

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2004, 15:22:20 ; Search time 141.124 Seconds
(without alignments)
2845.805 Million cell updates/sec

Title: US-09-743-818a-5
Perfect score: 3615
Sequence: 1 GGVPGAIPGGVPGVYFGA.....LSPIFGGACLGKACGRKXK 698

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Uniprot_02:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3602	99.6	730	1 ELS_HUMAN	P15502 homo sapien
2	3588.5	99.3	757	2 Q14234	Q14234 homo sapien
3	3584.5	99.2	757	2 Q75MU5	Q75MU5 homo sapien
4	3584.5	99.2	757	2 AAS07435	Aas07435 homo sapi
5	3474.5	96.1	711	2 Q723P5	Q723P5 homo sapien
6	3393.5	93.9	687	2 Q14235	Q14235 homo sapien
7	3318.5	91.8	687	2 Q72316	Q72316 homo sapien
8	3200	88.5	658	2 Q6P0L4	Q6P0L4 homo sapien
9	3200	88.5	658	2 AAH65566	AAH65566 homo sapi
10	3091.5	85.5	643	2 Q8NB14	Q8NB14 homo sapien
11	2896.5	80.1	602	2 Q15337	Q15337 homo sapien
12	2870	79.4	635	2 Q15336	Q15336 homo sapien
13	2692	74.5	570	2 Q6ZM66	Q6ZM66 homo sapien
14	2692	74.5	570	2 BAC85506	BAC85506 homo sapi
15	2537	70.2	707	2 Q28098	Q28098 bos taurus
16	2505.5	69.3	747	1 ELS_BOVIN	P04985 bos taurus
17	2431	67.2	679	2 Q28097	Q28097 bos taurus
18	2388.5	66.1	860	2 Q8C918	Q8C918 mus musculus
19	2385.5	66.0	860	1 ELS_MOUSE	P54320 mus musculus
20	2315.5	64.1	864	1 ELS_RAT	Q99372 rattus norv
21	2294.5	63.5	810	2 Q8ESZ9	Q8ESZ9 mus musculus
22	2288.5	63.3	666	2 Q28096	Q28096 bos taurus
23	2240.5	62.0	650	2 Q28099	Q28099 bos taurus
24	2023.5	56.0	559	2 Q4ZUN2	Q4ZUN2 homo sapien
25	2023.5	56.0	559	2 BAC86188	BAC86188 homo sapi
26	1679	46.4	472	2 Q8N2G0	Q8N2G0 homo sapien
27	1564	43.3	750	1 ELS_CHICK	P07916 gallus gall
28	1285	35.5	258	2 Q9UMF5	Q9UMF5 homo sapien
29	797.5	22.1	172	2 Q8BDZ0	Q8BDZ0 macaca mula
30	783.5	21.7	1953	2 Q8BI77	Q8BI77 nephila ina
31	770	21.3	1002	2 Q9BIU8	Q9BIU8 argiope tri

ALIGNMENTS

017434	nephila cla	2	017434	21.1	763	1071	988
Q7YU48	drosophila	2	Q7YU48	21.1	761	1071	1071
Q9VTR6	drosophila	2	Q9VTR6	21.1	761	1713	1713
Q9U617	drosophila	2	Q9U617	20.9	756.5	1729	1729
Q9HW42	nephila ina	2	Q9NHW2	20.4	738	1884	1884
Q9HW42	nephila cla	2	Q9NHW4	20.2	732	2249	2249
P05790	bombyx mori	1	FB0H_BOMMO	22.5	722.5	5263	5263
Q9GUB5	galleria me	2	Q9GUB5	19.5	706	1468	1468
Q9BIU9	argiope tri	2	Q9BIU9	19.3	697	651	651
Q44359	nephila cla	2	Q44359	19.3	696	907	907
Q8VI20	mycobacteri	2	Q8VI20	19.2	695	1715	1715
Q6Q294	agelenopsis	2	Q6Q294	18.9	681.5	897	897
Aat08436	agelenops	2	AAT08436	18.9	681.5	897	897
A44358	nephila cla	2	A44358	18.8	679.5	871	871
P19837	nephila cla	1	SPD1_NEPCL	18.6	673	747	747
Q7TWC3	mycobacteri	2	Q7TWC3	18.6	672	1460	1460
Q53553	mycobacteri	1	PG54_MYCTU	18.5	669.5	1901	1901
P17140	caenorhabdi	1	CA24_CAEEL	18.3	661	1758	1758
Q17163	brugia mala	2	Q17163	18.2	658.5	1802	1802
Q6PY84	kukulcania	2	Q6PY84	18.1	653.5	1760	1760
Aat08433	kukulcani	2	AAT08433	18.1	653.5	1760	1760
Q8VIY9	mycobacteri	2	Q8VIY9	18.0	650	1217	1217
Q7PT93	anopheles g	2	Q7PT93	17.7	641	1666	1666
Q964F4	antheraea y	2	Q964F4	17.7	639	2655	2655
Q6MW66	mycobacteri	2	Q6MW66	17.5	632.5	1489	1489
Cae55607	mycobacte	2	CAE55607	17.5	632.5	1489	1489
P27393	ascaris suu	1	CA24_ASCSU	17.5	632.5	1763	1763
Q76786	antheraea p	2	Q76786	17.4	630.5	2639	2639
Q7TWB8	mycobacteri	2	Q7TWB8	17.4	627.5	992	992
Q7U160	mycobacteri	2	Q7U160	17.3	626.5	773	773
Q8MW53	mytilus gal	2	Q8MW53	17.3	626.5	922	922
Q7D974	mycobacteri	2	Q7D974	17.3	624.5	749	749
Q6J6N0	araneus ven	2	Q6J6N0	17.2	623	563	563
Aat36347	araneus v	2	AAT36347	17.2	623	563	563
Q79FV7	mycobacteri	2	Q79FV7	17.2	622.5	749	749
Cae55328	mycobacte	2	CAE55328	17.2	622.5	749	749
O44367	mytilus edu	2	O44367	16.9	610	922	922
Q7U1Q7	mycobacteri	2	Q7U1Q7	16.7	605.5	1306	1306
Q6MX28	mycobacteri	2	Q6MX28	16.7	605.5	1306	1306
Cae55300	mycobacte	2	CAE55300	16.7	605.5	1306	1306
Q9BIU3	dolomedes t	2	Q9BIU3	16.7	604.5	1306	1306
Q7D9L6	mycobacteri	2	Q7D9L6	16.7	602.5	1408	1408
Q7U022	mycobacteri	2	Q7U022	16.5	598	16.5	16.5
Q9NHW1	nephila ina	2	Q9NHW1	16.5	597.5	854	854
Q9BIU4	dolomedes t	2	Q9BIU4	16.5	596.5	854	854
P29400	homo sapien	1	CAS4_HUMAN	16.5	595	1685	1685
Q8ESQ2	mus musculu	2	Q8ESQ2	16.4	592.5	1691	1691
Q8WSW4	nephila cla	2	Q8WSW4	16.4	591.5	644	644
P71933	mycobacteri	1	PG46_MYCTU	16.3	589.5	778	778
Q8VKD2	mycobacteri	2	Q8VKD2	16.3	589.5	879	879
Q79FD4	mycobacteri	2	Q79FD4	16.3	589.5	1660	1660
Cae55496	mycobacte	2	CAE55496	16.3	589.5	1660	1660
Q79FD4	mycobacteri	2	Q79FD4	16.3	589.5	1665	1665
Q79FV6	mycobacteri	2	Q79FV6	16.3	589	882	882
Cae55329	mycobacte	2	CAE55329	16.3	589	882	882
Q6P4U1	brachydanio	2	Q6P4U1	16.3	588	1447	1447
AaH63249	brachydan	2	AAH63249	16.3	588	1447	1447
Q46172	nephila cla	2	Q46172	16.3	587.5	617	617
Q9H4R9	homo sapien	2	Q9H4R9	16.2	587	1621	1621
P02462	homo sapien	2	CA14_HUMAN	16.2	587	1669	1669
Q79FP2	mycobacteri	1	CA14_HUMAN	16.2	586.5	1329	1329
Cae55390	mycobacte	2	CAE55390	16.2	586.5	1329	1329
Q7U1D4	canis fami	2	Q7U1D4	16.2	585.5	797	797
Q8HYC1	canis fami	2	Q8HYC1	16.2	585.5	1684	1684
Q866Z2	canis fam	2	Q866Z2	16.2	585.5	1691	1691
Aao33458	canis fam	2	AAO33458	16.2	585.5	648	648
Q9BIU7	argiope tri	2	Q9BIU7	16.2	582.5	774	774
Q7D9C6	mycobacteri	2	Q7D9C6	16.1	582.5	783	783

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OM protein - protein search, using sw model

Run on: November 19, 2004, 16:06:25 ; Search time 31.3948 Seconds
(without alignments)
2139.188 Million cell updates/sec

Title: US-09-743-818A-5
Perfect score: 3615
Sequence: 1 GGVPAICGVPGVPGVPCA.....LSPIPPGACLGACGRKK 698

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR 79:*

1: Pirl:*
2: Pirl:*
3: Pirl:*
4: Pirl:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3551	98.2	792	1 EAHU	elastin precursor,
2	2620	72.5	770	2 S59623	tropoelastin - she
3	2514.5	69.6	747	1 EABO	elastin precursor,
4	2385.5	66.0	860	1 EAMS	elastin precursor
5	2315.5	64.1	864	1 EART	elastin precursor
6	1718	47.5	784	2 A26601	elastin precursor
7	673	18.6	718	2 A36068	major ampullate fi
8	669.5	18.5	1901	2 F70806	hypothetical glyci
9	661	18.3	1758	2 T29350	hypothetical glyci
10	661	18.3	1759	2 T29351	hypothetical prote
11	632.5	17.5	1489	2 D70807	collagen alpha 2(I
12	632.5	17.5	1763	2 S16366	hypothetical glyci
13	630.5	17.4	2639	2 T31328	collagen alpha 2(I
14	622.5	17.2	749	2 A70812	fibroin - Chinese
15	605.5	16.7	1306	2 A70834	hypothetical glyci
16	595	16.5	1691	1 S22917	hypothetical glyci
17	589.5	16.3	778	2 F70963	collagen alpha 5(I
18	589.5	16.3	1660	2 A70869	hypothetical glyci
19	589	16.3	1669	1 B70812	hypothetical glyci
20	587	16.2	1669	1 CGHU4B	collagen alpha 1(I
21	586.5	16.2	1329	2 E70917	hypothetical glyci
22	579.5	16.0	767	2 E70895	hypothetical glyci
23	579.5	16.0	783	2 E70824	hypothetical glyci
24	577	16.0	1464	1 CGHULS	collagen alpha 1(I
25	569.5	15.8	1669	1 CGMS4B	collagen alpha 1(I
26	566.5	15.7	1049	1 CGBO7S	collagen alpha 1(I
27	564	15.6	1042	1 CGCH1S	collagen alpha 1(I
28	564	15.6	1466	1 CGHU7L	collagen alpha 1(I
29	563	15.6	812	2 S31521	collagen COLF1 - f

30	556.5	15.4	1373	1 A43291	collagen alpha 2(I
31	556	15.4	1381	2 E70806	hypothetical glyci
32	554	15.3	1079	2 B70807	hypothetical glyci
33	553.5	15.3	914	2 H70987	hypothetical glyci
34	553.5	15.3	1418	2 T45467	collagen alpha 1(I
35	553	15.3	957	2 D70835	hypothetical glyci
36	553	15.3	1453	2 S21626	collagen alpha 1(I
37	552.5	15.3	1487	1 CGHU6C	spidroin 2, dragli
38	549	15.2	627	2 A44112	collagen alpha 1(I
39	548	15.2	1464	2 S59856	hypothetical glyci
40	546	15.1	741	2 G70917	collagen alpha 2(I
41	546	15.1	1366	1 CGHU2S	hypothetical glyci
42	545.5	15.1	853	2 A70896	hypothetical glyci
43	541	15.0	801	2 F70824	collagen alpha 2(I
44	540.5	15.0	1712	1 CGHU2B	collagen alpha 6(I
45	540	14.9	1691	1 CGHU6B	collagen alpha 1(I
46	539.5	14.9	1419	2 A41182	collagen alpha 1(I
47	539.5	14.9	1487	2 B41182	collagen alpha 1(I
48	539	14.9	1027	2 S28774	collagen alpha cha
49	539	14.9	1492	2 A40333	collagen alpha 1'
50	532	14.7	1486	1 B40333	collagen alpha 1(I
51	530	14.7	837	2 E70835	hypothetical glyci
52	529	14.6	1538	2 H70846	hypothetical glyci
53	525.5	14.5	886	2 I50694	collagen alpha 1(I
54	524.5	14.5	1744	2 S40991	collagen alpha 2(I
55	520.5	14.4	1496	1 CGHU2V	collagen alpha 2(I
56	519.5	14.4	1707	2 A33526	collagen alpha 2(I
57	519	14.4	1497	2 I49607	procollagen type V
58	518	14.3	714	2 A70807	hypothetical glyci
59	516	14.3	779	1 CGBO1S	collagen alpha 1(I
60	508.5	14.1	694	2 F70868	hypothetical glyci
61	503.5	13.9	1690	1 CGHU1B	collagen alpha 4(I
62	501	13.9	2944	2 A54849	collagen alpha 1(V
63	500	13.8	1603	2 S23810	collagen alpha 1(X
64	496.5	13.7	1414	1 S23809	collagen alpha 2(I
65	496	13.7	603	2 A70770	hypothetical glyci
66	495.5	13.7	1806	1 CGHU1E	collagen alpha 1(X
67	493	13.6	1546	1 CGHU2E	collagen alpha 2(X
68	493	13.6	1670	1 CGHU3B	collagen alpha 3(I
69	492	13.6	1752	2 A45407	collagen alpha 3(I
70	488.5	13.5	923	2 E70820	hypothetical glyci
71	486.5	13.5	408	2 S57483	glycin-rich protei
72	486.5	13.5	635	2 A57131	collagen alpha 2(V
73	486.5	13.5	671	1 CGRT1S	collagen alpha 1(I
74	485.5	13.4	1775	2 A31893	collagen alpha 1(I
75	485	13.4	1747	2 A54121	collagen alpha-4 c
76	483.5	13.4	754	2 A55267	collagen alpha 5(I
77	482	13.3	964	1 CGCH2S	collagen alpha 2(I
78	481.5	13.3	677	2 S23296	collagen alpha 2(I
79	480.5	13.3	618	2 A70989	hypothetical glyci
80	478.5	13.2	744	2 S15435	collagen alpha 1(V
81	478	13.2	744	1 A34246	collagen alpha 1(V
82	478	13.2	744	1 S23298	collagen alpha 1(V
83	477	13.2	1843	2 S18803	collagen alpha 1(V
84	476.5	13.2	743	1 S23279	collagen alpha 1(X
85	476	13.2	680	1 CGHU1D	collagen alpha 1(V
86	474	13.1	1838	1 CGHU1V	collagen alpha 1(X
87	472.5	13.1	1142	2 JX0369	hypothetical glyci
88	471.5	13.0	731	2 C70974	hypothetical glyci
89	467	12.9	1011	2 F70620	collagen alpha 1(X
90	467	12.9	1024	2 S18251	collagen alpha 1(X
91	466.5	12.9	1549	2 I48103	type VII collagen
92	465.5	12.9	584	2 G70804	hypothetical glyci
93	465	12.9	3198	2 A43426	collagen alpha 2 f
94	463	12.8	469	2 A24450	collagen alpha 2(V
95	463	12.8	920	2 B34493	collagen alpha 1(I
96	459.5	12.7	667	2 A70893	hypothetical glyci
97	458.5	12.7	1958	2 B40505	hypothetical prote
98	456	12.6	606	2 H70816	hypothetical glyci
99	455	12.6	920	2 A45748	collagen alpha 1(V
100	449.5	12.4	591	2 B70523	hypothetical glyci

ALIGNMENTS

RESULT 1

EAHU

N;elastin precursor, long splice form - human

C;Species: Homo sapiens (man)

C;Date: 22-Jun-1990 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004

C;Accession: A32707; A33705; A30524; A53891

R.;Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Sheppard, P.; Anderson, N.; Rosenbloom, J.;

Proc. Natl. Acad. Sci. U.S.A. 84, 5680-5684, 1987

A;Title: Alternative splicing of human elastin mRNA indicated by sequence analysis of cDNA

A;Reference number: A32707; MUID:87289668; PMID:3039501

A;Accession: A32707

A;Molecule type: mRNA

A;Residues: 1-500,507-792 <IND>

R.;Bashir, M.M.; Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Rosenbloom, J.C.; Abrams, W.,

J. Biol. Chem. 264, 8887-8891, 1989

A;Title: Characterization of the complete human elastin gene. Delineation of unusual features

A;Reference number: A33705; MUID:89255358; PMID:2722804

A;Accession: A33705

A;Molecule type: DNA

A;Residues: 1-27 <BAS>

A;Cross-references: GB:J04821; NID:g182052; PIDN:AAA52379.1; PID:g553276

R.;Fazio, M.J.; Olsen, D.R.; Kauh, E.A.; Baldwin, C.T.; Indik, Z.; Ornstein-Goldstein, N.,

J. Invest. Dermatol. 91, 458-464, 1988

A;Title: Cloning of full-length elastin cDNAs from a human skin fibroblast recombinant cDNA

A;Reference number: A30524; MUID:89009960; PMID:3171221

A;Accession: A30524

A;Molecule type: mRNA

A;Residues: 1-453,483-617,651-792 <FAZ>

A;Cross-references: EMBL:M36860; NID:g182061; PIDN:AAA52382.1; PID:g182062

A;Note: this sequence represents a composite of several splice forms

R.;Fazio, M.J.; Olsen, D.R.; Kuivaniemi, H.; Chu, M.L.; Davidson, J.M.; Rosenbloom, J.; U

Lab. Invest. 58, 270-277, 1988

A;Title: Isolation and characterization of human elastin cDNAs, and age-associated variations

A;Reference number: A53891; MUID:88156138; PMID:2831431

A;Accession: A53891

A;Molecule type: mRNA

A;Residues: 164-453,483-500,507-617,651-792 <FA2>

A;Cross-references: GB:M24782; NID:g182063; PIDN:AAA53190.1; PID:g182064

C;Comment: the term tropoelastin refers to a soluble precursor form of the extracellular

line oxidase activity.

C;Genetics:

A;Gene: GDB:ELN

A;Cross-references: GDB:119107; OMIM:130160

A;Map position: 7q11.23-7q11.23

C;Superfamily: elastin

C;Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxyllysine

F;F1-26/Domain: signal sequence #status predicted <SIG>

F;F27-792/Product: elastin #status predicted <MAT>

F;F782-787/Disulfide bonds: #status predicted

Query Match 98.2%; Score 3551; DB 1; Length 792;

Best Local Similarity 91.1%; Pred. No. 6.2e-154;

Matches 698; Conservative 0; Mismatches 0; Indels 68; Gaps 3;

QY 1 GGVPGAIPGGVPGGVYFPAGLGGALGGGALPGGKPKLPVPVPGGLAGAGLGAIGAFPAVT 60

db 27 GGVPGAIPGGVPGGVYFPAGLGGALGGGALPGGKPKLPVPVPGGLAGAGLGAIGAFPAVT 86

QY 61 FPGALVPGGVADAARAAKAAKAGAGLGGVPGVGGI.GVSAGAVVPPQPGAGVKPKVPGVL 120

db 87 FPGALVPGGVADAARAAKAAKAGAGLGGVPGVGGI.GVSAGAVVPPQPGAGVKPKVPGVL 146

QY 121 PGVYPPGVLPGARFPGVLPVPTCAGVKPKAPGVGGAFAGIPGVGPGGPGQVPLGY 180

db 147 PGVYPPGVLPGARFPGVLPVPTCAGVKPKAPGVGGAFAGIPGVGPGGPGQVPLGY 206

QY 181 PIKAPKLPGGYGLPYTTGKLPGYGGPGGVAGAGKAGYPTGTGVPQAAAAAAXKAF 240

A:Accession: A53891
A:Molecule type: mRNA
A:Residues: 164-453; 483-500,507-617,651-792 <FA2>
A:Cross-references: GB:M24782; NID:g182063; PIDN:AAAS3130.1; PID:g182064
C:Comment: The term tropoelastin refers to a soluble precursor form of the extracellular matrix.
C:Genetics:
A:Gene: GDB:ELN
A:Cross-references: GDB:119107; OMIM:130160
A:Map position: 7q11.23-7q11.23
C:Superfamily: elastin
C:Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxyllysine
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-792/Product: elastin #status predicted <MAT>
F:782-787/Disulfide bonds: #status predicted

Query Match 98.2%; Score 3551; DB 1; Length 792;
Best Local Similarity 91.1%; Pred. No. 6.2e-154;
Matches 698; Conservative 0; Mismatches 0; Indels 68; Gaps 3;

QY 1 GGVPGAI PGGVPGGVFPY PGAGL GAGLGALGGGALGP GKPKLPV PGGLAGAGL GAGLGAPP AVT 60
dbb 27 GGVPGAI PGGVPGGVFPY PGAGL GAGLGALGGGALGP GKPKLPV PGGLAGAGL GAGLGAPP AVT 86
QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVSGAGAVVPPQGAGVKPKVP GGVL 120
dbb 87 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVSGAGAVVPPQGAGVKPKVP GGVL 146
QY 121 PGVTPGGVLPGARFFGVGLPVPTCAGVKRPA GPVGGA FAGIPGVGFPGG PQGPVPLCY 180
dbb 147 PGVTPGGVLPGARFFGVGLPVPTCAGVKRPA GPVGGA FAGIPGVGFPGG PQGPVPLGY 206
QY 181 PIKAPELPGGYGLPYTTTKLPYGVGPFGVAGAGKAGVTPTGTGVGPQAAAAAKAAKF 240

A:Accession: A53891
A:Molecule type: mRNA
A:Residues: 164-453; 483-500,507-617,651-792 <FA2>
A:Cross-references: GB:M24782; NID:g182063; PIDN:AAAS3130.1; PID:g182064
C:Comment: The term tropoelastin refers to a soluble precursor form of the extracellular matrix.
C:Genetics:
A:Gene: GDB:ELN
A:Cross-references: GDB:119107; OMIM:130160
A:Map position: 7q11.23-7q11.23
C:Superfamily: elastin
C:Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxyllysine
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-792/Product: elastin #status predicted <MAT>
F:782-787/Disulfide bonds: #status predicted

Query Match 98.2%; Score 3551; DB 1; Length 792;
Best Local Similarity 91.1%; Pred. No. 6.2e-154;
Matches 698; Conservative 0; Mismatches 0; Indels 68; Gaps 3;

QY 1 GGVPGAI PGGVPGGVFPY PGAGL GAGLGALGGGALGP GKPKLPV PGGLAGAGL GAGLGAPP AVT 60
dbb 27 GGVPGAI PGGVPGGVFPY PGAGL GAGLGALGGGALGP GKPKLPV PGGLAGAGL GAGLGAPP AVT 86

QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVSGAGAVVPPQGAGVKPKVPGVGL 120
dbb 87 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVSGAGAVVPPQGAGVKPKVPGVGL 146

QY 121 PGVTPGGVLPGARFFGVGLPVTGTCAGVKRPAQVGGGA FAGIPGVGFPGG PQGPVPLCY 180
dbb 147 PGVTPGGVLPGARFFGVGLPVTGTCAGVKRPAQVGGGA FAGIPGVGFPGG PQGPVPLGY 206

QY 181 PIKAPELPGGYGLPYTTGKLPGYGVPGGVAGAGKAGVPTGTGFGVQA AAAA AA AKAF 240

A:Accession: A53891
A:Molecule type: mRNA
A:Residues: 164-453; 483-500,507-617,651-792 <FA2>
A:Cross-references: GB:M24782; NID:g182063; PIDN:AAAS3130.1; PID:g182064
C:Comment: The term tropoelastin refers to a soluble precursor form of the extracellular matrix.
C:Genetics:
A:Gene: GDB:ELN
A:Cross-references: GDB:119107; OMIM:130160
A:Map position: 7q11.23-7q11.23
C:Superfamily: elastin
C:Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxyllysine
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-792/Product: elastin #status predicted <MAT>
F:782-787/Disulfide bonds: #status predicted

Query Match 98.2%; Score 3551; DB 1; Length 792;
Best Local Similarity 91.1%; Pred. No. 6.2e-154;
Matches 698; Conservative 0; Mismatches 0; Indels 68; Gaps 3;

QY 1 GGVPGAI PGGVPGGVFPY PGAGL GAGLGALGGGALGP GKPKLPV PGGLAGAGL GAGLGAPP AVT 60
dbb 27 GGVPGAI PGGVPGGVFPY PGAGL GAGLGALGGGALGP GKPKLPV PGGLAGAGL GAGLGAPP AVT 86

QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVSGAGAVVPPQGAGVKPKVPGVGL 120
dbb 87 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVSGAGAVVPPQGAGVKPKVPGVGL 146

QY 121 PGVTPGGVLPGARFFGVGLPVPTCAGVKRPAQVGGGA FAGIPGVGFPGG PQGPVPLCY 180
dbb 147 PGVTPGGVLPGARFFGVGLPVPTCAGVKRPAQVGGGA FAGIPGVGFPGG PQGPVPLGY 206

QY 181 PIKAPELPGGYGLPYTTTKLPYGVGPGGVAGAAGKAGVTFTGTGVPQA AAAA AA AKAF 240

A:Accession: A53891
A:Molecule type: mRNA
A:Residues: 164-453; 483-500,507-617,651-792 <FA2>
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C:Genetics:
A:Gene: GDB:ELN
A:Cross-references: GDB:119107; OMIM:130160
A:Map position: 7q11.23-7q11.23
C:Superfamily: elastin
C:Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxyllysine
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-792/Product: elastin #status predicted <MAT>
F:782-787/Disulfide bonds: #status predicted

Query Match 98.2%; Score 3551; DB 1; Length 792;
Best Local Similarity 91.1%; Pred. No. 6.2e-154;
Matches 698; Conservative 0; Mismatches 0; Indels 68; Gaps 3;

QY 1 GGVPGAI PGGVPGGVFPY PGAGL GAGLGALGGGALGP GKPKLPV PGGLAGAGL GAGLGAPP AVT 60
dbb 27 GGVPGAI PGGVPGGVFPY PGAGL GAGLGALGGGALGP GKPKLPV PGGLAGAGL GAGLGAPP AVT 86

QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVSGAGAVVPPQGAGVKPKVPGVGL 120
dbb 87 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVSGAGAVVPPQGAGVKPKVPGVGL 146

QY 121 PGVTPGGVLPGARFFGVGLPVPTCAGVKRPAQVGGGA FAGIPGVGFPGG PQGPVPLCY 180
dbb 147 PGVTPGGVLPGARFFGVGLPVPTCAGVKRPAQVGGGA FAGIPGVGFPGG PQGPVPLGY 206

QY 181 PIKAPELPGGYGLPYTTGKLPGYGVPGGVAGAGKAGVTGTGFGVQA AAAA AA AKAF 240

A:Accession: A53891
A:Molecule type: mRNA
A:Residues: 164-453; 483-500,507-617,651-792 <FA2>
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C:Genetics:
A:Gene: GDB:ELN
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A:Map position: 7q11.23-7q11.23
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F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-792/Product: elastin #status predicted <MAT>
F:782-787/Disulfide bonds: #status predicted

Query Match 98.2%; Score 3551; DB 1; Length 792;
Best Local Similarity 91.1%; Pred. No. 6.2e-154;
Matches 698; Conservative 0; Mismatches 0; Indels 68; Gaps 3;

QY 1 GGVPGAI PGGVPGGYFPAGI LGALGGALGP GPKPLKPV PGLLAGAGL GAGLGAPPVAVT 60
dbb 27 GGVPGAI PGGVPGGYFPAGI LGALGGALGP GPKPLKPV PGLLAGAGL GAGLGAPPVAVT 86

QY 61 FPGALVPGGVADAAAAYKA AKAGALGGVPGVGGLGVSGAGVVPOPGAGVKPKVPGVGL 120
dbb 87 FPGALVPGGVADAAAAYKA AKAGALGGVPGVGGLGVSGAGVVPOPGAGVKPKVPGVGL 146

QY 121 PGVTPGGVLPGARFFGVGLPVTGCAGVKRPA PGVGGAFAGIPGVGFPGGPQGVPGLCY 180
dbb 147 PGVTPGGVLPGARFFGVGLPVTGCAGVKRPA PGVGGAFAGIPGVGFPGGPQGVPGLCY 206

QY 181 PIKAPKLPGGYGLPYTTGKLPYGVGPFGVGAAGKAGVPTGTGVGPDQAAAAAKAAKPF 240

A:Accession: A53891
A:Molecule type: mRNA
A:Residues: 164-453; 483-500,507-617,651-792 <FA2>
A:Cross-references: GB:M24782; NID:g182063; PIDN:AAAS3130.1; PID:g182064
C:Comment: The term tropoelastin refers to a soluble precursor form of the extracellular matrix.
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A:Gene: GDB:ELN
A:Cross-references: GDB:119107; OMIM:130160
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C:Superfamily: elastin
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F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-792/Product: elastin #status predicted <MAT>
F:782-787/Disulfide bonds: #status predicted

Query Match 98.2%; Score 3551; DB 1; Length 792;
Best Local Similarity 91.1%; Pred. No. 6.2e-154;
Matches 698; Conservative 0; Mismatches 0; Indels 68; Gaps 3;

QY 1 GGVPGAI PGGVPGGVFPY PGAGL GAGLGALGGGALGP GKPKLPV PGGLAGAGL GAGLGAPP AVT 60
dbb 27 GGVPGAI PGGVPGGVFPY PGAGL GAGLGALGGGALGP GKPKLPV PGGLAGAGL GAGLGAPP AVT 86

QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVSGAGAVVPPQGAGVKPKVPGVGL 120
dbb 87 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVSGAGAVVPPQGAGVKPKVPGVGL 146

QY 121 PGVTPGGVLPGARFFGVGLPVTGTCAGVKRPAQVGGGA FAGIPGVGFPGG PQGPVPLCY 180
dbb 147 PGVTPGGVLPGARFFGVGLPVTGTCAGVKRPAQVGGGA FAGIPGVGFPGG PQGPVPLGY 206

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C:Comment: The term tropoelastin refers to a soluble precursor form of the extracellular matrix.
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A:Gene: GDB:ELN
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C:Superfamily: elastin
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F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-792/Product: elastin #status predicted <MAT>
F:782-787/Disulfide bonds: #status predicted

Query Match 98.2%; Score 3551; DB 1; Length 792;
Best Local Similarity 91.1%; Pred. No. 6.2e-154;
Matches 698; Conservative 0; Mismatches 0; Indels 68; Gaps 3;

QY 1 GGVPGAI PGGVPGGVFPY PGAGI GALGGAL GPGGKPL KPVPGLL AGAGI LAGLGAPPVAVT 60
dbb 27 GGVPGAI PGGVPGGVFPY PGAGI GALGGAL GPGGKPL KPVPGLL AGAGI LAGLGAPPVAVT 86
QY 61 FPGALV PGGVADAAAAY KAAKAG IGLGV VGGI GVSAGA VVPPGAGVKPKVPGVGL 120
dbb 87 FPGALV PGGVADAAAAY KAAKAG IGLGV VGGI GVSAGA VVPPGAGVKPKVPGVGL 146
QY 121 PGVTPGGVL PGARFFGV GLPVPT CAGVKR APGVGGAF AGIPGVGFPGGPQGVPLCY 180
dbb 147 PGVTPGGVL PGARFFGV GLPVPT CAGVKR APGVGGAF AGIPGVGFPGGPQGVPLGY 206
QY 181 PIKAPEL PGYGILP YTTGKL PYGVGPGGVAG AAGKAG VTGTGVG PQAAAAA AAAAKF 240

A:Accession: A53891
A:Molecule type: mRNA
A:Residues: 164-453; 483-500,507-617,651-792 <FA2>
A:Cross-references: GB:M24782; NID:g182063; PIDN:AAAS3130.1; PID:g182064
C:Comment: The term tropoelastin refers to a soluble precursor form of the extracellular matrix.
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F:27-792/Product: elastin #status predicted <MAT>
F:782-787/Disulfide bonds: #status predicted

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Matches 698; Conservative 0; Mismatches 0; Indels 68; Gaps 3;

QY 1 GGVPGAI PGGVPGGVFPY PGAGL GAGLGALGGGALGP GKPKLPV PGGLAGAGL GAGLGAPP AVT 60
dbb 27 GGVPGAI PGGVPGGVFPY PGAGL GAGLGALGGGALGP GKPKLPV PGGLAGAGL GAGLGAPP AVT 86

QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVSGAGAVVPPQGAGVKPKVPGVGL 120
dbb 87 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVSGAGAVVPPQGAGVKPKVPGVGL 146

QY 121 PGVTPGGVLPGARFFGVGLPVPTCAGVKRPAQVGGGA FAGIPGVGFPGG PQGPVPLCY 180
dbb 147 PGVTPGGVLPGARFFGVGLPVPTCAGVKRPAQVGGGA FAGIPGVGFPGG PQGPVPLGY 206

QY 181 PIKAPELPGGYGLPYTTGKLPGYGVPGGVAGAGKAGVTGTGFGVQA AAAA AA AKAF 240

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2004, 16:37:11 ; Search time 113.997 Seconds
(without alignments)
2168.321 Million cell updates/sec

Title: US-09-743-818A-5
Perfect score: 3615
Sequence: 1 GGVPAIFGVGGVYFGA.....LSPIFGGACLGKACGRK 698

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

- Database : Published Applications AA:*
- 1: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/prodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
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 - 12: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/prodata/2/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/prodata/2/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/prodata/2/pubpaa/US10_PUBCOMB.pep.*
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 - 18: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep.*
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 - 20: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	3602	99.6	730	10	US-09-961-403-8
2	3578.5	99.0	731	10	US-09-964-662-1
3	3486.5	96.4	711	15	US-10-210-172-38
4	3366	93.1	692	15	US-10-210-172-40
5	3233.5	89.4	663	15	US-10-108-260A-2477
6	2951.5	81.6	617	14	US-10-104-047-2915
7	1155	32.0	988	8	US-08-806-029-28
8	1154	31.9	965	16	US-10-800-179-31
9	1150.5	31.8	832	8	US-08-806-029-27
10	1139.5	31.5	936	8	US-08-806-029-26
11	1139.5	31.5	1038	16	US-10-800-179-30
12	1133	31.3	745	9	US-09-837-969A-38
13	1133	31.3	745	9	US-09-841-321A-38
Sequence 8, Appli					
Sequence 1, Appli					
Sequence 38, Appl					
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Sequence 2915, Ap					
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Sequence 31, Appl					
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Sequence 11, Appl

Query Match	99.6%	Score 3602	DB 10	Length 730
Best Local Similarity	99.1%	Pred. No. 5.6e-186		
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1	GGVPGATPGGVPGGVYPPGAGLTCALGGGALPGCGKPLKVPVGGLAGAGLGGAGLGAFFPAVT	60		
27	GGVPGALPGGVPGGVYPPGAGLTCALGGGALPGCGKPLKVPVGGLAGAGLGGAGLGAFFPAVT	86		
61	FPGALVPGGVADAAAAAATAKAKAGAGLGGVPGVGGGLGVSSAGAVVPPGAGVPGKVPVGGVL	120		
87	FPGALVPGGVADAAAAAATAKAKAGAGLGGVPGVGGGLGVSSAGAVVPPGAGVPGKVPVGGVL	146		
121	PGVYPGGVLPGARFPFGVGLVPGVPTCAGVKPKAPGVGGAFAGIPGVGPFPGQPQGVPLUGY	180		
147	PGVYPGGVLPGARFPFGVGLVPGVPTCAGVKPKAPGVGGAFAGIPGVGPFPGQPQGVPLUGY	206		
181	PIKAPKLPGYGLPYTTGKLPYGVYGGVAGAGKAGYPTGTGVGPQAAAAAATAKAAKF	240		
207	PIKAPKLPGYGLPYTTGKLPYGVYGGVAGAGKAGYPTGTGVGPQAAAAAATAKAAKF	266		
241	GAGAAAGLPGVGGAGVPGVPGALPGTGGTAGTGTAAAAAATAKAAKYGAAAGLVPGG	300		
267	GAGAAAGLPGVGGAGVPGVPGALPGTGGTAGTGTAAAAAATAKAAKYGAAAGLVPGG	326		
301	PGFGPGVGVPGAGVPGVPGAGIPVVPFCAGIPGAAVPGVVPSPAAAATAKAAKAYGAR	360		
327	PGFGPGVGVPGAGVPGVPGAGIPVVPFCAGIPGAAVPGVVPSPAAAATAKAAKAYGAR	386		
361	PGVGVGGIPYTVGVAGGFPFGVGGGIPGVAGVPSVGGVPGVGGVPGVGTGVSPEAQAAAA	420		

Sequence 89, Appl
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Sequence 49, Appl
Sequence 13, Appl
Sequence 22, Appl
Sequence 88, Appl
Sequence 51, Appl
Sequence 18, Appl
Sequence 10, Appl
Sequence 83, Appl
Sequence 7032, Ap
Sequence 1, Appl
Sequence 25, Appl

87 673 19.6 979 14 US-10-096-986-89
88 672.5 19.6 2016 17 US-10-479-638-52
89 672 19.6 1128 17 US-10-479-638-49
90 671 19.6 809 14 US-10-414-760-13
91 671 19.6 818 14 US-10-414-760-22
92 665 19.4 766 14 US-10-096-986-88
93 651 19.0 3420 17 US-10-479-638-51
94 650 19.0 761 17 US-10-479-638-18
95 649.5 19.0 1059 8 US-08-806-029-10
96 649.5 19.0 1101 14 US-10-096-986-83
97 645 18.8 1759 14 US-10-369-493-7032
98 639.5 18.7 651 9 US-09-861-597-1
99 639.5 18.7 651 14 US-10-414-760-1
100 639 18.7 780 15 US-10-441-965-25

ALIGNMENTS

RESULT 1
US-09-961-403-8
; Sequence 8, Application US/09961403
; Publication No. US20030077589A1
; GENERAL INFORMATION:
; APPLICANT: HE-STUMPP, HOLGER
; APPLICANT: HAENDLER, BERNARD
; APPLICANT: KRAETZSCHMAR, JOERN
; APPLICANT: KREFT, BERTHOLT
; APPLICANT: WINTERHAGER, ELKE
; APPLICANT: REGIDOR, PEDRO
; APPLICANT: SCOTTI, SIMONE
; TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS
; FILE REFERENCE: SCH-1789
; CURRENT APPLICATION NUMBER: US/09/961,403
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 8
; LENGTH: 730
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-961-403-8

Query Match 95.2%; Score 3261; DB 10; Length 730;
Best Local Similarity 91.2%; Pred. No. 1.8e-171;
Matches 646; Conservative 3; Mismatches 7; Indels 52; Gaps 6;

QY 2 GGVPAGVPGVGGVYFPGAGFGA-----25
DB 27 GGVPAGVPGVGGVYFPGAGFGA-----25
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DB 87 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVAGAVVPOPGAGVKGKVPVGL 146
QY 81 PGVYFPGVAGVPGARFPGVGLPVGPTGAGVKGKAPGVGGAFAGIPGVPGFGPQPGVPLG 140
DB 147 PGVYFPG-VGLPGARFPGVGLPVGPTGAGVKGKAPGVGGAFAGIPGVPGFGPQPGVPLG 205
QY 141 YPIKAPKLPGGYGLPYTTGKLPYGYGGVAGAGAGAGYPTGTGVPQAAAAAATAAK 200
DB 206 YPIKAPKLPGGYGLPYTTGKLPYGYGGVAGAGAGAGYPTGTGVPQAAAAAATAAK 265
QY 201 FGAGAGAGVAGVPGVGGVPGVPGAIPIGGIAGVGTAAAAAATAAKAAGV 260
DB 266 FGAGAA--GVLPGVGGVPGVPGAIPIGGIAGVGTAAAAAATAAKAAGV 323
QY 261 PGVPGFGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 320
DB 324 PGVPGFGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 382
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Db 383 YGARPVGVGIGIPTYGVGGAGGFGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGV 442
QY 381 AAAAAKAAKYGVGTAAAAAATAAKAAQF-----GLVPGVGVAGVPGVPGVPGVPGV 434
Db 443 AAAAAKAAKYGVGTAAAAAATAAKAAQFALLNLNLAGLVPGVGVAGVPGVPGVPGVPGV 502
QY 435 LAPGVGVAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 494
Db 503 LAPGVGVAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 562
QY 495 VGVFGLGVAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 553
Db 563 VGVFGLGVAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 622
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Db 623 GVWGAGPAAAAAATAAKAAQFGLVGAAGLGGVGGVGGVGGVGGVGGVGGVGGVGGVGGV 682
QY 614 YGAAGLGGVGGAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 661
Db 683 YGAAGLGGVGGAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 730

RESULT 2

US-09-964-662-1
; Sequence 1, Application US/09964662
; Publication No. US20030166846A1
; GENERAL INFORMATION:
; APPLICANT: PROTEIN SPECIALTIES LTD.
; APPLICANT: HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP
; TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN AND
; TITLE OF INVENTION: OTHER FIBROUS PROTEINS
; FILE REFERENCE: 041082/0112
; CURRENT APPLICATION NUMBER: US/09/964,662
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: 09/340,736
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 1
; LENGTH: 731
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-964-662-1

Query Match 94.5%; Score 3237.5; DB 10; Length 731;
Best Local Similarity 87.6%; Pred. No. 3.6e-170;
Matches 644; Conservative 3; Mismatches 9; Indels 79; Gaps 6;

QY 2 GGVPAGVPGVGGVYFPGAGFGA-----25
DB 1 GGVPAGVPGVGGVYFPGAGFGA-----25
QY 26 -----VPGGVADAAAAYKAAKAGAGLGGVPGVGGVAGAVVPOPGAGVKGKVPVGL 80
DB 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVAGAVVPOPGAGVKGKVPVGL 120
QY 81 PGVYFPGVAGVPGARFPGVGLPVGPTGAGVKGKAPGVGGAFAGIPGVPGFGPQPGVPLG 140
DB 121 PGVYFPG-VGLPGARFPGVGLPVGPTGAGVKGKAPGVGGAFAGIPGVPGFGPQPGVPLG 179
QY 141 YPIKAPKLPGGYGLPYTTGKLPYGYGGVAGAGAGAGYPTGTGVPQAAAAAATAAK 200
DB 180 YPIKAPKLPGGYGLPYTTGKLPYGYGGVAGAGAGAGYPTGTGVPQAAAAAATAAK 239
QY 201 FGAGAGAGVAGVPGVGGVPGVPGAIPIGGIAGVGTAAAAAATAAKAAGV 260
DB 240 FGAGAA--GVLPGVGGVPGVPGAIPIGGIAGVGTAAAAAATAAKAAGV 297
QY 261 PGVPGFGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 320
DB 298 PGVPGFGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 356

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OM protein - protein search, using sw model

Run on: November 19, 2004, 16:06:25 ; Search time 29.7306 Seconds
(without alignment)
2139.188 Million cell updates/sec

Title: US-09-743-818A-6

Perfect score: 3426

Sequence: 1 MGKVGAVPGVGGVFGVPG.....LSPIFFGGACLGKACGRKK 661

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : PIR 79:*

1: Pirl:*

2: Pirl:*

3: Pirl:*

4: Pirl:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3210	93.7	792	1 EAHU	elastin precursor,
2	2413	70.4	770	2 S59623	tropoelastin - she
3	2322.5	67.8	747	1 EABO	elastin precursor,
4	2162.5	63.1	860	1 EAMS	elastin precursor
5	2153.5	62.9	864	1 EART	elastin precursor
6	1587	46.3	784	2 A26601	elastin precursor
7	656.5	19.2	1901	2 F70806	hypothetical glyci
8	655	19.1	2639	2 T31328	fibroin - Chinese
9	645	18.8	1758	2 T29350	hypothetical prote
10	645	18.8	1759	2 T29351	collagen alpha 2(I
11	640.5	18.7	718	2 A36068	major amputate fi
12	617	18.0	1489	2 D70807	hypothetical glyci
13	609.5	17.8	1763	2 S16366	collagen alpha 2(I
14	592.5	17.3	1306	2 A70934	hypothetical glyci
15	587.5	17.1	778	2 F70963	hypothetical glyci
16	583	17.0	1660	2 A70869	hypothetical glyci
17	577.5	16.9	1669	1 CGHU4B	collagen alpha 1(I
18	577	16.8	1691	1 S22917	collagen alpha 5(I
19	576	16.8	1329	2 E70917	hypothetical glyci
20	572	16.7	882	2 B70812	hypothetical glyci
21	570.5	16.7	749	2 A70812	hypothetical glyci
22	570.5	16.6	767	2 E70895	hypothetical glyci
23	567.5	16.6	783	2 E70824	hypothetical glyci
24	558	16.3	1669	1 CGMS4B	collagen alpha 1(I
25	552	16.1	1042	1 CGH1S	collagen alpha 1(I
26	548.5	16.0	1373	1 A43291	collagen alpha 2(I
27	546.5	16.0	1464	1 CGHU1S	collagen alpha 1(I
28	546	15.9	1049	1 CGB07S	collagen alpha 1(I
29	545	15.9	1466	1 CGHU7L	collagen alpha 1(I

30	541	15.8	1381	2 E70806	hypothetical glyci
31	538	15.7	1418	2 T45467	collagen alpha 1(I
32	537.5	15.7	1079	2 B70807	hypothetical glyci
33	535	15.6	957	2 D70835	hypothetical glyci
34	534.5	15.6	812	2 S31521	collagen COL1 - f
35	534	15.6	1464	2 S59856	collagen alpha 1(I
36	534	15.6	1487	1 CGHU6C	collagen alpha 1(I
37	533	15.6	741	2 G70917	hypothetical glyci
38	532	15.5	1691	1 CGHU6B	collagen alpha 6(I
39	528	15.4	1027	2 S28774	collagen alpha cha
40	527.5	15.4	627	2 A44112	spidrin 2, dragli
41	527.5	15.4	914	2 F70987	hypothetical glyci
42	524	15.3	853	2 A70896	hypothetical glyci
43	523.5	15.3	1453	2 S21626	collagen alpha 1(I
44	523.5	15.3	1492	2 A40333	collagen alpha 1(I
45	523	15.3	1419	2 A41182	collagen alpha 1(I
46	523	15.3	1487	2 B41182	collagen alpha 1(I
47	521	15.2	1486	1 B40333	collagen alpha 1(I
48	519.5	15.2	1366	1 CGHU2S	collagen alpha 2(I
49	516.5	15.1	1707	2 A33526	collagen alpha 2(I
50	516	15.1	1538	2 H70846	hypothetical glyci
51	514.5	15.0	801	2 F70824	hypothetical glyci
52	514	15.0	1712	1 CGHU2B	collagen alpha 2(I
53	514	15.0	2944	2 A54849	collagen alpha 1(I
54	512	14.9	1744	2 S40991	collagen alpha 1(I
55	511	14.9	886	2 I50694	hypothetical glyci
56	510.5	14.9	694	2 F70868	hypothetical glyci
57	508.5	14.8	1497	2 I49607	procollagen type V
58	508	14.8	779	1 CGB01S	collagen alpha 1(I
59	505	14.7	837	2 E70835	hypothetical glyci
60	498	14.5	1603	2 S23810	collagen alpha 1(X
61	497	14.5	714	2 A70807	hypothetical glyci
62	494	14.4	408	2 S57483	glycin-rich protei
63	493	14.4	1496	1 CGHU2V	collagen alpha 2(V
64	492.5	14.4	744	1 A34246	collagen alpha 1(V
65	492.5	14.4	744	1 S23298	collagen alpha 1(V
66	492.5	14.4	744	2 S15435	collagen alpha 2(V
67	491	14.3	635	2 A57131	collagen alpha 3(I
68	490.5	14.3	1670	1 CGHU3B	collagen alpha 1(I
69	489	14.3	671	1 CGRT1S	collagen alpha 3(I
70	485.5	14.2	1752	2 A45407	hypothetical glyci
71	485	14.2	618	2 A70989	collagen alpha 4(I
72	485	14.2	1690	1 CGHU1B	hypothetical glyci
73	483.5	14.1	603	2 A70770	hypothetical glyci
74	482.5	14.1	923	2 E70820	hypothetical glyci
75	481.5	14.1	743	1 S23779	collagen alpha 1(V
76	479	14.0	1414	1 S23609	collagen alpha 2(I
77	478.5	14.0	1549	2 I48103	type VII collagen
78	476.5	13.9	964	1 CGCH2S	collagen alpha 2(I
79	476.5	13.9	1747	2 A54121	collagen alpha 2(I
80	474.5	13.8	469	2 A24450	collagen alpha 2(X
81	474	13.8	1546	1 CGHU2E	collagen alpha 2(X
82	473.5	13.8	754	2 A55267	collagen alpha 2(I
83	469.5	13.7	677	2 S23296	collagen alpha 2(I
84	469	13.7	1806	1 CGHU1E	collagen alpha 1(X
85	468	13.7	680	1 CGHU1D	collagen alpha 1(I
86	467.5	13.6	1775	2 A31893	hypothetical glyci
87	463	13.5	667	2 A70893	collagen alpha 2 f
88	462	13.5	3198	2 A43426	hypothetical glyci
89	461.5	13.5	606	2 H70816	collagen alpha 2(I
90	461.5	13.5	688	2 A53330	hypothetical glyci
91	461.5	13.5	731	2 G70974	hypothetical glyci
92	461.5	13.4	584	2 G70804	glycine-rich prote
93	453.5	13.2	608	2 T05442	hypothetical glyci
94	453	13.2	1011	2 F70620	collagen alpha 1(X
95	453	13.2	1024	2 S18251	hypothetical glyci
96	452.5	13.2	591	2 S18251	hypothetical glyci
97	451.5	13.2	674	2 B70523	collagen alpha 1(X
98	446	13.0	920	2 B34493	collagen alpha 1(I
99	444	13.0	921	2 S42617	collagen alpha 1(I
100	443.5	12.9	1843	2 S18803	collagen alpha 1(V

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OM protein - protein search, using sw model

Run on: November 19, 2004, 15:22:20 ; Search time 133.643 Seconds
(without alignments)
2845.805 Million cell updates/sec

Title: US-09-743-818A-6
Perfect score: 3426
Sequence: 1 MGVPGAVPGVGGVFPG.....LSPIFGGACLGKACGRKEK 661

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt 02.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3261	95.2	730	1	ELS_HUMAN
2	3247.5	94.8	757	2	Q14234
3	3243.5	94.7	757	2	Q75W05
4	3243.5	94.7	757	2	AAS07435
5	3133.5	91.5	711	2	Q723F5
6	3052.5	89.1	687	2	Q14235
7	3039.5	88.7	687	2	Q72316
8	2859	83.5	558	2	Q6P0L4
9	2859	83.5	558	2	AAR65566
10	2833.5	82.7	643	2	Q8NB14
11	2570	75.0	602	2	O15337
12	2543.5	74.2	635	2	O15336
13	2533	73.9	570	2	Q6ZWJ6
14	2533	73.9	570	2	BAC85506
15	2366.5	69.1	707	2	Q28098
16	2313.5	67.5	747	1	ELS_BOVIN
17	2270.5	66.3	679	2	Q28097
18	2165.5	63.2	860	2	Q8C9L8
19	2162.5	63.1	860	1	ELS_MOUSE
20	2153.5	62.9	864	1	ELS_RAT
21	2132.5	62.2	810	2	Q9ESZ9
22	2118	61.8	666	2	Q28096
23	2070	60.4	650	2	Q28099
24	1759	51.3	559	2	Q6ZUN2
25	1759	51.3	559	2	BAC86188
26	1531	44.7	472	2	Q8N2G0
27	1433	41.8	750	1	ELS_CHICK
28	1270.5	37.1	258	2	Q9UMF5
29	790	23.1	1071	2	Q7YU48
30	790	23.1	1713	2	Q9VTR6
31	775.5	22.6	1729	2	Q9U617

32	763.5	22.3	988	2	O17434	O17434	nephila cla
33	727.5	21.2	1002	2	Q9BIU8	Q9BIU8	argiope tri
34	724.5	21.1	5263	1	FB0H_BOMMO	FB0H_BOMMO	bombyx mori
35	716	20.9	1953	2	Q9BIT7	Q9BIT7	nephila ina
36	678	19.8	897	2	Q6Q294	Q6Q294	agelenopsis
37	678	19.8	897	2	AAT08436	AAT08436	agelenopsis
38	676.5	19.7	1884	2	Q9NHW2	Q9NHW2	nephila ina
39	674.5	19.7	651	2	Q9BIU9	Q9BIU9	argiope tri
40	663	19.4	1468	2	Q9GUB5	Q9GUB5	galleria me
41	661	19.3	1715	2	Q8VIZ0	Q8VIZ0	mycobacteri
42	660.5	19.3	2249	2	Q9NHW4	Q9NHW4	nephila cla
43	656.5	19.2	1901	1	PG54_MYCTU	PG54_MYCTU	mycobacteri
44	656.5	19.2	2655	2	Q964F4	Q964F4	antheraea y
45	655	19.2	2639	2	Q76786	Q76786	antheraea p
46	651.5	19.0	172	2	Q9BDZ0	Q9BDZ0	macaca mula
47	651.5	19.0	1460	2	Q7TWC3	Q7TWC3	mycobacteri
48	650	19.0	760	2	Q6PY84	Q6PY84	kukulcania
49	650	19.0	760	2	AAT08433	AAT08433	kukulcani
50	645.5	18.8	871	2	O44358	O44358	nephila cla
51	645	18.8	1758	1	CA24_CAEEL	CA24_CAEEL	caenorhabdi
52	640.5	18.7	747	1	SPD1_NEPCL	SPD1_NEPCL	nephila cla
53	631	18.4	1666	2	Q7PT93	Q7PT93	anopheles g
54	625	18.2	1802	2	Q17163	Q17163	brugia mala
55	621.5	18.1	907	2	O44359	O44359	nephila cla
56	617	18.0	1489	2	Q6MMW6	Q6MMW6	mycobacteri
57	617	18.0	1489	2	CAE55607	CAE55607	mycobacte
58	615.5	18.0	992	2	Q7TWB8	Q7TWB8	mycobacteri
59	611	17.8	922	2	Q8MW53	Q8MW53	mytilus gal
60	609.5	17.8	1763	1	CA24_ASCSU	CA24_ASCSU	ascaris suu
61	609	17.8	1217	2	Q8V1Y9	Q8V1Y9	mycobacteri
62	606	17.7	691	2	Q9BIU3	Q9BIU3	dolomedes t
63	602.5	17.6	617	2	O46172	O46172	nephila cla
64	599.5	17.5	922	2	O44367	O44367	mytilus edu
65	594	17.3	644	2	Q8WSM4	Q8WSM4	nephila cla
66	592.5	17.3	1306	2	Q7D9L6	Q7D9L6	mycobacteri
67	592.5	17.3	1306	2	Q7UIQ7	Q7UIQ7	mycobacteri
68	592.5	17.3	1306	2	Q6MX28	Q6MX28	mycobacteri
69	592.5	17.3	1306	2	CAE55300	CAE55300	mycobacte
70	589	17.2	563	2	Q6J6N0	Q6J6N0	araneus ven
71	589	17.2	563	2	AAT36347	AAT36347	araneus v
72	587.5	17.1	778	1	PG46_MYCTU	PG46_MYCTU	mycobacteri
73	583	17.0	1660	2	Q79FD4	Q79FD4	mycobacteri
74	583	17.0	1660	2	CAE55496	CAE55496	mycobacte
75	583	17.0	1665	2	Q7D721	Q7D721	mycobacteri
76	582.5	17.0	774	2	Q7U0P7	Q7U0P7	mycobacteri
77	582.5	17.0	854	2	Q9BIU4	Q9BIU4	dolomedes t
78	580.5	16.9	1691	2	Q9ESQ2	Q9ESQ2	mus muscucu
79	578.5	16.9	783	2	Q7D9C6	Q7D9C6	mycobacteri
80	577.5	16.9	1669	1	CA14_HUMAN	CA14_HUMAN	homo sapien
81	577	16.8	648	2	Q9BIU7	Q9BIU7	argiope tri
82	577	16.8	1685	1	CA54_HUMAN	CA54_HUMAN	homo sapien
83	576.5	16.8	1408	2	Q8VK17	Q8VK17	mycobacteri
84	576	16.8	1329	2	Q79FP2	Q79FP2	mycobacteri
85	576	16.8	1329	2	CAE55390	CAE55390	mycobacte
86	575	16.8	773	2	Q7UI60	Q7UI60	mycobacteri
87	575	16.8	1621	2	Q9H4R9	Q9H4R9	homo sapien
88	574.5	16.8	1408	2	Q7U022	Q7U022	mycobacteri
89	574	16.8	1075	2	Q86X41	Q86X41	homo sapien
90	572.5	16.7	749	2	Q7D974	Q7D974	mycobacteri
91	572.5	16.7	879	2	Q8VKD2	Q8VKD2	mycobacteri
92	572	16.7	882	2	Q79FV6	Q79FV6	mycobacteri
93	572	16.7	882	2	CAE55329	CAE55329	mycobacte
94	571.5	16.7	797	2	Q7UID4	Q7UID4	mycobacteri
95	571	16.7	626	2	Q9NHW1	Q9NHW1	nephila ina
96	570.5	16.7	749	2	Q79FV7	Q79FV7	mycobacteri
97	570.5	16.7	749	2	CAE55328	CAE55328	mycobacte
98	570	16.6	767	2	Q79FT0	Q79FT0	mycobacteri
99	570	16.6	767	2	CAE55354	CAE55354	mycobacte
100	569	16.6	831	2	Q7UI59	Q7UI59	mycobacteri

ALIGNMENTS

GenCore version 5.1.6
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QM protein - protein search, using sw model

Run on: November 19, 2004, 16:06:25 : Search time 0.584716 Seconds
(without alignments)
2139.188 Million cell updates/sec

Title: US-09-743-818A-13

Perfect score: 59

Sequence: 1 ALARAKAAKYGAA 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : PIR 79:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	100.0	792	1 EAHU	elastin precursor,
2	54	91.5	770	2 S59623	tropoelastin - sme
3	53	89.8	860	1 EAMS	elastin precursor
4	53	89.8	864	1 EART	elastin precursor
5	50	84.7	747	1 EABO	elastin precursor,
6	50	84.7	784	2 A26601	elastin precursor,
7	43	72.9	382	2 AH2361	endo-1,4-beta-xyla
8	40	67.8	375	2 AH3110	oxoreductase [limpo
9	40	67.8	375	2 D98176	hypothetical prote
10	39	66.1	253	2 A97052	probable lytic mur
11	39	66.1	336	2 D42653	dihydrolipoamide d
12	39	66.1	485	2 F87448	succinylglutamic s
13	38	64.4	704	2 A34337	propionyl-CoA carb
14	38	64.4	860	2 F71000	hypothetical prote
15	37	62.7	183	2 S33422	hypothetical prote
16	37	62.7	244	2 F95262	hypothetical prote
17	37	62.7	252	1 E36914	molybdate-binding
18	37	62.7	285	2 G75468	hypothetical prote
19	37	62.7	320	2 S05208	chorion protein s3
20	37	62.7	335	2 E71201	probable glucose-f
21	37	62.7	388	2 D91240	probable amino aci
22	37	62.7	388	2 A86088	probable hippurica
23	37	62.7	439	2 G70693	probable dinF prot
24	37	62.7	452	2 C83998	acetyl-CoA carboxy
25	37	62.7	453	2 E95367	probable methyltra
26	37	62.7	462	2 T36807	probable aldehyde
27	37	62.7	514	1 QJMWPB	photosystem II chl
28	37	62.7	524	2 T39993	N2,N2-dimethylguan
29	37	62.7	548	2 T46565	tRNA (guanine-N2-)

30	62.7	902	2 A86926	probable membrane
31	62.7	920	2 C70668	probable mmpL7 pro
32	61.0	115	2 C64160	hypothetical prote
33	61.0	154	2 T00556	60S ribosomal prot
34	61.0	251	2 A87651	conserved hypother
35	61.0	269	2 B82335	MutT/nudix family
36	61.0	295	2 A81318	probable lipid A b
37	61.0	322	2 E95985	probable sugar upt
38	61.0	325	2 G87344	alcohol dehydrogen
39	61.0	355	2 A12867	endo-1,4-beta-xyla
40	61.0	359	2 T44816	brp protein [impor
41	61.0	365	2 E97644	endo-1,4-beta-xyla
42	61.0	368	2 F84300	bacteriorhodopsin
43	61.0	607	2 S70106	probable arginine-
44	61.0	732	2 A43315	ETS domain protein
45	61.0	766	2 H81794	ATP-dependent DNA
46	61.0	766	2 G81216	ATP-dependent DNA
47	61.0	794	2 T40289	hypothetical prote
48	61.0	860	2 T14650	tail fiber protein
49	61.0	978	2 T14968	phage lambda-relat
50	61.0	1194	2 D49851	magnesium-protopor
51	59.3	113	2 T36789	hypothetical prote
52	59.3	122	2 C95157	ribosomal protein
53	59.3	127	2 B80023	50S ribosomal prot
54	59.3	184	2 H84780	probable Ap2 domai
55	59.3	251	2 B82839	3-oxoacyl-[ACP] re
56	59.3	252	2 G87289	hypothetical prote
57	59.3	268	2 H82757	hypothetical prote
58	59.3	302	1 A38097	urate oxidase (EC
59	59.3	309	2 E72784	probable dihydroor
60	59.3	319	2 B71332	conserved hypother
61	59.3	387	2 B90436	hypothetical prote
62	59.3	475	2 E81810	hypothetical prote
63	59.3	519	2 S54014	hypothetical prote
64	59.3	599	2 A57701	sterol esterase (E
65	59.3	600	2 E87665	arginyl-tRNA synth
66	59.3	612	2 A34967	sterol esterase (E
67	59.3	703	1 A27883	propionyl-CoA carb
68	59.3	943	2 C82559	isoleucyl-tRNA syn
69	59.3	1857	2 T50513	hypothetical prote
70	58.5	388	2 AE2412	aspartate aminotra
71	57.6	130	2 S41123	ribosomal protein
72	57.6	130	2 A70615	probable ribosomal
73	57.6	137	2 C75600	DNA-binding protei
74	57.6	154	2 T34818	hypothetical prote
75	57.6	182	2 T38587	probable semialdeh
76	57.6	226	2 T30695	probable uracil DN
77	57.6	229	2 I51227	histone H1A - Afri
78	57.6	249	2 T04300	probable proteasom
79	57.6	252	2 A49232	outer membrane pro
80	57.6	286	2 H88175	protein T24H7.1 [i
81	57.6	289	1 S39991	cytochrome-c oxida
82	57.6	289	2 F95344	FixP1 Di-heme cyto
83	57.6	342	2 T34348	hypothetical prote
84	57.6	386	2 T47234	O-succinylthiomoser
85	57.6	387	2 A82036	fatty oxidation co
86	57.6	398	2 C95378	hypothetical prote
87	57.6	481	2 B70179	conserved hypother
88	57.6	537	2 A55929	zinc finger protei
89	57.6	549	2 AH3224	two component sens
90	57.6	587	2 E84808	hypothetical prote
91	57.6	589	2 F87626	sensor histidine k
92	57.6	627	2 A96607	hypothetical prote
93	57.6	644	2 S39356	transcription fact
94	57.6	668	1 Q0BEW1	UL52 protein - hum
95	57.6	708	2 S70834	transcription init
96	57.6	724	2 T47149	hypothetical prote
97	57.6	741	2 B49555	enhancer of split
98	57.6	771	2 S35681	ESG protein - mous
99	57.6	772	2 D86695	transducin-like en
100	57.6	779	2 T20654	hypothetical prote

RESULT 1

A: Molecule type: mRNA
A: Residues: 1-500, 507-792 <IND>
A: Cross-references: UNIPROT: P15502; UNIPROT: Q9UMK5; GB: M16983; GB: J02948
R: Bashir, M.M.; Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Rosenbloom, J.C.; Abrams, W.
J. Biol. Chem. 264, 8897-8894, 1989
A: Title: Characterization of the complete human elastin gene. Delineation of unusual features.
A: Reference number: A33705; MUID: 89255358; PMID: 2722804

A.Morseclue type: mRNA
A.Morseclue 1: 453,483-617,651-792 <PAZ>
A.Cross-references: EMBL:M36860; NID:G182061; PID:AAA52382.1; PID:g182062
A.Note: this sequence represents a composite of several splice forms
R.Fazio, M.J.; Olsen, D.R.; Kuivaniemi, H.; Chu, M.L.; Davidson, J.M.; Rosenbloom, J.; U
Lab. Invest. 58, 270-277, 1988
A.Title: Isolation and characterization of human elastin cDNAs, and age-associated varia
A.Reference number: A53891; NUID:88156138; PMID:2831431

C:Genetics:
A:Gene: GDB:ELN
A:Cross-references: GDB:119107; OMIM:130160
A:Map position: 7q11.23-7q11.23
C:Superfamily: elastin
C:Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-792/Product: elastin #status predicted <MAT>
F:783-787/Disulfide bonds: #status predicted

Query Match	100.0%	Score 59	DB 1	Length 792
Best Local Similarity	100.0%	Pred. No. 0.028		
Matches 13	Conservative	0	Mismatches	0
			Indels	0
			Gaps	0

Oy	1	A	L	A	A	K	A	K	T	G	A		13
D6	654	A	L	A	A	K	A	K	T	G	A		666

RESULT 2

SS59623

tropoelastin - sheep

C.Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C.Date: 23-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C.Accession: S59623; A24758

C.RR:Mauch, J.C.; Sandberg, L.B.; Roos, P.J.; Jimenez, F.; Christiano, A.M.; Deak, S.B.; Bo

Matrix Biol. 14, 635-641, 1994

A.Title: Extensive alternate exon usage at the 5' end of the sheep tropoelastin gene.

A;Residues: I-170 <MAJ>

C;Keywords: alternative splicing
F;760-765/Disulfide bonds:

Query Match
Best Local Similarity
Matches 12; Conservation

QY 1 ALAAAKAAKYGAZ
| | | | | | | | | |
322 AAAAAKAAKYGAZ

RESULT 3

elastin precursor - mouse
N;Alternate names: tropoelastin

C;Species: Mus musculus (M)
C;Date: 18-Aug-1995 #sequer
C;Accession: A55721

Genomics 23, 125-131, 1994
A;Title: Use of an intron l

A;Reference number: A55721
A;Accession: A55721
A;Molecule type: mRNA

A;Residues: I-860 <WID>
A;Cross-references: UNIPROT
C;Genetics:

C;Superfamily: elastin
C;Keywords: alternative spl

F;1-2//Domain: signal sequence
F;28-860/Product: elastin #1
F;850-855/Diulfide bonds:

Query Match	Best Local Similarity
8	9

Matches 12; Conservati

QY 1 ALAAAKAAKYGA

db 363 AKAAKAAKYGAA

RESULT 4
EART

erastin precursor - rat
W;Alternate names: tropoelastin
C;Species: Rattus norvegicus

C; Date: 11-Jan-1991 #sequence
C; Accession: A36106; A308788
R; Pierce, R.A.; Deak, S.B.;

A;Title: Heterogeneity of r
A;Reference number: A36106;

A;Accession: A36106
A;Molecule type: mRNA
A;Residues: 1-864 <PIE>

A; Cross-References: UNIPROT

R;Deak, S.B.; Pierce, R.A.; Belsky, S.A.; Riley, D.J.; Boyd, C.D.
 J. Biol. Chem. 263, 13504-13507, 1988
 A;Title: Rat tropoelastin is synthesized from a 3.5-kilobase mRNA.
 A;Reference number: A30878; MUID:98330868; PMID:2971041
 A;Accession: A30878
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 781-864 <DEA>
 A;Cross-references: GB:J04035; NID:g207442; PIDN:AAA42268.1; PID:g207443
 R;Franzblau, C.; Pratt, C.A.; Faris, B.; Colaninno, N.M.; Offner, G.D.; Mogayzel Jr., P.
 J. Biol. Chem. 264, 15115-15119, 1989
 A;Title: Role of tropoelastin fragmentation in elastogenesis in rat smooth muscle cells.
 A;Reference number: A36523; MUID:9359327; PMID:2768256
 A;Accession: A36523
 A;Molecule type: protein
 A;Residues: 22-31 <FRA>
 R;Rich, C.B.; Foster, J.A.
 Arch. Biochem. Biophys. 268, 551-558, 1989
 A;Title: Characterization of rat heart tropoelastin.
 A;Reference number: S02173; MUID:89117149; PMID:2913947
 A;Accession: S02173
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 'ip', 369-545, 548-764, 770-864 <RIC>
 A;Experimental source: heart
 R;Pierce, R.A.; Alatawi, A.; Deak, S.B.; Boyd, C.D.
 Genomics 12, 651-658, 1992
 A;Title: Elements of the rat tropoelastin gene associated with alternative splicing.
 A;Reference number: I54172; MUID:92241859; PMID:1572637
 A;Accession: I54172
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 264-533 <RES>
 A;Cross-references: GB:M86372; NID:g207455; PIDN:AAA42271.1; PID:g554527
 A;Accession: I68505
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 558-864 <RE2>
 A;Cross-references: GB:M86376; NID:g207459; PIDN:AAA42272.1; PID:g207462
 C;Genetics:
 A;Introns: 277/1; 292/1; 308/1; 339/1; 359/1; 419/1; 437/1; 467/1; 484/1; 601/1; 621/1;
 A;Note: the list of introns may be incomplete
 C;Superfamily: elastin
 C;Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
 F;1-21/Domain: signal sequence #status predicted <SIG>
 F;22-864/Product: elastin #status predicted <MAT>
 F;854-859/Disulfide bonds: #status predicted

Query Match 89.8%; Score 53; DB 1; Length 864;
 Best Local Similarity 92.3%; Pred. No. 0.32; Mismatches 1; Indels 0; Gaps 0;
 Matches 12; Conservative 0;

QY 1 ALAAKAAKYGAA 13
 DB 349 AKAAKAAKYGAA 361

RESULT 5
 EABO
 N;Alternate names: tropoelastin
 N;Contains: elastin precursor, splice form b; elastin precursor, splice form c
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 08-Jun-1989 #sequence revision 26-Jul-1996 #text change 09-Jul-2004
 C;Accession: A31865; A26728; C26728; A22343; I45886
 R;Yeh, H.; Anderson, N.; Ornstein-Goldstein, N.; Bashir, M.M.; Rosenbloom, J.C.; Abrams,
 Biochemistry 28, 2365-2370, 1989
 A;Title: Structure of the bovine elastin gene and S1 nuclease analysis of alternative splicing.
 A;Reference number: A31865; MUID:89274159; PMID:2543440
 A;Accession: A31865
 A;Molecule type: DNA
 A;Residues: 1-27 <YEH>
 A;Cross-references: UNIPROT:P04985; UNIPROT:Q28101; GB:J02855; NID:g340504; PIDN:AAA3077

R;Raju, K.; Anwar, R.A.
 J. Biol. Chem. 262, 5755-5762, 1987
 A;Title: Primary structures of bovine elastin a, b, and c deduced from the sequences of cDNA clones.
 A;Reference number: A92640; MUID:87194772; PMID:3032943
 A;Accession: A26728
 A;Molecule type: mRNA
 A;Residues: 1, 'RS', 4-11, 'E', 13-636, 'V', 638-747 <RAU>
 A;Cross-references: GB:J02717; NID:g163019; PIDN:AAA30503.1; PID:g163020
 A;Accession: B26728
 A;Molecule type: mRNA
 A;Residues: 1, 'RS', 4-11, 'E', 13-225, 240-636, 'V', 638-747 <RA2>
 A;Cross-references: GB:K03505; NID:g163025; PIDN:AAA30505.1; PID:g163026
 A;Accession: C26728
 A;Molecule type: mRNA
 A;Residues: 1, 'RS', 4-11, 'E', 13-225, 260-636, 'V', 638-747 <RA3>
 A;Cross-references: GB:K03506; NID:g163027; PIDN:AAA30506.1; PID:g163028
 R;Cicila, G.; May, M.; Ornstein-Goldstein, N.; Indik, Z.; Morrow, S.; Yeh, H.S.; Rosenbloom,
 Biochemistry 24, 3075-3080, 1985
 A;Title: Structure of the 3' portion of the bovine elastin gene.
 A;Reference number: A22343; MUID:85280426; PMID:2992576
 A;Accession: A22343
 A;Molecule type: DNA
 A;Residues: 613-747 <CIC>
 A;Cross-references: GB:M20415
 R;Rosenbloom, J.
 Lab. Invest. 51, 605-623, 1984
 A;Title: Biology of disease: Elastin: Relation of protein and gene structure to disease.
 A;Reference number: I45885; MUID:95059254; PMID:6150137
 A;Accession: I45886
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 678-683, 685-747 <ROS>
 A;Cross-references: GB:M31898; NID:g163015; PIDN:AAA96417.1; PID:g163018
 R;Brown, P.L.; Mecham, L.; Tisdale, C.; Mecham, R.P.
 Biochem. Biophys. Res. Commun. 186, 549-555, 1992
 A;Title: The cysteine residues in the carboxy terminal domain of tropoelastin form an intramolecular disulfide bond.
 A;Reference number: A58621; MUID:92337651; PMID:1632791
 C;Contents: annotation, disulfide bonds
 C;Comment: The term tropoelastin refers to a soluble precursor form of the extracellular matrix elastin.
 C;Genetics:
 A;Introns: 634/3; 653/3; 676/3; 689/3; 707/3; 716/3; 733/3
 A;Note: the list of introns is incomplete
 C;Superfamily: elastin
 C;Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
 F;1-747/Product: elastin precursor, splice form a #status predicted <EPA>
 F;1-225,260-747/Product: elastin precursor, splice form c #status predicted <EPC>
 F;1-225,240-747/Product: elastin precursor, splice form b #status predicted <EPB>
 F;1-26/Domain: signal sequence #status predicted <SIG>
 F;27-747/Product: elastin #status predicted <MAT>
 F;105,109,252,271,275,324,327,400,404,407,445,448,489,493,544,548,552,606,609,645,649,681,682,683,684,685,686,687,688,689,690,691,692,693,694,695,696,697,698,699,700,701,702,703,704,705,706,707,708,709,710,711,712,713,714,715,716,717,718,719,720,721,722,723,724,725,726,727,728,729,730,731,732,733,734,735,736,737,738,739,740,741,742,743,744,745,746,747,748,749,750,751,752,753,754,755,756,757,758,759,760,761,762,763,764,765,766,767,768,769,770,771,772,773,774,775,776,777,778,779,780,781,782,783,784,785,786,787,788,789,790,791,792,793,794,795,796,797,798,799,800,801,802,803,804,805,806,807,808,809,810,811,812,813,814,815,816,817,818,819,820,821,822,823,824,825,826,827,828,829,830,831,832,833,834,835,836,837,838,839,840,841,842,843,844,845,846,847,848,849,850,851,852,853,854,855,856,857,858,859,860,861,862,863,864,865,866,867,868,869,870,871,872,873,874,875,876,877,878,879,880,881,882,883,884,885,886,887,888,889,890,891,892,893,894,895,896,897,898,899,900,901,902,903,904,905,906,907,908,909,910,911,912,913,914,915,916,917,918,919,920,921,922,923,924,925,926,927,928,929,930,931,932,933,934,935,936,937,938,939,940,941,942,943,944,945,946,947,948,949,950,951,952,953,954,955,956,957,958,959,960,961,962,963,964,965,966,967,968,969,970,971,972,973,974,975,976,977,978,979,980,981,982,983,984,985,986,987,988,989,990,991,992,993,994,995,996,997,998,999,1000

Query Match 84.7%; Score 50; DB 1; Length 747;
 Best Local Similarity 84.6%; Pred. No. 0.9;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALAAKAAKYGAA 13
 DB 319 AAAKAAKYGAA 331

RESULT 6
 A26601
 N;Alternate names: tropoelastin
 N;Alternate names: chicken (fragment)
 C;Species: Gallus gallus (chicken)
 C;Date: 05-Oct-1988 #sequence revision 26-Jul-1996 #text change 09-Jul-2004
 C;Accession: A26601; A30795; A27264
 R;Bressan, G.M.; Argos, P.; Stanley, K.K.
 Biochemistry 26, 1497-1503, 1987
 A;Title: Repeating structure of chick tropoelastin revealed by complementary DNA cloning.
 A;Reference number: A26601; MUID:87242320; PMID:3593675

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan, K.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, A.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan, K.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; MUID:21608550; PMID:11743193

A:Cross-references: UNIPROT:Q8U7E1; GB:AE008689; PIDN:AA45302.1; PID:g17742991; GSPDB:C58

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: Atu4508

A:Map position: linear chromosome

Query Match 67.8%; Score 40; DB 2; Length 375;

Best Local Similarity 75.0%; Pred. No. 24;

Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LAAKAAKYGAA 13

DB 47 LAAKAAKFGFA 58

RESULT 9

D98176

hypothetical protein AGR_L720 [imported] - Agrobacterium tumefaciens (strain C58, Cerso

C:Species: Agrobacterium tumefaciens

C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004

C:Accession: D98176

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens C58

A:Reference number: A97359; MUID:21608551; PMID:11743194

A:Accession: D98176

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-375 <KUR>

A:Cross-references: UNIPROT:Q8U7E1; GB:AE007870; PIDN:AAK8934.1; PID:g15158710; GSPDB:C58

C:Genetics:

A:Gene: AGR_L 720

A:Map position: linear chromosome

Query Match 67.8%; Score 40; DB 2; Length 375;

Best Local Similarity 75.0%; Pred. No. 24;

Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LAAKAAKYGAA 13

DB 47 LAAKAAKFGFA 58

RESULT 10

A97052

probable lytic murin transglycosylase (N-term. LysM motif repeat domain) CAC1232 [import

C:Species: Clostridium acetobutylicum

C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004

C:Accession: A97052

R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum ATCC824

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: A97052

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-253 <KUR>

A:Cross-references: UNIPROT:Q97JF1; GB:AE001437; PIDN:AAK79204.1; PID:g15024157; GSPDB:C58

A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A;Gene: CAC1232

Query Match 66.1%; Score 39; DB 2; Length 253;
Best Local Similarity 66.7%; Pred. No. 25;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALAAAKAAYG 12

Db 207 SLGAAKAAYGS 218

RESULT 11

D42653 dihydrolipoamide dehydrogenase (EC 1.8.1.4) - Acholeplasma laidlawii (fragment)

N;Alternate names: 36k protein

C;Species: Acholeplasma laidlawii

C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: D42653

R;Wallbrant, P.; Tegman, V.; Jonsson, B.H.; Wieslander, A.

J. Bacteriol. 174, 1388-1396, 1992

A;Title: Identification and analysis of the genes coding for the putative pyruvate dehydrogenase complex in A. laidlawii

A;Reference number: A42653; MUID:92138635; PMID:1735725

A;Accession: D42653

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-336 <WAL>

A;Cross-references: UNIPROT:P35484; GB:M81753; NID:G141807; PIDN:AAA21910.1; PID:G141811

A;Note: sequence extracted from NCBI backbone (NCBI:79683, NCBI:P:79691)

C;Keywords: FAD; flavoprotein; lipoamide; NAD; oxidoreductase; redox-active disulfide

Query Match 66.1%; Score 39; DB 2; Length 336;

Best Local Similarity 72.7%; Pred. No. 33; Gaps 0;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LAATAAKAYG 12

Db 18 VAATKAAYG 28

RESULT 12

F87448

succinylglutamic semialdehyde dehydrogenase [imported] - Caulobacter crescentus

C;Species: Caulobacter crescentus

C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C;Accession: F87448

R;Nierman, W.C.; Felblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MUID:21173698; PMID:11259647

A;Accession: F87448

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-485 <STO>

A;Cross-references: UNIPROT:Q9ATW2; GB:AE005673; NID:G13423006; PIDN:AAK23586.1; GSPDB:C

C;Genetics:

A;Gene: CCL607

C;Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology

Query Match 66.1%; Score 39; DB 2; Length 485;

Best Local Similarity 72.7%; Pred. No. 45; Gaps 0;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALAAAKAAYG 11

Db 391 ALAANATRYG 401

RESULT 13

A34337

propionyl-CoA carboxylase (EC 6.4.1.3) alpha chain precursor - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 11-Jan-2002

C;Accession: A34337; A30871

R;Browner, M.F.; Taroni, F.; Sztul, E.; Rosenberg, L.E.

J. Biol. Chem. 264, 12680-12685, 1989

A;Title: Sequence analysis, biogenesis, and mitochondrial import of the alpha-subunit of

A;Reference number: A34337; MUID:89308706; PMID:2745462

A;Accession: A34337

A;Molecule type: mRNA

A;Residues: MPYERFCATRCWNSG', 1-704 <BR1>

A;Cross-references: GB:M22631

R;Browner, M.F.; Taroni, F.; Sztul, E.; Rosenberg, L.E.

submitted to GenBank, February 1989

A;Reference number: A30871

A;Accession: A30871

A;Molecule type: mRNA

A;Residues: MPYERFCATRCWNSG', 1-298, 'WP', 301-704 <BR2>

A;Cross-references: GB:M22631; NID:G206049; PIDN:AAA88512.1; PID:G206050

R;Browner, M.F.; Taroni, F.; Sztul, E.; Rosenberg, L.E.

J. Biol. Chem. 266, 4660, 1991

A;Reference number: A43040

A;Contents: annotation; correction

A;Note: the first 17 residues in the original paper were derived from bacterial DNA as ar

C;Genetics:

A;Gene: PCCA

C;Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipoyl

C;Keywords: biotin binding; heterododecamer; ligase; mitochondrial matrix; mitochondrion

F;1-27/Domain: transit peptide (mitochondrion) (fragment) #status predicted <TNP>

F;28-704/Product: propionyl-CoA carboxylase alpha chain #status predicted <MAT>

F;41-492/Domain: biotin carboxylase homology <BCH>

F;631-704/Domain: lipoyl/biotin-binding homology <LPB>

F;670/Binding site: biotin (Lys) (covalent) #status predicted

Query Match 64.4%; Score 38; DB 2; Length 704;

Best Local Similarity 61.5%; Pred. No. 93; Gaps 0;

Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALAAAKAAYGAA 13

Db 296 AVALAKAVKYSSA 308

RESULT 14

F71000

hypothetical protein PH1302 - Pyrococcus horikoshii

C;Species: Pyrococcus horikoshii

C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004

C;Accession: F71000

R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,

DNA Res. 5, 55-76, 1998

A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic ar

A;Reference number: A71000; MUID:98344137; PMID:9679194

A;Accession: F71000

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-860 <KAW>

A;Cross-references: UNIPROT:O59003; GB:AP000006; NID:G3236133; PIDN:BAA30406.1; PID:dl031

A;Experimental source: strain OT3

A;Note: this accession replaces an interim accession for a sequence replaced by GenBank

C;Genetics:

A;Gene: PH1302

Query Match 64.4%; Score 38; DB 2; Length 860;

Best Local Similarity 66.7%; Pred. No. 1.1e+02; Gaps 0;

Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 LAATAAKAAYGAA 13

Db 826 LTAAGVKYGEA 837

RESULT 15

S33422

hypothetical protein 183 - Streptomyces ambofaciens
 C:Species: Streptomyces ambofaciens
 C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
 C:Accession: S33422
 R:Hagege, J.M.; Boccard, F.; Smokvina, T.; Pernodet, J.L.; Friedmann, A.; Guerineau, M.
 submitted to the EMBL Data Library, January 1993
 A:Description: Identification of a gene encoding the replication initiator protein of the
 A:Reference number: S33422
 A:Accession: S33422
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-183 <HAG>
 A:Cross-references: UNIPROT:P36892; EMBL:Z19594; NID:g298046; PIDN:CAA79646.1; PID:g5753
 C:Genetics:
 A:Start codon: GTG

Query Match 62.7%; Score 37; DB 2; Length 183;
 Best Local Similarity 75.0%; Pred. No. 41;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGA 12
 ||||| |||||
 Db 160 ALAAADAANYAA 171

RESULT 16
 F95262
 hypothetical protein Sma0013 [imported] - Sinorhizobium meliloti (strain 1021) magaplaem
 C:Species: Sinorhizobium meliloti
 C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
 C:Accession: F95262
 R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
 ; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
 Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
 A>Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
 A:Reference number: A95262; MUID:21396509; PMID:11481432
 A:Accession: F95262
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-244 <KUR>

A:Cross-references: UNIPROT:Q931D6; GB:AE006469; PIDN:AAK64664.1; PID:g14523061; GSPDB:G
 A:Experimental source: strain 1021, megaplasmid pSymA
 R:Galbert, F.; Finan, T.W.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
 P.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
 heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A>Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: Sma0013
 A:Genome: plasmid

Query Match 62.7%; Score 37; DB 2; Length 244;
 Best Local Similarity 61.5%; Pred. No. 54;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGA 13
 ||||| |||||
 Db 4 ALARAQAGYGA 16

RESULT 17
 E36914
 molybdate-binding protein homolog ModA - Rhodobacter capsulatus
 C:Species: Rhodobacter capsulatus
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004
 C:Accession: E36914
 R:Wang, G.; Angermuller, S.; Klipp, W.
 J. Bacteriol. 175, 3031-3042, 1993
 A>Title: Characterization of Rhodobacter capsulatus genes encoding a molybdenum transpor

A:Reference number: A36914; MUID:93259949; PMID:8491722
 A:Accession: E36914
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-252 <WAN>
 A:Cross-references: UNIPROT:Q08383; GB:L06254; NID:g310272; PIDN:AAA71911.1; PID:g310276
 A>Note: sequence extracted from NCBI backbone (NCBIN:131915, NCBI:P131920)
 C:Superfamily: Molybdate-binding periplasmic protein ModA

Query Match 62.7%; Score 37; DB 1; Length 252;
 Best Local Similarity 61.5%; Pred. No. 55;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGA 13
 ||||| |||||
 Db 135 ATADPKSAPYGA 147

RESULT 18
 G75468
 hypothetical protein - Deinococcus radiodurans (strain RL)
 C:Species: Deinococcus radiodurans
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: G75468
 R:White, O.; Eisen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 ; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma.
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999

A>Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: G75468
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-285 <WHI>

A:Cross-references: UNIPROT:Q9RM12; GB:AE001939; GB:AE000513; NID:g6458563; PIDN:AAF1043
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR0857
 A:Map position: 1

Query Match 62.7%; Score 37; DB 2; Length 285;
 Best Local Similarity 61.5%; Pred. No. 62;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGA 13
 ||||| |||||
 Db 12 ALGAGAAAHGAA 24

RESULT 19
 S09208
 chorion protein s36 - Mediterranean fruit fly
 C:Species: Ceratitis capitata (Mediterranean fruit fly)
 C>Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Jul-2004
 C:Accession: S09208
 R:Konsolaki, M.; Komitopoulou, K.; Tolia, P.P.; King, D.L.; Swimmer, C.; Kafatos, F.C.
 Nucleic Acids Res. 18, 1731-1737, 1990
 A>Title: The chorion genes of the medfly, Ceratitis capitata, I: structural and regulato
 A:Reference number: S09208; MUID:90245561; PMID:1692403
 A:Accession: S09208
 A:Molecule type: DNA
 A:Residues: 1-320 <KON>
 A:Cross-references: UNIPROT:P17110; EMBL:X51342; NID:g5973; PIDN:CAA35723.1; PID:g295730
 C:Genetics:
 A:Introns: 14/3

Query Match 62.7%; Score 37; DB 2; Length 320;
 Best Local Similarity 72.7%; Pred. No. 68;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 AAAAKAAKYGA 13
 ||||| |||||
 Db 273 SAAPAAASYGA 283

RESULT 20

E71201
probable glucose-fructose oxidoreductase - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C:Accession: E71201
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: E71201
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-335 <KAW>
A:Cross-references: UNIPROT:O59537; GB:AF000007; NID:g3236134; PIDN:BAA31004.1; PID:g325
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH1882

Query Match 62.7%; Score 37; DB 2; Length 335;
Best Local Similarity 66.7%; Pred. No. 71;
Matches 8; Conservative 1; Mismatches 0; Indels 3; Gaps 0;

QY 1 ALAAAKAAYGA 12
||| : |||
Db 40 ALAKVEAKYGA 51

RESULT 21

D91240
probable amino acid amidohydrolase [imported] - Escherichia coli (strain O157:H7, substa
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: D91240
R:Havashi, T.; Makino, K.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: D91240
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-388 <HAY>
A:Cross-references: UNIPROT:O8X726; GB:BA000007; PIDN:BA838315.1; PID:g13364368; GSPDB:G
A:Experimental source: strain O157:H7, substrain RIND 0509952
C:Genetics:
A:Gene: ECS4892
C:Superfamily: hippurate hydrolase

Query Match 62.7%; Score 37; DB 2; Length 388;
Best Local Similarity 66.7%; Pred. No. 81;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALAAAKAAYGA 12
||| : |||
Db 273 ALAQQAASFGA 284

RESULT 22

A86088
probable hippuricase Z5522 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: A86088
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: A86088

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-388 <STO>

A:Cross-references: UNIPROT:Q8X726; GB:AE005174; NID:g12518888; PIDN:AAG59165.1; GSPDB:GN
A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: Z5522

C:Superfamily: hippurate hydrolase

Query Match 62.7%; Score 37; DB 2; Length 388;
Best Local Similarity 66.7%; Pred. No. 81;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALAAAKAAYGA 12
||| : |||
Db 273 ALAQQAASFGA 284

RESULT 23

G70693
probable dinF protein - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: G70693
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hollroyd, S.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: G70693
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-439 <COL>
A:Cross-references: UNIPROT:P71616; GB:Z81331; GB:AL123456; NID:g3261650; PIDN:CAB03650.1
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: dinF
C:Superfamily: conserved hypothetical protein H11612

Query Match 62.7%; Score 37; DB 2; Length 439;
Best Local Similarity 72.7%; Pred. No. 91;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 AAACAAYGAA 13
||| : |||
Db 252 AAACAAYGAA 262

RESULT 24

C83998
acetyl-CoA carboxylase biotin carboxylase subunit accC [imported] - Bacillus halodurans
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: C83998
R:Takami, H.; Nakabone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: C83998
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-452 <STO>
A:Cross-references: UNIPROT:Q9K963; GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BA8065
A:Experimental source: strain C-125
C:Genetics:
A:Gene: accC
C:Superfamily: biotin carboxylase; biotin carboxylase homology

Query Match 62.7%; Score 37; DB 2; Length 452;
Best Local Similarity 61.5%; Pred. No. 93;

Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGAA 13
 :|||||
 Db 259 AVAAAKAVNSGA 271
 :|||||

RESULT 25
 E95367
 probable methyltransferase - chemotaxis [imported] - Sinorhizobium meliloti (strain 1021)
 C:Species: Sinorhizobium meliloti
 C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
 C:Accession: E95367
 R; Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
 ; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
 Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
 A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
 A:Reference number: A95262; MUID:21396509; PMID:11481432
 A:Accession: E95367
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-453 <RUR>
 A:Cross-references: UNIPROT:Q92YM8; GB:AE006469; PIDN:AAK65503.1; PID:gl4523976; GSPDB:G
 A:Experimental source: strain 1021, megaplasmid pSymA
 R; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
 peia, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
 heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: SMal552
 A:Genome: plasmid

Query Match 62.7%; Score 37; DB 2; Length 453;
 Best Local Similarity 72.7%; Pred. No. 93;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYG 11
 :|||||
 Db 142 ALAAAKTGDYG 152
 :|||||

RESULT 26
 T36807
 probable aldehyde dehydrogenase - Streptomyces coelicolor
 C:Species: Streptomyces coelicolor
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: T36807
 R; Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, July 1999
 A:Reference number: Z21614
 A:Accession: T36807
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-462 <OLI>
 A:Cross-references: UNIPROT:Q9S246; EMBL:AL096811; PIDN:CAB46804.1; GSPDB:GN00070; SCORP
 A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: SCORDB:SC130A.27C
 C:Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology

Query Match 62.7%; Score 37; DB 2; Length 462;
 Best Local Similarity 72.7%; Pred. No. 95;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYG 11
 :|||||
 Db 297 SLAAEAAAKYG 307
 :|||||

RESULT 27

QJWNPB

photosystem II chlorophyll a-binding protein psbB precursor - Prochlorothrix hollandica
 N; Alternate names: photosystem II CP-47 protein
 C; Species: Prochlorothrix hollandica
 C; Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C; Accession: S17739
 R; Greer, K.L.; Golden, S.S.
 Plant Mol. Biol. 17, 915-917, 1991
 A; Title: Nucleotide sequence of psbB from Prochlorothrix hollandica.
 A; Reference number: S17739; MUID:92003701; PMID:1840692
 A; Accession: S17739
 A; Molecule type: DNA
 A; Residues: 1-514 <GRE>
 A; Cross-references: UNIPROT:P27200; EMBL:X59614; NID:G45537; PIDN:CAA42177.1; PID:G45538
 A; Note: the authors translated the codon CCC for residue 134 as O
 C; Genetics:

A; Gene: psbB

C; Superfamily: photosystem II chlorophyll a-binding protein psbB
 C; Keywords: chlorophyll; photosynthesis; photosystem II; transmembrane protein
 F; 19-40/Domain: transmembrane #status predicted <TM1>
 F; 104-120/Domain: transmembrane #status predicted <TM2>
 F; 146-162/Domain: transmembrane #status predicted <TM3>
 F; 211-227/Domain: transmembrane #status predicted <TM4>
 F; 245-261/Domain: transmembrane #status predicted <TM5>
 F; 459-475/Domain: transmembrane #status predicted <TM6>

Query Match 62.7%; Score 37; DB 1; Length 514;
 Best Local Similarity 69.2%; Pred. No. 1e+02;
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGAA 13

|||:|:|:|

Db 245 ALASATAAVFGAA 257

RESULT 28

T39993

N2,N2-dimethylguanosine tRNA methyltransferase - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T39993
 R; Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Whithead, S.; Chillingworth, T.; Churcher,
 submitted to the EMBL Data Library, July 1998
 A:Reference number: Z21897

A; Accession: T39993

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: DNA

A; Residues: 1-524 <LYN>

A; Cross-references: EMBL:AL031158; PIDN:CAA20101.1; GSPDB:GN00067; SPDB:SPBC25D12.05
 A; Experimental source: strain 972h-; cosmid c25D12

C; Genetics:

A; Gene: SPDB:SPBC25D12.05

A; Map position: 2

Query Match 62.7%; Score 37; DB 2; Length 524;
 Best Local Similarity 80.0%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AAKAAKYGAA 13

|||:|:|:|

Db 245 AASAAKYGRA 254

RESULT 29

T46565

tRNA (guanine-N2-) -methyltransferase (EC 2.1.1.32) [imported] - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C; Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 09-Jul-2004
 C; Accession: T46565
 R; Niederberger, C.

submitted to the EMBL Data Library, February 1998

A;Description: Cloning and characterization of the putative tRNA (guanine-N2-)-methyltra

A;Reference number: Z23073

A;Accession: I46585

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-548 <NIE>

A;Cross-references: UNIPROT:Q9P804; EMBL:AJ224000; PIDN:CAA11801.1

C;Genetics:

A;Gene: trml

C;Keywords: methyltransferase; S-adenosylmethionine

Query Match 62.7%; Score 37; DB 2; Length 548;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AAKAAKYGAA 13
|||
Db 269 AASAAKYGRA 278

RESULT 30

A86926

probable membrane protein [imported] - Mycobacterium leprae

C;Species: Mycobacterium leprae

C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C;Accession: A86926

R;Cole, S.T.; Bigmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho

R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,

eam, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq

A;Title: Massive gene decay in the leprosy bacillus

A;Reference number: A86909; MUID:21128732; PMID:11234002

A;Accession: A86926

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-902 <STO>

A;Cross-references: GB:AL450380; NID:gl3092515; PIDN:CAC29645.1; GSPDB:GN00147

C;Genetics:

A;Gene: mmpL7

Query Match 62.7%; Score 37; DB 2; Length 902;
Best Local Similarity 63.6%; Pred. No. 1.7e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LAAAKAAKYGA 12
:|:|:|:|:
Db 699 IAAGKAMKYGS 709

Search completed: November 19, 2004, 15:38:49
Job time : 4.58472 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2004, 15:22:20 ; Search time 2.62838 Seconds

(without alignments)
2845.805 Million cell updates/sec

Title: US-09-743-818A-13

Perfect score: 59

Sequence: 1 ALAAAKAAKYCAA 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt 02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	258	2	Q9UMF5
2	59	100.0	472	2	Q8N2G0
3	59	100.0	570	2	Q8ZW60
4	59	100.0	570	2	BAC85506
5	59	100.0	658	2	Q6P0L4
6	59	100.0	658	2	AAH65566
7	59	100.0	687	2	Q14235
8	59	100.0	687	2	Q72316
9	59	100.0	711	2	Q7Z3F5
10	59	100.0	730	1	ELUS_HUMAN
11	59	100.0	757	2	Q14234
12	59	100.0	757	2	Q75MU5
13	59	100.0	757	2	AA07435
14	54	91.5	559	2	Q5ZUM2
15	54	91.5	559	2	BAC86188
16	54	91.5	602	2	Q15337
17	54	91.5	635	2	Q15336
18	54	91.5	643	2	Q8NB14
19	53	89.8	810	2	Q9ESZ9
20	53	89.8	860	1	ELUS_MOUSE
21	53	89.8	860	2	Q8C9L8
22	53	89.8	864	1	ELUS_RAT
23	50	84.7	650	2	Q28099
24	50	84.7	666	2	Q28096
25	50	84.7	679	2	Q28097
26	50	84.7	707	2	Q28098
27	50	84.7	747	1	ELUS_BOVIN
28	50	84.7	750	1	ELUS_CHICK
29	47	79.7	69	2	Q28101
30	47	79.7	100	1	ELUS_SHEEP
31	43	72.9	382	2	Q8YFW3

32	41	69.5	277	2	Q7X738	O7x738 oryza sativ
33	41	69.5	277	2	CAE03060	CaE03060 oryza sat
34	40	67.8	375	2	Q7CV49	Q7cv49 agrobacteri
35	40	67.8	375	2	Q8U7E1	Q8u7e1 agrobacteri
36	40	67.8	393	2	Q758U3	Q758u3 ashbya goss
37	40	67.8	393	2	AA552343	AA552343 ashbya go
38	40	67.8	421	2	Q88UY9	Q88uy9 lactobacill
39	40	67.8	649	2	Q6CXW7	Q6cmx7 kluyveromyc
40	39	66.1	133	2	Q9RL42	Q9rl42 streptomyce
41	39	66.1	253	2	Q97JF1	Q97jfp1 clostridium
42	39	66.1	329	2	Q9NHE0	Q9nhe0 meloidogyne
43	39	66.1	336	1	DLDH_ACHLA	P35484 acholeplasm
44	39	66.1	448	2	Q9A7W2	Q9a7w2 caulobacter
45	38	64.4	145	1	AROQ_CORGL	O52377 corynebacte
46	38	64.4	145	1	AAQ64007	AAq64007 corynebac
47	38	64.4	149	2	Q9S6G5	Q9s6g5 corynebacte
48	38	64.4	155	2	Q9LMB3	Q9lwb3 spinacia ol
49	38	64.4	177	2	Q9SNF2	Q9snf2 oryza sativ
50	38	64.4	275	1	HXDC_HUMAN	P35452 homo sapien
51	38	64.4	294	2	Q6J7W5	O6j7w5 actinoplane
52	38	64.4	294	2	AAT36814	Aat36814 actinopla
53	38	64.4	474	2	Q7VFP30	Q7vf30 helicobacte
54	38	64.4	531	2	Q8L476	Q8l476 oryza sativ
55	38	64.4	724	2	Q8OVU5	Q8ovv5 mus musculu
56	38	64.4	724	2	Q91ZA3	Q91za3 mus musculu
57	38	64.4	724	2	Q922N3	Q922n3 mus musculu
58	38	64.4	860	2	Q59003	Q59003 pyrococcus
59	38	64.4	1401	2	Q7S799	Q7s799 neurospora
60	38	64.4	1472	2	Q9L2I4	Q9l2i4 streptomyce
61	37	62.7	76	2	Q28100	Q28100 bos taurus
62	37	62.7	76	2	AAA96416	AAa96416 bos tauru
63	37	62.7	152	2	Q7XT75	Q7xt75 oryza sativ
64	37	62.7	152	2	Q9FSP3	Q9fsp3 oryza sativ
65	37	62.7	183	1	YREP_STRAM	P36892 streptomyce
66	37	62.7	183	2	Q9ADC3	Q9adc3 streptomyce
67	37	62.7	183	2	CAA06454	CAa06454 streptomy
68	37	62.7	244	2	Q931D6	Q931d6 rhizobium m
69	37	62.7	252	1	MODA_RHOCA	Q8383 rhodobacter
70	37	62.7	277	2	Q73XE9	Q73xr9 mycobacteri
71	37	62.7	277	2	AA04557	AA04557 mycobacte
72	37	62.7	285	2	Q9RM12	Q9rm12 deinococcus
73	37	62.7	289	2	Q6NJK4	Q6njk4 corynebacte
74	37	62.7	289	2	CAE48901	CAe48901 corynebac
75	37	62.7	320	1	CH36_CERCA	P17110 ceratitidis c
76	37	62.7	332	2	Q939Q8	Q939q8 streptomyce
77	37	62.7	335	2	Q59537	Q59537 pyrococcus
78	37	62.7	336	2	Q6N298	Q6n298 rhodopseu
79	37	62.7	336	2	CAE29593	CAe29593 rhodopseu
80	37	62.7	349	2	Q8LGO6	Q8lgo6 chlamydomon
81	37	62.7	353	2	Q6H521	Q6h521 oryza sativ
82	37	62.7	371	2	Q8I2E7	Q8i2e7 plasmodium
83	37	62.7	385	2	Q82DF6	Q82df6 streptomyce
84	37	62.7	388	2	Q7A966	Q7a966 escherichia
85	37	62.7	388	2	Q8FB92	Q8fb92 escherichia
86	37	62.7	388	2	Q8X726	Q8x726 escherichia
87	37	62.7	436	2	Q7D6H3	Q7d6h3 mycobacteri
88	37	62.7	439	2	P71616	P71616 mycobacteri
89	37	62.7	439	2	Q7TXR0	Q7txr0 mycobacteri
90	37	62.7	452	2	Q9K963	Q9k963 bacillus ha
91	37	62.7	453	2	Q92YN8	Q92ym8 rhizobium m
92	37	62.7	462	2	Q9S246	Q9s246 streptomyce
93	37	62.7	487	2	Q6W253	Q6w253 rhizobium s
94	37	62.7	487	2	AAQ87165	AAq87165 rhizobium
95	37	62.7	501	2	Q8HS72	Q8hs72 hordeum vul
96	37	62.7	501	2	Q6NBI9	Q6nbi9 rhodopseu
97	37	62.7	501	2	CAE26283	CAe26283 rhodopseu
98	37	62.7	514	1	PSBB_PROHO	P27200 prochloroth
99	37	62.7	531	2	Q826R5	Q826r5 streptomyce
100	37	62.7	548	1	TRM1_SCHPO	Q9p804 schizosacch

ALIGNMENTS

```
RESULT 1
Q9UMF5 Q9UMF5 PRELIMINARY; PRT; 258 AA.
AC Q9UMF5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Elastin (Fragment).
GN Name=ELN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96411691; PubMed=8812460;
RA Osborne L.R., Martindale D.W., Scherer S.W., Shi X.-M., Huizenga J.,
RA Heng H.H.Q., Costa T., Pober B., Lew L., Brinkman J., Rommens J.,
RA Koop B.F., Tsui L.-C.;
RT "Identification of genes from a 500-kb region at 7q11.23 that is
RT commonly deleted in Williams syndrome patients.";
RL Genomics 36:328-336(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20458868; PubMed=11003705;
RA Martindale D.W., Wilson M.D., Wang D., Burke R.D., Chen X.,
RA Duronio V., Koop B.F.;
RT "Comparative genomic sequence analysis of the Williams syndrome region
RT (LIMK1-RFC2) of human chromosome 7q11.23.";
RL Mamm. Genome 11:890-898(2000).
DR EMBL; U63721; AAC13884.1; -.
DR InterPro; IPR001451; Hexapep.transf.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 258 AA; 21990 MW; C39BF7298D0E05D2 CRC64;

Query Match 100.0%; Score 59; DB 2; Length 258;
Best Local Similarity 100.0%; Pred. No. 0.086;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGAA 13
Db 120 ALAAAKAAKYGAA 132

RESULT 2
Q8N2G0 Q8N2G0 PRELIMINARY; PRT; 472 AA.
AC Q8N2G0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein PSEC0191.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole embryo;
RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
RA Nagahari K., Sugano S., Isogai T.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK075494; BAC11651.1; -.
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro; IPR001451; Hexapep.transf.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROP0ELASTIN.
DR PROSITE; PSC0101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
FT NON_TER 472
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SQ SEQUENCE 472 AA; 42265 MW; 8D7A0F3A9BF971F3 CRC64;

Query Match 100.0%; Score 59; DB 2; Length 472;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGAA 13
Db 360 ALAAAKAAKYGAA 372

RESULT 3
Q6ZMJ6 Q6ZMJ6 PRELIMINARY; PRT; 570 AA.
AC Q6ZMJ6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ16246.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,
RA Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
RA Masuho Y., Nagai K., Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK122731; BAC85506.1; -.
DR InterPro; IPR001451; Hexapep.transf.
DR PRINTS; PR01500; TROP0ELASTIN.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
SQ SEQUENCE 570 AA; 48941 MW; 3117B028D06D4F7B CRC64;

Query Match 100.0%; Score 59; DB 2; Length 570;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGAA 13
Db 450 ALAAAKAAKYGAA 462

RESULT 4
BAC85506 BAC85506 PRELIMINARY; PRT; 570 AA.
AC BAC85506;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE CDNA FLJ16246 fis, clone HCHON2001577, highly similar to Human elastin
DE gene.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,
RA Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
RA Masuho Y., Nagai K., Isogai T.;
```

RT "NEDO human cDNA sequencing project."
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK122731; BC85506.1; -
SQ SEQUENCE 570 AA; 48941 MW; 3117B028D06D4F7B CRC64;

Query Match 100.0%; Score 59; DB 2; Length 570;

Best Local Similarity 100.0%; Pred. No. 0.17;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAAAKAAYGAA 13

Db 450 ALAAAKAAYGAA 462

RESULT 5

Q6P0L4 PRELIMINARY; PRT; 658 AA.

ID Q6P0L4
AC Q6P0L4
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE ELN protein.
GN Name=ELN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.

RC TISSUE=Eye;

RA Strausberg R.;

RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC065566; AAH65566.1; -

DR InterPro; IPR001451; Hexapep transf.

DR InterPro; IPR003979; tropoelastin.

DR PRINTS; PR01500; TROPOELASTIN.

DR PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.

SQ SEQUENCE 658 AA; 56680 MW; 5DAFC00D16A2F94E CRC64;

Query Match 100.0%; Score 59; DB 2; Length 658;

Best Local Similarity 100.0%; Pred. No. 0.19;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAAAKAAYGAA 13

Db 538 ALAAAKAAYGAA 550

RESULT 6

AAH65566 PRELIMINARY; PRT; 658 AA.
ID AAH65566
AC AAH65566;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE ELN protein.
GN ELN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.

RC TISSUE=Eye;

RA Strausberg R.;

RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC065566; AAH65566.1; -

SQ SEQUENCE 658 AA; 56680 MW; 5DAFC00D16A2F94E CRC64;

Query Match 100.0%; Score 59; DB 2; Length 658;

Best Local Similarity 100.0%; Pred. No. 0.19;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAAAKAAYGAA 13

Db 538 ALAAAKAAYGAA 550

RESULT 7

Q14235 PRELIMINARY; PRT; 687 AA.

AC Q14235;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Elastin.

GN Name=ELN;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=87289668; PubMed=3039501;

RA Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,

RA Rosenbloom J.C., Peltonen L., Rosenbloom J.;

RT "Alternative splicing of human elastin mRNA indicated by sequence

RT analysis of cloned genomic and complementary DNA.";

```

Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
[2]
SEQUENCE FROM N.A.
RA Indik Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J.,
RA Rosenbloom J., Ornstein-Goldstein N.;
RT "Structure of the 3' region of the human elastin gene: great abundance
RT of Alu repetitive sequences and few coding sequences.";
RL Connect. Tissue Res. 16:197-211(1987).
DR EMBL; M17282; AAC98393.1; JOINED.
DR EMBL; M16983; AAC98393.1; JOINED.
DR EMBL; M17265; AAC98393.1; JOINED.
DR EMBL; M17266; AAC98393.1; JOINED.
DR EMBL; M17267; AAC98393.1; JOINED.
DR EMBL; M17268; AAC98393.1; JOINED.
DR EMBL; M17271; AAC98393.1; JOINED.
DR EMBL; M17272; AAC98393.1; JOINED.
DR EMBL; M17273; AAC98393.1; JOINED.
DR EMBL; M17275; AAC98393.1; JOINED.
DR EMBL; M17276; AAC98393.1; JOINED.
DR EMBL; M17277; AAC98393.1; JOINED.
DR EMBL; M17278; AAC98393.1; JOINED.
DR EMBL; M17279; AAC98393.1; JOINED.
DR EMBL; M17281; AAC98393.1; JOINED.
DR HSP; P50099; IZFU.
DR GO; GO:0005578; C:extracellular matrix; NAS.
DR GO; GO:0030023; F:extracellular matrix constituent conferring. . .; NAS.
DR InterPro; IPR001451; Hexapep.transf.
DR PRINTS; P01500; TROPOLASTIN.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
SQ SEQUENCE 687 AA; 59529 MW; 864068C4C8E9F88F CRC64;

Query Match 100.0%; Score 59; DB 2; Length 687;
Best Local Similarity 100.0%; Pred. No. 0.19; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0;

QY 1 ALAATAAKAYGAA 13
Db 567 ALAATAAKAYGAA 579

RESULT 8
Q72316
ID Q72316 PRELIMINARY; PRT; 687 AA.
AC Q72316;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686O21208 (Fragment).
GN Name=DKFZp686O21208;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538199; CAD98065.1; -.
DR InterPro; IPR001451; Hexapep.transf.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 687 AA; 59847 MW; 79232A191DC1F10F CRC64;

Query Match 100.0%; Score 59; DB 2; Length 687;
Best Local Similarity 100.0%; Pred. No. 0.19; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0;

QY 1 ALAATAAKAYGAA 13
Db 567 ALAATAAKAYGAA 579

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Db 567 ALAATAAKAYGAA 579
|||||
RESULT 9
Q723F5
ID Q723F5 PRELIMINARY; PRT; 711 AA.
AC Q723F5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686F06102.
GN Name=DKFZp686F06102;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human fetal kidney;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX537939; CAD97910.1; -.
DR InterPro; IPR001451; Hexapep.transf.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 711 AA; 61765 MW; 95B624A99B4A989B CRC64;

Query Match 100.0%; Score 59; DB 2; Length 711;
Best Local Similarity 100.0%; Pred. No. 0.2; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0;

QY 1 ALAATAAKAYGAA 13
Db 591 ALAATAAKAYGAA 603

RESULT 10
ELS_HUMAN
ID ELS_HUMAN STANDARD; PRT; 730 AA.
AC P15502; Q14233; Q14238;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Elastin precursor (Tropoelastin).
GN Name=ELN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM B).
RX MEDLINE=87289668; PubMed=3039501;
RA Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
RA Rosenbloom J.C., Peltonen L., Rosenbloom J.;
RT "Alternative splicing of human elastin mRNA indicated by sequence
RT analysis of cloned genomic and complementary DNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX TISSUE=Skin fibroblast;
RX MEDLINE=89009960; PubMed=3171221;
RA Fazio M.J., Olsen D.R., Kauh E.A., Baldwin C.T., Indik Z.,
RA Ornstein-Goldstein N., Yeh H., Rosenbloom J., Uitto J.;
RT "Cloning of full-length elastin cDNAs from a human skin fibroblast
RT recombinant cDNA library: further elucidation of alternative splicing
RT utilizing exon-specific oligonucleotides.";
RL J. Invest. Dermatol. 91:458-464(1988).
RN [3]
RP SEQUENCE OF 164-724 FROM N.A. (ISOFORM B).
RX TISSUE=Placenta; PubMed=2831431;
RX MEDLINE=88156138; PubMed=2831431;

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RA Fazio M.J., Olsen D.R., Kuivaniemi H., Chu M.L., Davidson J.M.,
RA Rosenbloom J., Uitto J.;
RT "Isolation and characterization of human elastin cDNAs, and age-
RT associated variation in elastin gene expression in cultured skin
RT fibroblasts.";
RL Lab. Invest. 58:270-277 (1988).
RN [4]
RP SEQUENCE OF 603-730 FROM N.A.
RC TISSUE=Hippocampus, and Placenta;
RX MEDLINE=96291399; PubMed=6689686;
RA Frangiskakis J.M., Ewart A.K., Morris C.A., Mervis C.B., Bertrand J.,
RA Robinson B.F., Klein B.P., Ensing G.J., Everett L.A., Green E.D.,
RA Proeschel C., Gutowski N.J., Noble M., Atkinson D.L., Odelberg S.J.,
RA Keating W.T.;
RT "LIM-Kinase1 hemizygosity implicated in impaired visuospatial
RT constructive cognition.";
RL Cell 86:59-69 (1996).
RN [5]
RP INVOLVEMENT IN CUTIS LAXA.
RX MEDLINE=99091639; PubMed=9873040;
RA Zhang M.-C., He L., Giro M., Yong S.L., Tiller G.E., Davidson J.M.;
RT "Cutis laxa arising from frameshift mutations in exon 30 of the
RT elastin gene (ELN).";
RL J. Biol. Chem. 274:981-986 (1999).
RN [6]
RP INVOLVEMENT IN SVAS.
RX PubMed=10942104;
RA Urban Z., Michels V.V., Thibodeau S.N., Davis E.C., Bonnefont J.-P.,
RA Munnich A., Eyskens B., Gewillig M., Devriendt K., Boyd C.D.;
RT "Isolated supravalvular aortic stenosis: functional haploinsufficiency
RT of the elastin gene as a result of nonsense-mediated decay.";
RL Hum. Genet. 106:577-588 (2000).
CC -1- FUNCTION: Major structural protein of tissues such as aorta and
CC nuchal ligament, which must expand rapidly and recover completely.
CC -1- SUBUNIT: The polymeric elastin chains are cross-linked together
CC into an extensible 3D network.
CC -1- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=1;
CC IsoId=P15502-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P15502-2; Sequence=VSP_004243;
CC -1- PM: The crosslinks are made of deaminated Lys.
CC -1- DISEASE: Defects in ELN are a cause of autosomal dominant cutis
CC laxa [MIM:123700]. Cutis laxa is a rare connective tissue disorder
CC characterized by loose, hyperextensible skin with decreased
CC resilience and elasticity leading to a premature aged appearance.
CC The skin changes are often accompanied by extracutaneous
CC manifestations, including pulmonary emphysema, bladder
CC diverticula, pulmonary artery stenosis and pyloric stenosis.
CC -1- DISEASE: Haploinsufficiency of ELN may be the cause of certain
CC cardiovascular and musculo-skeletal abnormalities observed in
CC Williams-Beuren syndrome (WBS) [MIM:194050]. WBS is a rare
CC developmental disorder and a contiguous gene deletion syndrome
CC involving genes from chromosome band 7q11.23.
CC -1- DISEASE: Defects in ELN are the cause of supravalvular aortic
CC stenosis (SVAS) [MIM:185500]. SVAS is a congenital narrowing of
CC the ascending aorta which can occur sporadically, as an autosomal
CC dominant condition, or as one component of Williams-Beuren
CC syndrome.
CC -----
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CC European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M17282; AAC98394.1; JOINED.
DR EMBL; M16983; AAC98394.1; JOINED.

DR EMBL; M17265; AAC98394.1; JOINED.
DR EMBL; M17266; AAC98394.1; JOINED.
DR EMBL; M17267; AAC98394.1; JOINED.
DR EMBL; M17268; AAC98394.1; JOINED.
DR EMBL; M17270; AAC98394.1; JOINED.
DR EMBL; M17271; AAC98394.1; JOINED.
DR EMBL; M17272; AAC98394.1; JOINED.
DR EMBL; M17273; AAC98394.1; JOINED.
DR EMBL; M17275; AAC98394.1; JOINED.
DR EMBL; M17276; AAC98394.1; JOINED.
DR EMBL; M17277; AAC98394.1; JOINED.
DR EMBL; M17278; AAC98394.1; JOINED.
DR EMBL; M17279; AAC98394.1; JOINED.
DR EMBL; M17280; AAC98394.1; JOINED.
DR EMBL; M17281; AAC98394.1; JOINED.
DR EMBL; M36860; AAA52382.1; -.
DR EMBL; M24782; AAB17544.1; -.
DR EMBL; U62292; AAB17544.1; -.
DR EMBL; X15603; CAA33627.1; -.
DR PIR; A32707; EAHU.
DR HSP; P50099; IZFU.
DR Genew; HGNC:3327; ELN.
DR MIM; 130160; -.
DR MIM; 123700; -.
DR MIM; 194050; -.
DR MIM; 185500; -.
DR GO; GO:0005578; C:extracellular matrix; TAS.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005201; F:extracellular matrix structural constituent; TAS.
DR GO; GO:0008283; P:cell proliferation; TAS.
DR GO; GO:0008015; P:circulation; TAS.
DR GO; GO:0009887; P:organogenesis; TAS.
DR GO; GO:0007585; P:respiratory gaseous exchange; TAS.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN.
DR KW Alternative splicing; Connective tissue; Repeat; Signal;
DR Structural protein; Williams-Beuren syndrome.
FT SIGNAL 1 26
FT CHAIN 27 730 Elastin.
FT DSULFID 720 725 By similarity.
FT VARSPPLIC 472 477 Missing (in isoform 2).
FT FTID=VSP_004243.
SQ SEQUENCE 730 AA; 63260 MW; AB06D15BA567AE46 CRC64;
Query Match 100.0%; Score 59; DB 1; Length 730;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ALAAKAAKYGAA 13
Db 592 ALAAKAAKYGAA 604
RESULT 11
Q14234
ID Q14234 PRELIMINARY; PRT; 757 AA.
AC Q14234;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Elastin.
GN Name=ELN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87289668; PubMed=3039501;
RA Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
RA Rosenbloom J.C., Peltonen L., Rosenbloom J.;
RT "Alternative splicing of human elastin mRNA indicated by sequence
RT analysis of cloned genomic and complementary DNA.";

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Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
[2]
SEQUENCE FROM N.A.
MEDLINE=87274906; PubMed=3038460;
Indk Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J.,
Rosenbloom J., Ornstein-Goldstein N.;
"Structure of the 3' region of the human elastin gene: great abundance
of Alu repetitive sequences and few coding sequences.";
Connect. Tissue Res. 16:197-211(1987).
EMBL; M17282; AAC98395.1; -.
EMBL; M16983; AAC98395.1; JOINED.
EMBL; M17265; AAC98395.1; JOINED.
EMBL; M17266; AAC98395.1; JOINED.
EMBL; M17267; AAC98395.1; JOINED.
EMBL; M17268; AAC98395.1; JOINED.
EMBL; M17270; AAC98395.1; JOINED.
EMBL; M17271; AAC98395.1; JOINED.
EMBL; M17272; AAC98395.1; JOINED.
EMBL; M17273; AAC98395.1; JOINED.
EMBL; M17274; AAC98395.1; JOINED.
EMBL; M17275; AAC98395.1; JOINED.
EMBL; M17276; AAC98395.1; JOINED.
EMBL; M17277; AAC98395.1; JOINED.
EMBL; M17278; AAC98395.1; JOINED.
EMBL; M17279; AAC98395.1; JOINED.
EMBL; M17280; AAC98395.1; JOINED.
EMBL; M17281; AAC98395.1; JOINED.
GO; GO:0005578; C:extracellular matrix; NAS.
GO; GO:0030023; F:extracellular matrix constituent conferring. .; NAS.
InterPro; IPR001451; Hexapep transf.
InterPro; IPR003979; tropoelastin.
PRINTS; PR01500; TROP0ELASTIN.
PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN 1.
SEQUENCE 757 AA; 66136 MW; 2387F5B8AF8SCA8_CRC64;

Query Match 100.0%; Score 59; DB 2; Length 757;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAATAKAAKYGAA 13
Db 619 ALAATAKAAKYGAA 631
|||||
619 ALAATAKAAKYGAA 631

RESULT 12
Q75MU5
ID Q75MU5 PRELIMINARY; PRT; 757 AA.
AC Q75MU5;
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DE Hypothetical protein ELN.
GN Name=ELN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22737999; PubMed=12853948;
RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
Fell G.A., Delhaunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
Vanbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
Ozersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
Kozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
Tin-Wollam A.M., Abbott A., Minx P., Maupin R., Stromatt J.P.,
Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,
Wend M.C., Yang S.P., Schultz B.R., Wallis J.W., Spieth J.,
Baertsch R.A., Portnoy M.E., Torrens D., Chinwalla A.T., Gish W.R.,
Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
Waterston R.H., Wilson R.K.;
"The DNA sequence of human chromosome 7.";
MEDLINE=22737999; PubMed=12853948;
RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
Fell G.A., Delhaunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
Vanbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
Ozersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
Kozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
Tin-Wollam A.M., Abbott A., Minx P., Maupin R., Stromatt J.P.,
Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,
Wend M.C., Yang S.P., Schultz B.R., Wallis J.W., Spieth J.,
Baertsch R.A., Portnoy M.E., Torrens D., Chinwalla A.T., Gish W.R.,
Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
Waterston R.H., Wilson R.K.;
"The DNA sequence of human chromosome 7.";
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RA Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
RA Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen E.,
RA Gillitt W., Zhou Y., James R., Phelps K., Iadamoto S., Bubb K.,
RA Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,
RA Baertsch R.A., Brent M.R., Keibler E., Flicek P., Bork P., Suyama M.,
RA Bailey J.A., Portnoy M.E., Torrens D., Chinwalla A.T., Gish W.R.,
RA Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
RA Waterston R.H., Wilson R.K.;
"The DNA sequence of human chromosome 7.";
Nature 424:157-164(2003).
[2]
SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Wilson R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005056; AAS07435.1; -.
InterPro; IPR001451; Hexapep transf.
InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROP0ELASTIN.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 757 AA; 66106 MW; 2B24F955D8360738_CRC64;

Query Match 100.0%; Score 59; DB 2; Length 757;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAATAKAAKYGAA 13
Db 619 ALAATAKAAKYGAA 631
|||||
619 ALAATAKAAKYGAA 631

RESULT 13
AAS07435
ID AAS07435 PRELIMINARY; PRT; 757 AA.
AC AAS07435;
DT 02-MAR-2004 (TREMELrel. 27, Created)
DT 02-MAR-2004 (TREMELrel. 27, Last sequence update)
DE Hypothetical protein ELN.
GN ELN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22737999; PubMed=12853948;
RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
Fell G.A., Delhaunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
Vanbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
Ozersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
Kozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
Tin-Wollam A.M., Abbott A., Minx P., Maupin R., Stromatt J.P.,
Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,
Wend M.C., Yang S.P., Schultz B.R., Wallis J.W., Spieth J.,
Baertsch R.A., Portnoy M.E., Torrens D., Chinwalla A.T., Gish W.R.,
Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
Waterston R.H., Wilson R.K.;
"The DNA sequence of human chromosome 7.";
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RL Nature 424:157-164 (2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Du H., Rohlfing T., Strong C.;
RT "The sequence of Homo sapiens BAC clone CTB-51J22.";
RT Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Waterston R.H.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Wilson R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; AC005056; AAS07435.1; -.
RW Hypothetical protein.
SQ SEQUENCE 757 AA; 66106 MW; 2B24F955D8360738 CRC64;

Query Match 100.0%; Score 59; DB 2; Length 757;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAYGAA 13
Db 619 ALAAAKAAYGAA 631

RESULT 14
Q6ZUN2 PRELIMINARY; PRT; 559 AA.
AC Q6ZUN2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ43523.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK125511; BAC6188.1; -.
SQ SEQUENCE 559 AA; 53787 MW; 20938FFEC5492A01 CRC64;

Query Match 91.5%; Score 54; DB 2; Length 559;
Best Local Similarity 92.3%; Pred. No. 1.1;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALAAAKAAYGAA 13
Db 302 ALAAAKAAYGAA 314

RESULT 16
O15337 PRELIMINARY; PRT; 602 AA.
ID AC O15337;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Elastin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=97359574; PubMed=9215670;
RA Li D.Y., Toland A.E., Boak B.B., Atkinson D.L., Ensing G.J.,
RA Morris C.A., Keating M.T.;
RT "Elastin point mutations cause an obstructive vascular disease,
RT supralvalvular aortic stenosis.";
RL Hum. Mol. Genet. 6:1021-1028 (1997).
DR EMBL; U93037; AAB65620.1; -.
DR EMBL; U93034; AAB65620.1; JOINED.
DR EMBL; U93035; AAB65620.1; JOINED.
DR EMBL; U93036; AAB65620.1; JOINED.
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro; IPR001451; Hexapep transf.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
FT NON TER 1
FT NON TER 602
SQ SEQUENCE 602 AA; 51807 MW; 53B5B9A71EF04807 CRC64;

Query Match 91.5%; Score 54; DB 2; Length 602;
Best Local Similarity 92.3%; Pred. No. 1.2;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALAAAKAAYGAA 13
Db 302 ALAAAKAAYGAA 314

RESULT 15
BAC6188 PRELIMINARY; PRT; 559 AA.
ID BAC6188
AC BAC6188;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)

```

```
Db 279 AAAAAAACYGAA 291
Query Match 91.5%; Score 54; DB 2; Length 643;
Best Local Similarity 92.3%; Pred. No. 1.3;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 17
O15336 PRELIMINARY; PRT; 635 AA.
ID O15336
AC O15336;
DT 01-JAN-1998 (TREMELrel. 05, Created)
DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Elastin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97358574; PubMed=9215670;
RA Li D.Y., Toland A.E., Boak B.B., Atkinson D.L., Ensing G.J.,
RA Morris C.A., Keating M.T.;
RT "Elastin point mutations cause an obstructive vascular disease,
RT supraaortic aortic stenosis.";
RL Hum. Mol. Genet. 6:1021-1028(1997).
DR EMBL; U93037; AAB65621.1; -.
DR EMBL; U93034; AAB65621.1; JOINED.
DR EMBL; U93035; AAB65621.1; JOINED.
DR EMBL; U93036; AAB65621.1; JOINED.
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro; IPR001451; Hexapep.transf.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 635
SQ SEQUENCE 635 AA; 55279 MW; 72950C364127B2A4 CRC64;

Query Match 91.5%; Score 54; DB 2; Length 635;
Best Local Similarity 92.3%; Pred. No. 1.2;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAAAAACYGAA 13
Db 279 AAAAAAACYGAA 291

RESULT 18
Q8NB14 PRELIMINARY; PRT; 643 AA.
ID Q8NB14;
AC Q8NB14;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Hypothetical protein PSEC0254.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Meta K., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
RA Nagahari K., Sugano S., Isogai T.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK075554; BAC11696.1; -.
DR HSP; F50099; IZFU.
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro; IPR001451; Hexapep.transf.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
SQ SEQUENCE 643 AA; 55629 MW; FDFC042617E72A69 CRC64;

Db 279 AAAAAAACYGAA 291
Query Match 91.5%; Score 54; DB 2; Length 643;
Best Local Similarity 92.3%; Pred. No. 1.3;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAAAAACYGAA 13
Db 313 AAAAAAACYGAA 325

RESULT 20
ELSMOUSE STANDARD; PRT; 860 AA.
ID ELSMOUSE
AC P54320;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Elastin precursor (Tropoelastin).
GN Name=Elm;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/c; TISSUE=Lung;
RX MEDLINE=95130069; PubMed=7829060;
RA Wyder K.S., Sechler J.L., Boyd C.D., Passmore H.C.;
RT "Use of an intron polymorphism to localize the tropoelastin gene to
RT mouse chromosome 5 in a region of linkage conservation with human
RT chromosome 7.";
RL Genomics 23:125-131(1994).
CC -!- FUNCTION: Major structural protein of tissues such as aorta and
CC nuchal ligament, which must expand rapidly and recover completely.
CC -!- SUBUNIT: The polymeric elastin chains are cross-linked together
CC into an extensible 3D network.
CC -!- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
CC -!- PTM: The crosslinks are made of deaminated lys.
-----
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DR EMBL; U08210; AAA80155.1; -;
 DR PIR; A55721; EAMS.
 DR MGD; MGI:95317; Eln.
 DR PRINTS; IPR003979; tropoelastin.
 DR INTERPro; PRO1500; TROPOLASTIN.
 KW Connective tissue; Repeat; Signal; Structural protein.
 FT SIGNAL 1 27 Potential.
 FT CHAIN 28 860 Elastin.
 FT DISULFID 850 855 By similarity.
 SQ SEQUENCE 860 AA; 71955 MW; 0C0B55AAE1EDD7F1 CRC64;

Query Match 89.8%; Score 53; DB 1; Length 860;
 Best Local Similarity 92.3%; Pred. No. 2.4;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ALAAKAAKYGAA 13

Db 363 AKAAKAAKYGAA 375

RESULT 21

Q8C9L8 PRELIMINARY; PRT; 860 AA.
 AC Q8C9L8;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
 DE library, clone:A630042119 product:elastin, full insert sequence
 DE (Elastin).
 DE Name=Eln;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RX MEDLINE=21085660; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RX MEDLINE=20499374; PubMed=11042159;
 RA The FANTOM Consortium,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";

Genome Res. 10:1617-1630(2000).
 [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Kitsuai T., Tashiro H., Itoh M.,
 RA Konno H., Akiyama J., Nishi K., Katsura S., Hazama T., Harada A.,
 RA Sumi N., Ishii Y., Nakamura S., Ikegami T., Kashiwagi K.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Kikuchi T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume M.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akaiura S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickens M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 RX Strausberg R.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 RA EMBL; AK041860; BAC31084.1; -;
 DR EMBL; BC051649; AAHS1649.1; -;
 DR MGD; MGI:95317; Eln.
 DR GO; GO:0007519; P:myogenesis; IMP.
 DR GO; GO:0030833; P:regulation of actin filament polymerization; IMP.
 DR GO; GO:0043149; P:stress fiber formation; IMP.
 DR InterPro; IPR003979; tropoelastin.
 DR PRINTS; PR01500; TROPOLASTIN.
 SQ SEQUENCE 860 AA; 71938 MW; 7C340F2FFDC92E5 CRC64;

Query Match 89.8%; Score 53; DB 2; Length 860;
 Best Local Similarity 92.3%; Pred. No. 2.4;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 ALAAAKAAKYGAA 13
Db 363 AKAAAKAAKYGAA 375

RESULT 22
ELS RAT STANDARD; PRT; 864 AA.
AC Q99372;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Elastin precursor (Tropoelastin) (Fragment).
GN Name=Eln;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN [2]
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=91104868; PubMed=1702999;
RA Pierce R.A., Deak S.B., Stolle C.A., Boyd C.D.;
RT "Heterogeneity of rat tropoelastin mRNA revealed by cDNA cloning.";
RL Biochemistry 29:9677-9683(1990).
RN [2]
RN PARTIAL SEQUENCE FROM N.A.
RX PubMed=2913947;
RA Rich C.B., Foster J.A.;
RT "Characterization of rat heart tropoelastin.";
RL Arch. Biochem. Biophys. 268:551-558(1989).
RN [3]
RN SEQUENCE OF 22-31 FROM N.A.
RX PubMed=2768256;
RA Franzblau C., Pratt C.A., Faris B., Colanino N.M., Offner G.D.,
RA Mogyayzel P.J. Jr., Troxler R.F.;
RT "Role of tropoelastin fragmentation in elastogenesis in rat smooth
RT muscle cells.";
RL J. Biol. Chem. 264:15115-15119(1989).
RN [4]
RN SEQUENCE OF 264-533 AND 558-864 FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=92241859; PubMed=1572637;
RA Pierce R.A., Alatawi A., Deak S.B., Boyd C.D.;
RT "Elements of the rat tropoelastin gene associated with alternative
RT splicing.";
RL Genomics 12:651-658(1992).
RN [5]
RN SEQUENCE OF 781-864 FROM N.A.
RX MEDLINE=89330868; PubMed=2971041;
RA Deak S.B., Pierce R.A., Belsky S.A., Riley D.J., Boyd C.D.;
RT "Rat tropoelastin is synthesized from a 3.5-kilobase mRNA.";
RL J. Biol. Chem. 263:13504-13507(1988).
CC -!- FUNCTION: Major structural protein of tissues such as aorta and
CC nuchal ligament, which must expand rapidly and recover completely.
CC -!- SUBUNIT: The polymeric elastin chains are cross-linked together
CC into an extensible 3D network.
CC -!- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=8;
CC Comment=Experimental confirmation may be lacking for some
CC isoforms;
CC Name=1;
CC IsoId=Q99372-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q99372-2; Sequence=VSP_004244;
CC Name=3;
CC IsoId=Q99372-3; Sequence=VSP_004245;
CC Name=4;
CC IsoId=Q99372-4; Sequence=VSP_004246;
CC Name=5;
CC IsoId=Q99372-5; Sequence=VSP_004244, VSP_004245;
CC Name=6;
CC IsoId=Q99372-6; Sequence=VSP_004245, VSP_004246;
CC Name=7;

CC IsoId=Q99372-7; Sequence=VSP_004244, VSP_004246;
CC Name=8;
CC IsoId=Q99372-8; Sequence=VSP_004244, VSP_004245, VSP_004246;
CC -!- PTM: The crosslinks are made of deaminated Lys.
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DR EMBL; M60647; AAA42269.1; --
DR EMBL; J04035; AAA42268.1; --
DR EMBL; M86372; AAA42271.1; --
DR EMBL; M86355; AAA42271.1; JOINED.
DR EMBL; M86363; AAA42271.1; JOINED.
DR EMBL; M86364; AAA42271.1; JOINED.
DR EMBL; M86366; AAA42271.1; JOINED.
DR EMBL; M86371; AAA42271.1; JOINED.
DR EMBL; M86376; AAA42272.1; --
DR EMBL; M86373; AAA42272.1; JOINED.
DR EMBL; M86375; AAA42272.1; JOINED.
DR PIR; A36106; EART.
DR RGD; 67394; Eln.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN.
KW Alternative splicing; Connective tissue; Repeat; Signal;
KW Structural protein.
FT NON_TER 1
FT SIGNAL <1 21 By similarity.
FT CHAIN 22 864 Elastin.
FT DISULFID 854 859 By similarity.
FT VARSPPLIC 263 307 Missing (in isoform 2, isoform 5, isoform
FT 7 and isoform 8).
FT VARSPPLIC 308 308 Missing (in isoform 3, isoform 5, isoform
FT 6 and isoform 8).
FT VARSPPLIC 809 823 Missing (in isoform 4, isoform 6, isoform
FT 7 and isoform 8).
FT SEQUENCE 864 AA; 72786 MW; 456894BB09E79FD4 CRC64;

Query Match 89.8%; Score 53; DB 1; Length 864;
Best Local Similarity 92.3%; Pred. No. 2.4;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGAA 13
Db 349 AKAAAKAAKYGAA 361

RESULT 23
Q28099
ID Q28099 PRELIMINARY; PRT; 650 AA.
AC Q28099;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Elastin-cBEL1; NCBI gi: 163003 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=85280426; PubMed=2992576;
RA Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow S.,
RA Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;
RT "Structure of the 3' portion of the bovine elastin gene.";

```

```
RL Biochemistry 24:3075-3080(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=8028442; PubMed=3665402;
RA Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N.,
RA Rosenbloom J.C., Cicila G., Yoon K., Rosenbloom J.;
RT "Sequence variation of bovine elastin mRNA due to alternative
RT splicing.";
RL Coll. Relat. Res. 7:235-247(1987).
DR EMBL; M19372; AAA30499.1; -.
DR EMBL; M11422; AAA30499.1; JOINED.
DR EMBL; M19366; AAA30499.1; JOINED.
DR EMBL; M19368; AAA30499.1; JOINED.
DR EMBL; M19369; AAA30499.1; JOINED.
DR EMBL; M19370; AAA30499.1; JOINED.
DR EMBL; M19371; AAA30499.1; JOINED.
DR EMBL; M22771; AAA30499.1; JOINED.
DR EMBL; M22772; AAA30499.1; JOINED.
DR EMBL; M22773; AAA30499.1; JOINED.
DR EMBL; M22774; AAA30499.1; JOINED.
DR EMBL; M22775; AAA30499.1; JOINED.
DR EMBL; M22988; AAA30499.1; JOINED.
DR EMBL; M23010; AAA30499.1; JOINED.
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN.
FT NON TER 1
SQ SEQUENCE 650 AA; 55373 MW; CD21ABB3E9076AD7 CRC64;

Query Match 84.7%; Score 50; DB 2; Length 650;
Best Local Similarity 84.6%; Pred.No. 5.9;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ALAAKAAKYGAA 13
Db 230 ALAAKAAKFGAA 242

RESULT 24
Q28096 PRELIMINARY; PRT; 666 AA.
AC Q28096;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Elastin-CBE13; NCBI gi: 163005 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85280426; PubMed=2992576;
RA Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow S.,
RA Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;
RT "Structure of the 3' portion of the bovine elastin gene.";
RL Biochemistry 24:3075-3080(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=8028442; PubMed=3665402;
RA Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N.,
RA Rosenbloom J.C., Cicila G., Yoon K., Rosenbloom J.;
RT "Sequence variation of bovine elastin mRNA due to alternative
RT splicing.";
RL Coll. Relat. Res. 7:235-247(1987).
DR EMBL; M19372; AAA30501.1; -.
DR EMBL; M11422; AAA30500.1; JOINED.
DR EMBL; M19366; AAA30500.1; JOINED.
DR EMBL; M19367; AAA30500.1; JOINED.
DR EMBL; M19368; AAA30500.1; JOINED.
DR EMBL; M19369; AAA30500.1; JOINED.
DR EMBL; M19370; AAA30500.1; JOINED.
DR EMBL; M19371; AAA30500.1; JOINED.
DR EMBL; M22771; AAA30500.1; JOINED.
DR EMBL; M22772; AAA30500.1; JOINED.
DR EMBL; M22773; AAA30500.1; JOINED.
DR EMBL; M22774; AAA30500.1; JOINED.
DR EMBL; M22988; AAA30500.1; JOINED.
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN.
FT NON TER 1
SQ SEQUENCE 679 AA; 57652 MW; EB3C019E3BD7618D CRC64;

Query Match 84.7%; Score 50; DB 2; Length 679;
```

```
DR EMBL; M19370; AAA30501.1; JOINED.
DR EMBL; M19371; AAA30501.1; JOINED.
DR EMBL; M22771; AAA30501.1; JOINED.
DR EMBL; M22772; AAA30501.1; JOINED.
DR EMBL; M22773; AAA30501.1; JOINED.
DR EMBL; M22774; AAA30501.1; JOINED.
DR EMBL; M22775; AAA30501.1; JOINED.
DR EMBL; M22988; AAA30501.1; JOINED.
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN.
FT NON TER 1
SQ SEQUENCE 666 AA; 56435 MW; BCB5E62632BE1B71 CRC64;

Query Match 84.7%; Score 50; DB 2; Length 666;
Best Local Similarity 84.6%; Pred.No. 6.1;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ALAAKAAKYGAA 13
Db 230 ALAAKAAKFGAA 242

RESULT 25
Q28097 PRELIMINARY; PRT; 679 AA.
AC Q28097;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Elastin-CBE12; NCBI gi: 163004 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85280426; PubMed=2992576;
RA Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow S.,
RA Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;
RT "Structure of the 3' portion of the bovine elastin gene.";
RL Biochemistry 24:3075-3080(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=8028442; PubMed=3665402;
RA Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N.,
RA Rosenbloom J.C., Cicila G., Yoon K., Rosenbloom J.;
RT "Sequence variation of bovine elastin mRNA due to alternative
RT splicing.";
RL Coll. Relat. Res. 7:235-247(1987).
DR EMBL; M19372; AAA30500.1; -.
DR EMBL; M11422; AAA30500.1; JOINED.
DR EMBL; M19366; AAA30500.1; JOINED.
DR EMBL; M19367; AAA30500.1; JOINED.
DR EMBL; M19368; AAA30500.1; JOINED.
DR EMBL; M19369; AAA30500.1; JOINED.
DR EMBL; M19370; AAA30500.1; JOINED.
DR EMBL; M19371; AAA30500.1; JOINED.
DR EMBL; M22771; AAA30500.1; JOINED.
DR EMBL; M22772; AAA30500.1; JOINED.
DR EMBL; M22773; AAA30500.1; JOINED.
DR EMBL; M22774; AAA30500.1; JOINED.
DR EMBL; M22988; AAA30500.1; JOINED.
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN.
FT NON TER 1
SQ SEQUENCE 679 AA; 57652 MW; EB3C019E3BD7618D CRC64;

Query Match 84.7%; Score 50; DB 2; Length 679;
```

```
Best Local Similarity 84.6%; Pred. No. 6.2;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALAAAKAAYGAA 13
Db 264 ALAAAKAAYGAA 276

RESULT 26
Q28098 PRELIMINARY; PRT; 707 AA.
AC Q28098;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Elastin; NCBI gi: 163002 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]_TaxID=9913;
RP SEQUENCE FROM N.A.
RX MEDLINE=85280426; PubMed=2992576;
RA Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow S.,
RA Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;
RT "Structure of the 3' portion of the bovine elastin gene.";
RL Biochemistry 24:3075-3080(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85280426; PubMed=2992576;
RA Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow S.,
RA Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;
RT "Structure of the 3' portion of the bovine elastin gene.";
RL Biochemistry 24:3075-3080(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88028442; PubMed=3665402;
RA Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N.,
RA Rosenbloom J.C., Cicila G., Yoon K., Rosenbloom J.;
RT "sequence variation of bovine elastin mRNA due to alternative
RT splicing.";
RL Coll. Relat. Res. 7:235-247(1987).
DR EMBL; M19372; AAA30498.1; -.
DR EMBL; M11422; AAA30498.1; JOINED.
DR EMBL; M19366; AAA30498.1; JOINED.
DR EMBL; M19367; AAA30498.1; JOINED.
DR EMBL; M19368; AAA30498.1; JOINED.
DR EMBL; M19369; AAA30498.1; JOINED.
DR EMBL; M19370; AAA30498.1; JOINED.
DR EMBL; M19371; AAA30498.1; JOINED.
DR EMBL; M22771; AAA30498.1; JOINED.
DR EMBL; M22772; AAA30498.1; JOINED.
DR EMBL; M22773; AAA30498.1; JOINED.
DR EMBL; M22774; AAA30498.1; JOINED.
DR EMBL; M22775; AAA30498.1; JOINED.
DR EMBL; M22988; AAA30498.1; JOINED.
DR EMBL; M23010; AAA30498.1; JOINED.
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN.
FT NON_TER 1
SQ SEQUENCE 707 AA; 60346 MW; FDFD559BAB34CE33 CRC64;

Query Match 84.7%; Score 50; DB 2; Length 707;
Best Local Similarity 84.6%; Pred. No. 6.4;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALAAAKAAYGAA 13
Db 264 ALAAAKAAYGAA 276

RESULT 27
ELI BOVIN
ID ELS BOVIN STANDARD; PRT; 747 AA.
AC P04985; P04986; P04987; Q29421;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
```

```
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Elastin precursor (Tropoelastin).
GN Name=ELN;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]_TaxID=9913;
RP SEQUENCE FROM N.A.
RX MEDLINE=87194772; PubMed=3032943;
RA Raju K., Anwar R.A.;
RT "Primary structures of bovine elastin a, b, and c deduced from the
RT sequences of cDNA clones.";
RL J. Biol. Chem. 262:5755-5762(1987).
RN [2]
RP SEQUENCE OF 1-27 FROM N.A.
RX TISSUE=Nuchal ligament;
RT TISSUE=Nuchal ligament;
RA Yeh H., Anderson N., Ornstein-Goldstein N., Bashir M.M.,
RA Rosenbloom J.C., Abrams W.R., Indik Z., Yoon K., Parks W., Mecham R.,
RA Rosenbloom J.;
RT "Structure of the bovine elastin gene and SI nuclease analysis of
RT alternative splicing of elastin mRNA in the bovine nuchal ligament.";
RL Biochemistry 28:2365-2370(1989).
RN [3]
RP SEQUENCE OF 1-27 FROM N.A.
RX MEDLINE=91234332; PubMed=2031719;
RA Manohar A., Shi W., Anwar R.A.;
RT "Partial characterization of bovine elastin gene; comparison with the
RT gene for human elastin.";
RL Biochem. Cell Biol. 69:185-192(1991).
RN [4]
RP DISULFIDE BOND.
RX MEDLINE=92337851; PubMed=1632791;
RA Brown P.L., Mecham L., Tisdale C., Mecham R.P.;
RT "The cysteine residues in the carboxy terminal domain of tropoelastin
RT form an intrachain disulfide bond that stabilizes a loop structure and
RT positively charged pocket.";
RL Biochem. Biophys. Res. Commun. 186:549-555(1992).
CC -!- FUNCTION: Major structural protein of tissues such as aorta and
CC nuchal ligament, which must expand rapidly and recover completely.
CC -!- SUBUNIT: The polymeric elastin chains are cross-linked together
CC into an extensible 3D network.
CC -!- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=A;
CC ISOID=P04985-1; Sequence=Displayed;
CC Name=2; Synonyms=B;
CC ISOID=P04985-2; Sequence=VSP_004239;
CC Name=3; Synonyms=C;
CC ISOID=P04985-3; Sequence=VSP_004240;
CC -!- PTM: The crosslinks are made of deaminated Lys.
CC -----
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CC -----
DR EMBL; J02717; AAA30503.1; -.
DR EMBL; K03505; AAA30505.1; -.
DR EMBL; K03506; AAA30506.1; -.
DR EMBL; J02855; AAA30776.1; -.
DR EMBL; M58652; AAA03519.2; -.
DR PIR; A31865; EABO.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN
KW Alternative splicing; Connective tissue; Repeat; Signal;
KW Structural protein.
```



```

FT SIGNAL 1 26
FT CHAIN 27 747 Elastin.
FT DISULFID 737 742
FT MOD RES 105 105 Alllysine.
FT MOD RES 109 109 Alllysine.
FT MOD RES 252 252 Alllysine.
FT MOD RES 271 271 Alllysine.
FT MOD RES 275 275 Alllysine.
FT MOD_RES 324 324 Alllysine.
FT MOD_RES 327 327 Alllysine.
FT MOD_RES 400 400 Alllysine.
FT MOD_RES 404 404 Alllysine.
FT MOD_RES 407 407 Alllysine.
FT MOD_RES 448 448 Alllysine.
FT MOD_RES 489 489 Alllysine.
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FT MOD_RES 544 544 Alllysine.
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FT MOD_RES 606 606 Alllysine.
FT MOD_RES 609 609 Alllysine.
FT MOD_RES 645 645 Alllysine.
FT MOD_RES 649 649 Alllysine.
FT MOD_RES 685 685 Alllysine.
FT MOD_RES 688 688 Alllysine.
FT VARSPLIC 226 239 Missing (in isoform 2).
FT VARSPLIC /FTid=VSP 004239.
FT VARSPLIC Missing (in isoform 3).
FT VARSPLIC /FTid=VSP 004240.
FT CONFLICT 1 3 MRS -> MAG (in Ref. 2 and 3).
FT CONFLICT 12 12 E -> G (in Ref. 2 and 3).
SQ SEQUENCE 747 AA; 64229 MW; 633C03E411643D83 CRC64;

Query Match 84.7%; Score 50; DB 1; Length 747;
Best Local Similarity 84.6%; Pred. No. 6.7;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAAAKAAKVGAA 13
Db 319 AAAAAKAAKFGAA 331

RESULT 28
ELS_CHICK STANDARD; PRT; 750 AA.
AC P07916;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Elastin precursor (Tropoelastin) (Fragment).
GN Name=ELN;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87242320; PubMed=3593675;
RA Bressan G.M., Argos P., Stanley K.K.;
RT "Repeating structure of chick tropoelastin revealed by complementary
RT DNA cloning.";
RN Biochemistry 26:1497-1503(1987).
RN [2]
RP SEQUENCE OF 85-750 FROM N.A. (ISOFORM 2).
RX MEDLINE=88309083; PubMed=2841924;
RA Baule V.J., Foster J.A.;
RT "Multiple chick tropoelastin mRNAs.";
RN Biochem. Biophys. Res. Commun. 154:1054-1060(1988).
RN [3]
RP SEQUENCE OF 457-750 FROM N.A.
RC TISSUE=Aorta;
RX MEDLINE=87297534; PubMed=3502711;

```

Tokimitsu I., Tajima S., Nishikawa T., Tajima M., Fukasawa T.;
 "Sequence analysis of elastin cDNA from chick aorta and tissue-
 specific transcription of the elastin gene in developing chick
 embryo.";
 Arch. Biochem. Biophys. 256:455-461(1987).
 -!- FUNCTION: Major structural protein of tissues such as aorta and
 nuchal ligament, which must expand rapidly and recover completely.
 -!- SUBUNIT: The polymeric elastin chains are cross-linked together
 into an extensible 3D network.
 -!- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
 -!- ALTERNATIVE PRODUCTS:
 Event=Alternative splicing; Named isoforms=2;
 Comment=Additional isoforms seem to exist;
 Name=1;
 IsoId=P07916-1; Sequence=Displayed;
 Name=2; Synonyms=Embryonic;
 IsoId=P07916-2; Sequence=VSP_004241, VSP_004242;
 -!- PTM: The crosslinks are made of deaminated Lys.

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 or send an email to license@isb-sib.ch).

 EMBL; M18633; AAA48761.1; -;
 EMBL; M21880; AAA49082.1; -;
 EMBL; M15889; AAA49108.1; -;
 PIR; A26601; A26601.
 InterPro; IPR008160; Collagen.
 InterPro; IPR003979; tropoelastin.
 Pfam; PF01391; Collagen; 1.
 PRINTS; PR01500; TROPOELASTIN.
 KW Alternative splicing; Connective tissue; Repeat; Signal;
 Structural protein.
 FT NON_TER 1 1
 FT SIGNAL <1 24 Elastin.
 FT CHAIN 25 750 8 X tandem repeats.
 FT DOMAIN 83 686 1.
 FT REPEAT 83 127 2.
 FT REPEAT 219 262 3.
 FT REPEAT 263 318 4.
 FT REPEAT 319 393 5.
 FT REPEAT 394 482 6.
 FT REPEAT 483 554 7.
 FT REPEAT 555 619 8.
 FT REPEAT 620 686 By similarity.
 FT DISULFID 739 745 Alllysine (Potential).
 FT MOD_RES 63 63 Alllysine (Potential).
 FT MOD_RES 66 66 Alllysine (Potential).
 FT MOD_RES 111 111 Alllysine (Potential).
 FT MOD_RES 115 115 Alllysine (Potential).
 FT MOD_RES 156 156 Alllysine (Potential).
 FT MOD_RES 159 159 Alllysine (Potential).
 FT MOD_RES 198 198 Alllysine (Potential).
 FT MOD_RES 200 200 Alllysine (Potential).
 FT MOD_RES 235 235 Alllysine (Potential).
 FT MOD_RES 252 252 Alllysine (Potential).
 FT MOD_RES 256 256 Alllysine (Potential).
 FT MOD_RES 297 297 Alllysine (Potential).
 FT MOD_RES 301 301 Alllysine (Potential).
 FT MOD_RES 354 354 Alllysine (Potential).
 FT MOD_RES 357 357 Alllysine (Potential).
 FT MOD_RES 427 427 Alllysine (Potential).
 FT MOD_RES 431 431 Alllysine (Potential).
 FT MOD_RES 513 513 Alllysine (Potential).
 FT MOD_RES 517 517 Alllysine (Potential).
 FT MOD_RES 520 520 Alllysine (Potential).
 FT MOD_RES 586 586 Alllysine (Potential).
 FT MOD_RES 590 590 Alllysine (Potential).
 FT MOD_RES 593 593 Alllysine (Potential).

FT MOD_RES 655 655 Allysine (Potential).
FT MOD_RES 658 658 Allysine (Potential).
FT MOD_RES 719 719 Allysine (Potential).
FT MOD_RES 722 722 Allysine (Potential).
FT MOD_RES 743 743 Allysine (Potential).
FT MOD_RES 748 748 Allysine (Potential).
FT MOD_RES 750 750 Allysine (Potential).
FT VARSPLIC 212 212 G -> GLGGFGQQPGVPLGYPIKAPKLP (in isoform 2).
FT /FTID=VSP 004241.
FT G -> GVGPGVGVP (in isoform 2).
FT /FTID=VSP 004242.
FT A -> G (in Ref. 3).
FT CONFLICT 536 536 A -> G (in Ref. 3).
FT CONFLICT 571 571 G -> A (in Ref. 3).
FT CONFLICT 610 610 P -> A (in Ref. 3).
FT CONFLICT 654 654 A -> R (in Ref. 3).
FT CONFLICT 667 667 P -> R (in Ref. 3).
SQ SEQUENCE 750 AA; 63697 MW; E57BCD60C6EE556F CRC64;

Query Match 84.7%; Score 50; DB 1; Length 750;

Best Local Similarity 91.7%; Pred. No. 6.7; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; Indels 0; Gaps 0;

QY 1 ALAAKAAKYGA 12

Db 349 AAAKAAKYGA 360

RESULT 29

Q28101
ID Q28101 PRELIMINARY; PRT; 69 AA.
AC Q28101;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Elastin (Fragment).
GN Name=elastin;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85059254; PubMed=6150137;
RA Rosenbloom J.;
RT "Elastin: relation of protein and gene structure to disease.";
RL Lab. Invest. 51:605-623(1984).
DR EMBL; M31898; AAA96417.1; -.
DR EMBL; M31898; AAA96417.1; JOINED.
DR EMBL; M31895; AAA96417.1; JOINED.
DR EMBL; M31896; AAA96417.1; JOINED.
DR EMBL; M31897; AAA96417.1; JOINED.
DR PIR; A31865; EABO.
FT NON_TER 1
SQ SEQUENCE 69 AA; 6202 MW; 2309361CA7D0662F CRC64;

Query Match 79.7%; Score 47; DB 2; Length 69;

Best Local Similarity 90.9%; Pred. No. 3; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAAKAAKYGA 13

Db 4 AAAKAAKYGA 14

RESULT 30

ELS SHEEP
ID ELS SHEEP STANDARD; PRT; 100 AA.
AC P11547;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Elastin (Tropoelastin) (Fragment).
GN Name=ELN;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85305763; PubMed=3839997;
RA Yoon K., Davidson J.M., Boyd C., May M., Luvalle P.,
RA Ornstein-Goldstein N., Smith J., Indik Z., Ross A., Golub E.,
RA Rosenbloom J.;
RT "Analysis of the 3' region of the sheep elastin gene.";
RL Arch. Biochem. Biophys. 241:684-691(1985).
CC -!- FUNCTION: Major structural protein of tissues such as aorta and nuchal ligament, which must expand rapidly and recover completely.
CC -!- SUBUNIT: The polymeric elastin chains are cross-linked together into an extensible 3D network.
CC -!- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
CC -!- PTM: The crosslinks are made of deaminated Lys.
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DR EMBL; M26188; AAA31515.1; ALT_SEQ.
DR EMBL; M26189; AAA31516.1; -.
DR PIR; S59623; S59623
KW Connective tissue; Repeat; Structural protein.
FT NON_TER 1
FT DISULFID 90 95 By similarity.
SQ SEQUENCE 100 AA; 8662 MW; 5C680C6A5AEE6786 CRC64;

Query Match 79.7%; Score 47; DB 1; Length 100;

Best Local Similarity 90.9%; Pred. No. 4; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAAKAAKYGA 13

Db 35 AAAKAAKYGA 45

Search completed: November 19, 2004, 16:36:44

Job time : 7.62838 secs

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OM protein - protein search, using sw model
Run on: November 19, 2004, 16:06:25 ; Search time 23.1638 Seconds
(without alignments)
2139.188 Million cell updates/sec

Title: US-09-743-818A-71
Perfect score: 2680
Sequence: 1 GGVPGAIPGGVPGGVFPYGA.....GGVAAAKSAKVAQAQLR 515

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database :

PIR 79:**

1: PIR1:**

2: PIR2:**

3: PIR3:**

4: PIR4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2642.5	98.6	792	1 EAHU	elastin precursor,
2	1964.5	73.3	770	2 S59623	tropoelastin - she
3	1842.5	68.8	747	1 EABO	elastin precursor,
4	1728.5	64.5	860	1 EAMS	elastin precursor
5	1675.5	62.5	864	1 EART	elastin precursor
6	1432.5	53.5	784	2 A26601	elastin precursor
7	509	19.0	1758	2 T29350	hypothetical prote
8	509	19.0	1759	2 T29351	collagen alpha 2(I
9	494.5	18.5	1763	2 S16366	collagen alpha 2(I
10	489.5	18.3	627	2 A44112	spidiroin 2, dragli
11	488.5	18.2	718	2 A36068	major ampullate fi
12	484.5	18.1	1901	2 F70806	hypothetical glyci
13	478	17.8	1669	1 CGHU4B	collagen alpha 1(I
14	466	17.4	1489	2 D70807	hypothetical glyci
15	456.5	17.0	1669	1 CGMS4B	collagen alpha 1(I
16	456	17.0	1691	1 S22917	collagen alpha 5(I
17	453.5	16.9	749	2 A70812	hypothetical glyci
18	450	16.8	1329	2 E70917	hypothetical glyci
19	446	16.6	767	2 E70895	hypothetical glyci
20	445.5	16.6	1049	1 CGB07S	collagen alpha 1(I
21	445.5	16.6	2639	2 T31328	fibroin - Chinese
22	444	16.6	1466	1 CGHU7L	collagen alpha 1(I
23	443.5	16.5	1464	2 S59856	collagen alpha 1(I
24	439	16.4	1464	1 CGHU1S	collagen alpha 1(I
25	437.5	16.3	882	2 E70812	hypothetical glyci
26	436.5	16.3	1042	1 CGCHLS	collagen alpha 1(I
27	436	16.3	741	2 G70917	hypothetical glyci
28	434.5	16.2	783	2 E70824	hypothetical glyci
29	434	16.2	1306	2 A70934	hypothetical glyci

30	432	16.1	1373	1 A43291	collagen alpha 2(I
31	430	16.0	754	2 A55267	collagen alpha 5(I
32	429	16.0	812	2 S31521	collagen COLP1 - f
33	428	16.0	778	2 F70963	hypothetical glyci
34	427	15.9	1366	1 CGHU2S	collagen alpha 2(I
35	425.5	15.9	744	1 A34246	collagen alpha 1(V
36	425.5	15.9	744	1 S23298	collagen alpha 1(V
37	425	15.9	1418	2 T45467	collagen alpha 1(I
38	424.5	15.8	779	1 CGB01S	collagen alpha 1(I
39	423.5	15.8	1453	2 S21626	collagen alpha 1(I
40	423	15.8	671	1 CGRT1S	collagen alpha 1(I
41	423	15.8	1492	2 A40333	collagen alpha 1(I
42	422.5	15.8	618	2 A70989	hypothetical glyci
43	421.5	15.7	603	2 A70770	hypothetical glyci
44	421.5	15.7	1712	1 CGHU2B	collagen alpha 2(I
45	420	15.7	801	2 F70824	hypothetical glyci
46	420	15.7	914	2 H70987	hypothetical glyci
47	420	15.7	1660	2 A70869	hypothetical glyci
48	419.5	15.7	1487	1 CGHU6C	collagen alpha 1(I
49	415	15.5	1486	1 B40333	collagen alpha 1(I
50	414	15.4	584	2 G70804	hypothetical glyci
51	412	15.4	744	2 S15435	collagen alpha 1(V
52	412	15.4	1419	2 A41182	collagen alpha 1(I
53	412	15.4	1487	2 B41182	collagen alpha 1(I
54	411	15.3	1381	2 E70806	hypothetical glyci
55	410.5	15.3	2944	2 A54849	collagen alpha 1(V
56	410	15.3	384	1 A26099	glycine-rich cell
57	409	15.3	1691	1 CGHU6B	collagen alpha 6(I
58	406.5	15.2	635	2 A57131	collagen alpha 2(V
59	406.5	15.2	964	1 CGCH2S	collagen alpha 2(I
60	405	15.1	743	1 S23779	collagen alpha 1(V
61	405	15.1	1497	2 I49607	procollagen type V
62	403.5	15.1	957	2 D70835	hypothetical glyci
63	403.5	15.1	1707	2 A33526	collagen alpha 2(I
64	403	15.0	853	2 A70896	hypothetical glyci
65	402.5	15.0	1079	2 B70807	hypothetical glyci
66	401.5	15.0	1690	1 CGHU1B	collagen alpha 4(I
67	401	15.0	674	2 S23297	collagen alpha 1(X
68	401	15.0	1496	1 CGHU2V	collagen alpha 2(V
69	400.5	14.9	408	2 S57483	glycin-rich protei
70	400.5	14.9	694	2 F70868	hypothetical glyci
71	399	14.9	1744	2 S40991	collagen alpha 1(I
72	398	14.9	680	1 CGHU1D	collagen alpha 1(X
73	396.5	14.8	907	2 A45560	sporozoite surface
74	395	14.7	641	1 QCB531	nuclear antigen EB
75	394	14.7	837	2 E70835	hypothetical glyci
76	393.5	14.7	1603	2 S23810	collagen alpha 1(X
77	393.5	14.7	1752	2 A45407	collagen alpha 3(I
78	392	14.6	606	2 H70816	hypothetical glyci
79	391.5	14.6	469	2 A24450	collagen alpha 2(V
80	390	14.6	921	2 S42617	collagen alpha 1(I
81	389.5	14.5	886	2 I50694	collagen alpha 1(I
82	388.5	14.5	1027	2 S28774	collagen alpha cha
83	386	14.4	1806	1 CGHU1E	collagen alpha 1(X
84	385.5	14.4	615	2 H70589	hypothetical glyci
85	384.5	14.3	714	2 A70807	hypothetical glyci
86	384.5	14.3	1538	2 H70846	hypothetical glyci
87	384	14.3	1024	2 S18251	collagen alpha 1(X
88	383.5	14.3	731	2 C70974	collagen alpha 2(I
89	382	14.3	677	2 S23296	collagen alpha 2(I
90	382	14.3	923	2 E70820	hypothetical glyci
91	381.5	14.2	673	1 CGB06C	collagen alpha 1(I
92	381.5	14.2	1670	1 CGHU3B	collagen alpha 3(I
93	381	14.2	921	2 S40495	collagen alpha 1(I
94	378	14.1	674	2 S13301	collagen alpha 1(X
95	377.5	14.1	920	2 B34493	collagen alpha 1(I
96	376.5	14.0	1775	2 A31893	collagen alpha 1(I
97	376	14.0	1414	1 S23809	collagen alpha 2(I
98	375.5	14.0	1549	2 I48103	type VII collagen
99	375	14.0	680	2 S31216	collagen alpha 1(X
100	373.5	13.9	1838	1 CGHU1V	collagen alpha 1(V

ALIGNMENTS

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RESULT 1
EAAHU
elastin precursor, long splice form - human
N/Alternate names: tropoelastin
C/Species: Homo sapiens (man)
C/Date: 22-Jun-1990 #sequence revision 26-Jul-1996 #text_change 09-Jul-2004
C/Accession: A32707; A33705; A30524; A53891
R/Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Sheppard, P.; Anderson, N.; Rosenbloom, J.
Proc. Natl. Acad. Sci. U.S.A. 84, 5680-5684, 1987
A/Title: Alternative splicing of human elastin mRNA indicated by sequence analysis of cDNA
A/Reference number: A32707; MUID:87289668; PMID:3039501
A/Accession: A32707
A/Molecule type: mRNA
A/Residues: 1-500,507-792 <IND>
A/Cross-references: UNIPROT:P15502; UNIPROT:Q9UMK5; GB:M16983; GB:J02948
R/Baehir, M.M.; Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Rosenbloom, J.C.; Abrams, W.
J. Biol. Chem. 264, 8887-8891, 1989
A/Title: Characterization of the complete human elastin gene. Delineation of unusual features
A/Reference number: A33705; MUID:89255358; PMID:2722804
A/Accession: A33705
A/Molecule type: DNA
A/Residues: 1-27 <BAS>
A/Cross-references: GB:J04821; NID:g182052; PIDN:AAAS2379.1; PID:g553276
R/Fazio, M.J.; Olsen, D.R.; Kauh, E.A.; Baldwin, C.T.; Indik, Z.; Ornstein-Goldstein, N.
J. Invest. Dermatol. 91, 458-464, 1988
A/Title: Cloning of full-length elastin cDNAs from a human skin fibroblast recombinant cDNA
A/Reference number: A30524; MUID:89009960; PMID:3171221
A/Accession: A30524
A/Molecule type: mRNA
A/Residues: 1-453,483-617,651-792 <PAZ>
A/Cross-references: EMBL:M36860; NID:g182061; PIDN:AAAS2382.1; PID:g182062
A/Note: this sequence represents a composite of several splice forms
R/Fazio, M.J.; Olsen, D.R.; Kuivaniemi, H.; Chu, M.L.; Davidson, J.M.; Rosenbloom, J.; U
Lab. Invest. 58, 270-277, 1988
A/Title: Isolation and characterization of human elastin cDNAs, and age-associated variation
A/Reference number: A53891; MUID:188156138; PMID:2831431
A/Accession: A53891
A/Molecule type: mRNA
A/Residues: 164-453,483-500,507-617,651-792 <PAZ>
A/Cross-references: GB:M24782; NID:g182063; PIDN:AAAS3190.1; PID:g182064
C/Comment: The term tropoelastin refers to a soluble precursor form of the extracellular
matrix protein.
C/Genetics:
A/Gene: GDB:ELN
A/Map position: 7q11.23-7q11.23
C/Superfamily: elastin
C/Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-792/Product: elastin #status predicted <MAT>
F:782-787/Disulfide bonds: #status predicted
Query Match 98.6%; Score 2642.5; DB 1; Length 792;
Best Local Similarity 93.6%; Pred. No. 2.1e-118; Indels 35; Gaps 2;
Matches 515; Conservative 0; Mismatches 0;
QY 1 GGVPGAIPGGVPGVFPYPCAGLGGALGGGKPLKVPVGGLAGAGLGAFFAVT 60
DB 27 GGVPGAIPGGVPGVFPYPCAGLGGALGGGKPLKVPVGGLAGAGLGAFFAVT 86
QY 61 FFGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVSAGAVVPPQAGVKPGVGL 120
DB 87 FFGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVSAGAVVPPQAGVKPGVGL 146
QY 121 PGVPGVGLPGARFPGVGLPGVPTCAGVKPKAPGVGGAFAGIPGVPGPGVPLGY 180
DB 147 PGVPGVGLPGARFPGVGLPGVPTCAGVKPKAPGVGGAFAGIPGVPGPGVPLGY 206
QY 181 PIKAPKLPGGYGLPYTTGKLPYGVGPGVAGAGKAGYPTGTGVGPAAAAAAXKAF 240

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DB 207 PIKAPKLPGGYGLPYTTGKLPYGVGPGVAGAGKAGYPTGTGVGPAAAAAAXKAF 266
QY 241 GAGAAAGVLPVGGAGVPGVPGAIPOIGGIAGVGTTPAAAAAAXKAAKAYGAAAGLVPGG 300
DB 267 GAGAAAGVLPVGGAGVPGVPGAIPOIGGIAGVGTTPAAAAAAXKAAKAYGAAAGLVPGG 326
QY 301 PGFGPGVGVPGAGVPGVPGAGIPVVPAGIPCAAVPGVVSPEAAAKAAKAAKYGAR 360
DB 327 PGFGPGVGVPGAGVPGVPGAGIPVVPAGIPCAAVPGVVSPEAAAKAAKAAKYGAR 386
QY 361 PGVGVGGIPTYTGAGAGGPGFGVGGIPGVAGVPSVGGVPGVGGVPGVGGISPEAQAAA 420
DB 387 PGVGVGGIPTYTGAGAGGPGFGVGGIPGVAGVPSVGGVPGVGGVPGVGGISPEAQAAA 446
QY 421 AKAAKY-----GVGTAAAAAAXKAAKAAQF----- 445
DB 447 AKAAKYAGAGAGVGLGLVPGQAAVPGVGTGTVGTEAAAAAAXKAAKAAQFALLNLA 506
QY 446 GLVPGVGVAPGVGVPAGVPGVGLAPGVGVPAGVGVAGVPGVPGVGGVAAAAAKSA 505
DB 507 GLVPGVGVAPGVGVPAGVPGVGLAPGVGVPAGVGVAGVPGVPGVGGVAAAAAKSA 566
QY 506 AKVAAKAQLR 515
DB 567 AKVAAKAQLR 576
RESULT 2
tropoelastin - sheep
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C/Date: 23-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S59623; A24758
R/Mauch, J.C.; Sandberg, L.B.; Roos, P.J.; Jimenez, F.; Christiano, A.M.; Deak, S.B.; B
Matrix Biol. 14, 635-641, 1994
A/Title: Extensive alternate exon usage at the 5' end of the sheep tropoelastin gene.
A/Reference number: S59623
A/Accession: S59623
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-770 <MAU>
A/Cross-references: UNIPROT:P11547
R/Yoon, K.; Davidson, J.M.; Boyd, C.; May, M.; LuValle, P.; Ornstein-Goldstein, N.; Smit
Arch. Biochem. Biophys. 241, 684-691, 1985
A/Title: Analysis of the 3' region of the sheep elastin gene.
A/Reference number: A24758; MUID:85305763; PMID:3839997
A/Accession: A24758
A/Molecule type: mRNA
A/Residues: 655-669,671-716,732-770 <YOO>
C/Superfamily: elastin
C/Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
F:760-765/Disulfide bonds: #status predicted
Query Match 73.3%; Score 1964.5; DB 2; Length 770;
Best Local Similarity 72.2%; Pred. No. 2.3e-86;
Matches 411; Conservative 18; Mismatches 55; Indels 85; Gaps 16;
QY 1 GGVPGAIPGGVPGVFPYPCAGLGGALGGGKPLKVPVGGLAGAGLGA-GLGAFFAV 59
DB 27 GGVLGAVPGVPGVPGVFPYPCAGLGGVGLGVPKPAKPGVGLVPGVGLGAGSGLLPAG 86
QY 60 TTPGAL--VPGGVADAAAAYK--AAKAGA---GLGSGVPGVGLGVSAGAVVPPQGA--- 108
DB 87 APFGFFGAGGGAAGAAAAYKAAKAGAGLGGVGGIGVGGVGLGVSTGAVFQLGAGVGV 146
QY 109 GVKPKVPGVGLPGVPGVGLP--GARFPGVGLFVPTGAGVKPKAPGVGGAFAGIPGV 166
DB 147 GVKPKVPGVGLPGVPGVGLP--GARFPGVGLP--GARFPGVGLP--GARFPGVGLP-- 206
QY 167 GFPGPGVPGVPLGYPIKAPKLPGGYGLPYTTGKLPYGVGPGVAGAGKAGYPTGTGVGP 226
DB 207 GFPGPGVPGVPLGYPIKAPKLPGGYGLPYTTGKLPYGVGPGVAGAGKAGYPTGTGVGP 266

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RESULT 1
Q14234 PRELIMINARY; PRT; 757 AA.
AC Q14234;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Elastin.
OS Name=ELN;
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87289668; PubMed=3039501;
RA Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
RA Rosenbloom J.C., Peltonen-Lindfors J., Rosenbloom J.,
RT "Alternative splicing of human elastin mRNA indicated by sequence
RT analysis of cloned genomic and complementary DNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87274906; PubMed=3038460;
RA Indik Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J.,
RA Rosenbloom J., Ornstein-Goldstein N.;
RT "Structure of the 3' region of the human elastin gene: great abundance
RT of Alu repetitive sequences and few coding sequences.";
RL Connect. Tissue Res. 16:197-211(1987).
DR EMBL; M17282; AAC98395.1; JOINED.
DR EMBL; M16983; AAC98395.1; JOINED.
DR EMBL; M17265; AAC98395.1; JOINED.
DR EMBL; M17266; AAC98395.1; JOINED.
DR EMBL; M17267; AAC98395.1; JOINED.
DR EMBL; M17268; AAC98395.1; JOINED.
DR EMBL; M17270; AAC98395.1; JOINED.
DR EMBL; M17271; AAC98395.1; JOINED.
DR EMBL; M17272; AAC98395.1; JOINED.
DR EMBL; M17273; AAC98395.1; JOINED.
DR EMBL; M17274; AAC98395.1; JOINED.
DR EMBL; M17275; AAC98395.1; JOINED.
DR EMBL; M17276; AAC98395.1; JOINED.
DR EMBL; M17277; AAC98395.1; JOINED.
DR EMBL; M17278; AAC98395.1; JOINED.
DR EMBL; M17279; AAC98395.1; JOINED.
DR EMBL; M17280; AAC98395.1; JOINED.
DR EMBL; M17281; AAC98395.1; JOINED.
DR GO; GO:0005578; C:extracellular matrix; NAS.
DR GO; GO:0030023; F:extracellular matrix constituent conferring...; NAS.
DR InterPro; IPR001451; Hexapep.transf.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; HEXAPEP TRANSFERASES.
DR PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.
SQ SEQUENCE 757 AA; 66136 MW; 23B7FE58AF85CA8 CRC64;

Query Match 100.0%; Score 2680; DB 2; Length 757;
Best Local Similarity 100.0%; Pred. No. 1.3e-99;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGVPGAIPGGVPGGVFPYAGLGGALGGALGGKPLKVPVGGLAGAGLGGAGLGAFAVPT 60
DB 27 GGVPGAIPGGVPGGVFPYAGLGGALGGALGGKPLKVPVGGLAGAGLGGAGLGAFAVPT 86
QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVAGAVVPPQAGVKKPQVPGVGL 120
DB 87 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVAGAVVPPQAGVKKPQVPGVGL 146
QY 121 PGVYPGVGLPGARFPGGVLPVPGVTPGAGVKKPAGVCGAFAGVPGVPGVPLGY 180
DB 147 PGVYPGVGLPGARFPGGVLPVPGVTPGAGVKKPAGVCGAFAGVPGVPGVPLGY 206
QY 181 PIKAPKLPGGYGLPYTTTCKLPYGYGPGVGAAGAKAGYPTGTGVPQAAAAAKAAKF 240
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RESULT 2

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Q75MU5 PRELIMINARY; PRT; 757 AA.
ID Q75MU5;
AC Q75MU5;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical protein ELN.
GN Name=ELN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22737999; PubMed=12853948;
RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
RA Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
RA Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
RA Fewell G.A., Delehaunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
RA Vanbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
RA Ozersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris J.,
RA Strong C.M., Hou S., Tomlinson C., Rohlfing T., Rock S.M.,
RA Kozlowicz-Reilly A., Leonard S., Daughin-Kohlberg S.,
RA Tin-Wollam A.M., Abbott A., Minx P., Maupin R., Strowmatt C.,
RA Latreille P., Miller N., Johnson D., Mullis J.W., Spieth J.,
RA Bieri T.A., Nelson J.O., Berkowicz N., Wohlmann P.E., Cook L.L.,
RA Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
RA Clifton S.W., Chisoe S.L., Marra M.A., Raymond C., Haugen E.,
RA Gillett W., Zhou Y., James R., Phelps K., Iadamoto S., Bubb K.,
RA Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,
RA Baerisch R.A., Brent M.R., Keibler E., Flicke P., Bork P., Suyama M.,
RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,
RA Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
RA Waterston R.H., Wilson R.K.;
RT "The DNA sequence of human chromosome 7.";
RL Nature 424:157-164(2003).
RN [2]
RP SEQUENCE FROM N.A.
RX Waterston R.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX Wilson R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005056; AAS07435.1; -.
DR InterPro; IPR001451; Hexapep.transf.
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DR InterPro; IPR003979; tropoelastin.
 DR PRINTS; PRO1500; TROPOLASTIN.
 DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 757 AA; 66106 MW; 2824F955D8360738 CRC64;
 Query Match 99.9%; Score 2676; DB 2; Length 757;
 Best Local Similarity 99.8%; Pred. No. 1.8e-99;
 Matches 514; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGVPGALPGGVPGGVFPVPGAGLGGALGPGGKPLKPVPGGLAGLGGAGLGAFAFPAVT 60
 DB 27 GGVPGALPGGVPGGVFPVPGAGLGGALGPGGKPLKPVPGGLAGLGGAGLGAFAFPAVT 86
 QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVSAGAVVPGAGVKGKVPVGVGL 120
 DB 87 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVSAGAVVPGAGVKGKVPVGVGL 146
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 QY 181 PIKAPKLPGGYGLPYTTGKLPYGVPGGVGAGAAKAGAYPTGTGTGVPQAAAAAATAAKAF 240
 DB 207 PIKAPKLPGGYGLPYTTGKLPYGVPGGVGAGAAKAGAYPTGTGTGVPQAAAAAATAAKAF 266
 QY 241 GAGAAGVLPVGGAGVPGVPGAIPGIGIAGVGTTPAAAAAAAATAAKAAGLVPGG 300
 DB 267 GAGAAGVLPVGGAGVPGVPGAIPGIGIAGVGTTPAAAAAAAATAAKAAGLVPGG 326
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 QY 481 VGVAPGVGVPAGIPGGVAAAAAATAAKAQAQLR 515
 DB 507 VGVAPGVGVPAGIPGGVAAAAAATAAKAQAQLR 541
 RESULT 3
 ID AAS07435 PRELIMINARY; PRT; 757 AA.
 AC AAS07435;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DE 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein ELN.
 GN ELN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=22737999; PubMed=12853948;
 RA Hallier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
 RA Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
 RA Wyllie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
 RA Fewell G.A., Delehaunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
 RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
 RA Vanbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
 RA Ozersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
 RA Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
 RA Kozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
 RA Tin-Wollam A.M., Abbott A., Minx P., Maupin R., Strowmatt C.,

RA Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,
 RA Wendt M.C., Yang S.P., Schultz B.R., Wallis J.W., Spieth J.,
 RA Bieri T.A., Nelson J.O., Berkowicz N., Wohldmann P.E., Cook L.L.,
 RA Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
 RA Clifton S.W., Chisoe S.L., Marra M.A., Raymond C., Haugen E.,
 RA Gillett W., Zhou Y., James R., Phelps K., Iadonato S., Bub K.,
 RA Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,
 RA Baertsch R.A., Brent M.R., Keibler E., Flicek P., Bork P., Suyama M.,
 RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.F., Gish W.R.,
 RA Bady S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
 RA Waterston R.H., Wilson R.K.;
 RT "The DNA sequence of human chromosome 7.";
 RL Nature 424:157-164(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Du H., Rohlfing T., Strong C.;
 RT "The sequence of Homo sapiens BAC clone CTB-51J22.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Waterston R.H.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Waterston R.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Wilson R.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 RL EMBL; ACO05056; AAS07435.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 757 AA; 66106 MW; 2B24F955D8360738 CRC64;
 Query Match 99.9%; Score 2676; DB 2; Length 757;
 Best Local Similarity 99.8%; Pred. No. 1.8e-99;
 Matches 514; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGVPGALPGGVPGGVFPVPGAGLGGALGPGGKPLKPVPGGLAGLGGAGLGAFAFPAVT 60
 DB 27 GGVPGALPGGVPGGVFPVPGAGLGGALGPGGKPLKPVPGGLAGLGGAGLGAFAFPAVT 86
 QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVSAGAVVPGAGVKGKVPVGVGL 120
 DB 87 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVSAGAVVPGAGVKGKVPVGVGL 146
 QY 121 PGVYPGGVLPGARFPVPGVGLPGVPTGAGVKPKAPGVGGAFAGIPGVGPGPGQPGVPLGY 180
 DB 147 PGVYPGGVLPGARFPVPGVGLPGVPTGAGVKPKAPGVGGAFAGIPGVGPGPGQPGVPLGY 206
 QY 181 PIKAPKLPGGYGLPYTTGKLPYGVPGGVGAGAAKAGAYPTGTGTGVPQAAAAAATAAKAF 240
 DB 207 PIKAPKLPGGYGLPYTTGKLPYGVPGGVGAGAAKAGAYPTGTGTGVPQAAAAAATAAKAF 266
 QY 241 GAGAAGVLPVGGAGVPGVPGAIPGIGIAGVGTTPAAAAAAAATAAKAAGLVPGG 300
 DB 267 GAGAAGVLPVGGAGVPGVPGAIPGIGIAGVGTTPAAAAAAAATAAKAAGLVPGG 326
 QY 301 PFGPGVGVPGAGVPGVPGAGIPVVPVPGAGIPGAAPVGVSPVPGVPGVPGVGLSPVPAQAAAA 420
 DB 327 PFGVGVGIPVYGVGAGFPFGVGVGIPGVAGVPGVPGVPGVPGVPGVGLSPVPAQAAAA 446
 QY 421 AKAAKGVGTTPAAAAAATAAKAAGLVPGVPGVPGVPGVPGVPGVPGVGLSPVPAQAAAA 480
 DB 447 AKAAKGVGTTPAAAAAATAAKAAGLVPGVPGVPGVPGVPGVPGVPGVGLSPVPAQAAAA 506
 QY 481 VGVAPGVGVPAGIPGGVAAAAAATAAKAQAQLR 515
 DB 507 VGVAPGVGVPAGIPGGVAAAAAATAAKAQAQLR 541

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RESULT 4
ELS_HUMAN
ID ELS_HUMAN STANDARD; PRT; 730 AA.
AC P1502; Q14233; Q14238;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Elastin precursor (Tropoelastin).
GN Name=ELN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A. (ISOFORM B).
RP MEDLINE=87289668; PubMed=3039501;
RA Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
RA Rosenbloom J.C., Peltonen L., Rosenbloom J.
RT "Alternative splicing of human elastin mRNA indicated by sequence
RT analysis of cloned genomic and complementary DNA."
RL Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
[2]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RP TISSUE=Skin fibroblast;
RC TISSUE=Skin fibroblast;
RX MEDLINE=89009960; PubMed=3171221;
RA Fazio M.J., Olsen D.R., Kauh E.A., Baldwin C.T., Indik Z.,
RA Ornstein-Goldstein N., Yeh H., Rosenbloom J., Vitto J.;
RT "Cloning of full-length elastin cDNAs from a human skin fibroblast
RT recombinant cDNA library; further elucidation of alternative splicing
RT utilizing exon-specific oligonucleotides."
RL J. Invest. Dermatol. 91:458-464(1988).
[3]
RN SEQUENCE OF 164-724 FROM N.A. (ISOFORM B).
RP TISSUE=Placenta;
RX MEDLINE=88156138; PubMed=2831431;
RA Fazio M.J., Olsen D.R., Kuivaniemi H., Chu M.L., Davidson J.M.,
RA Rosenbloom J., Vitto J.;
RT "Isolation and characterization of human elastin cDNAs, and age-
RT associated variation in elastin gene expression in cultured skin
RT fibroblasts."
RL Lab. Invest. 58:270-277(1988).
[4]
RN SEQUENCE OF 603-730 FROM N.A.
RP TISSUE=Hippocampus, and Placenta;
RX MEDLINE=96291399; PubMed=8689688;
RA Frangiskakis J.M., Ewart A.K., Morris C.A., Bertrand J.,
RA Robinson B.F., Klein B.P., Ensing G.J., Everett L.A., Green E.D.,
RA Proeschel C., Gutowski N.J., Noble M., Atkinson D.L., Odelberg S.J.,
RA Keating M.T.;
RT "LIM-kinase1 hemizyosity implicated in impaired visuospatial
RT constructive cognition."
RL Cell 86:59-69(1996).
[5]
RN INVOLVEMENT IN CUTIS LAXA.
RX MEDLINE=99091639; PubMed=9873040;
RA Zhang M.-C., He L., Giro M., Yong S.L., Tiller G.E., Davidson J.M.;
RT "Cutis laxa arising from frameshift mutations in exon 30 of the
RT elastin gene (ELN)."
RL J. Biol. Chem. 274:981-986(1999).
[6]
RN INVOLVEMENT IN SVAS.
RP PubMed=10942104;
RX Urban Z., Michels V.V., Thibodeau S.N., Davis E.C., Bonnefont J.-P.,
RX Munnich A., Eyskens B., Gewillig M., Devriendt K., Boyd C.D.;
RT "Isolated supravalvular aortic stenosis: functional haploinsufficiency
RT of the elastin gene as a result of nonsense-mediated decay."
RL Hum. Genet. 106:577-588(2000).
CC -!- FUNCTION: Major structural protein of tissues such as aorta and
CC nuchal ligament, which must expand rapidly and recover completely.
CC -!- SUBUNIT: The polymeric elastin chains are cross-linked together
CC into an extensible 3D network.
CC
```

```
CC -!- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=1;
CC IsoId=PI5502-1; Sequence=Displayed;
CC Name=2;
CC IsoId=PI5502-2; Sequence=VSP_004243;
CC -!- PTM: The crosslinks are made of deaminated Lys.
CC -!- DISEASE: Defects in ELN are a cause of autosomal dominant cutis
CC laxa [MIM:123700]. Cutis laxa is a rare connective tissue disorder
CC characterized by loose, hyperextensible skin with decreased
CC resilience and elasticity leading to a premature aged appearance.
CC The skin changes are often accompanied by extracutaneous
CC manifestations, including pulmonary emphysema, bladder
CC diverticula, pulmonary artery stenosis and pyloric stenosis.
CC -!- DISEASE: Haploinsufficiency of ELN may be the cause of certain
CC cardiovascular and musculo-skeletal abnormalities observed in
CC Williams-Beuren syndrome (WBS) [MIM:194050]. WBS is a rare
CC developmental disorder and a contiguous gene deletion syndrome
CC involving genes from chromosome band 7q11.23.
CC -!- DISEASE: Defects in ELN are the cause of supravalvular aortic
CC stenosis (SVAS) [MIM:185500]. SVAS is a congenital narrowing of
CC the ascending aorta which can occur sporadically, as an autosomal
CC dominant condition, or as one component of Williams-Beuren
CC syndrome.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M17282; AAC98394.1; -
CC EMBL; M16983; AAC98394.1; JOINED.
CC EMBL; M17265; AAC98394.1; JOINED.
CC EMBL; M17266; AAC98394.1; JOINED.
CC EMBL; M17267; AAC98394.1; JOINED.
CC EMBL; M17268; AAC98394.1; JOINED.
CC EMBL; M17270; AAC98394.1; JOINED.
CC EMBL; M17271; AAC98394.1; JOINED.
CC EMBL; M17272; AAC98394.1; JOINED.
CC EMBL; M17273; AAC98394.1; JOINED.
CC EMBL; M17275; AAC98394.1; JOINED.
CC EMBL; M17276; AAC98394.1; JOINED.
CC EMBL; M17277; AAC98394.1; JOINED.
CC EMBL; M17278; AAC98394.1; JOINED.
CC EMBL; M17279; AAC98394.1; JOINED.
CC EMBL; M17280; AAC98394.1; JOINED.
CC EMBL; M17281; AAC98394.1; JOINED.
CC EMBL; M36860; AAA52382.1; -
CC EMBL; M24782; AAA53190.1; -
CC EMBL; U62292; AAB17544.1; -
CC EMBL; X15603; CAA33627.1; -
CC PIR; A32707; EAHU
CC HSSP; P50099; 1ZFU.
CC Genew; HGNC:3327; ELN.
CC MIM; 130160; -
CC MIM; 123700; -
CC MIM; 194050; -
CC MIM; 185500; -
CC GO; GO:0005578; C:extracellular matrix; TAS.
CC GO; GO:0005615; C:extracellular space; TAS.
CC GO; GO:0005201; F:extracellular matrix structural constituent; TAS.
CC GO; GO:0008283; P:cell proliferation; TAS.
CC GO; GO:0008015; P:circulation; TAS.
CC GO; GO:0009887; P:organogenesis; TAS.
CC GO; GO:0007585; P:respiratory gaseous exchange; TAS.
CC InterPro; IPR003979; tropoelastin.
CC PRINTS; PRO1500; TROPOLASTIN.
CC Alternative splicing; Connective tissue; Repeat; Signal;
CC KW
```

KW Structural protein; Williams-Beuren syndrome.

FT SIGNAL 1 26
FT CHAIN 27 730 Elastin.
FT DISULFID 720 725 By similarity.
FT VARSPLIC 472 477 Missing (in isoform 2).
FT /FTID=VSP_004243.
SQ SEQUENCE 730 AA; 63260 MW; AB06D15BA567AE46 CRC64;

Query Match 99.5%; Score 2667; DB 1; Length 730;
Best Local Similarity 98.8%; Pred. No. 4e-99;
Matches 515; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

QY 1 GGVPCAI PGVPGGVYFPCAGLGGALGGKPLKPVPGGLAGLGGALGAGLGAFFAVT 60
Db 27 GGVPCAI PGVPGGVYFPCAGLGGALGGKPLKPVPGGLAGLGGALGAGLGAFFAVT 86
QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVLSAGAVVPPQAGVPGKVPVGL 120
Db 87 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVLSAGAVVPPQAGVPGKVPVGL 146
QY 121 PGVPGVLPGARFPFGVGLPGVPTGAGVKPKPCVGGAFAGIPGVPGPQPCVPLGY 180
Db 147 PGVPGVLPGARFPFGVGLPGVPTGAGVKPKPCVGGAFAGIPGVPGPQPCVPLGY 206
QY 181 PIKAPLPGGYLPTTGTGKLPYGYGPGVAGAGKAGYPTGTGVPQAAAAAKAAKF 240
Db 207 PIKAPLPGGYLPTTGTGKLPYGYGPGVAGAGKAGYPTGTGVPQAAAAAKAAKF 266
QY 241 GAGAAGVLPVGGAGVPGVPCAIPIGIGIAGVGTTPAAAAAAYKAAKAGLVPFG 300
Db 267 GAGAAGVLPVGGAGVPGVPCAIPIGIGIAGVGTTPAAAAAAYKAAKAGLVPFG 326
QY 301 PGFGPVGVPGAGVPGVPGAGIPVVPVPGAGIPGAAVPGVVSPEAAKAAKAAKYGAR 360
Db 327 PGFGPVGVPGAGVPGVPGAGIPVVPVPGAGIPGAAVPGVVSPEAAKAAKAAKYGAR 386
QY 361 PGVGVGIPVTVGAGGFPFGVPGVGGIPGVAGVPSVGGVPGVPGVGSPEAQAAA 420
Db 387 PGVGVGIPVTVGAGGFPFGVPGVGGIPGVAGVPSVGGVPGVPGVGSPEAQAAA 446
QY 421 AKAAKYGVTTPAAAAAAYKAAKAGF-----GLVPGVPGVPGVAGVPGVPGVGLAPG 474
Db 447 AKAAKYGVTTPAAAAAAYKAAKAGFALLNLNLAGLVPGVPGVPGVAGVPGVPGVGLAPG 506
QY 475 VGVAPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 515
Db 507 VGVAPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 547

RESULT 5

Q7Z3F5
ID Q7Z3F5 PRELIMINARY; PRT; 711 AA.
AC Q7Z3F5
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFp686F06102.
GN Name=DKFp686F06102;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Human fetal kidney;
RC Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Anid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX537939; CAD97910.1;
DR InterPro; IPR001451; Hexapep.transf.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 711 AA; 61765 MW; 95B624A99B4A989B CRC64;

Query Match

Best Local Similarity 99.2%; Score 2659.5; DB 2; Length 711;
Matches 514; Conservative 0; Mismatches 1; Indels 5; Gaps 1;

QY 1 GGVPCAI PGVPGGVYFPCAGLGGALGGKPLKPVPGGLAGLGGALGAGLGAFFAVT 60
Db 27 GGVPCAI PGVPGGVYFPCAGLGGALGGKPLKPVPGGLAGLGGALGAGLGAFFAVT 86
QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVLSA-----GAVVPPQAGVPGKVP 115
Db 87 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVLSA-----GAVVPPQAGVPGKVP 146
QY 116 PGVGLPGVPGVLPGARFPFGVGLPGVPTGAGVKPKAPGVGGAFAGIPGVPGPQPG 175
Db 147 PGVGLPGVPGVLPGARFPFGVGLPGVPTGAGVKPKAPGVGGAFAGIPGVPGPQPG 206
QY 176 VPLGVPTIKAPLPGGYGLPYTTGKLPYGYGPGVAGAGKAGYPTGTGVPQAAAAAK 235
Db 207 VPLGVPTIKAPLPGGYGLPYTTGKLPYGYGPGVAGAGKAGYPTGTGVPQAAAAAK 266
QY 236 AAAXFGAAGVLPVGGAGVPGVPGAIPIGIGIAGVGTTPAAAAAAYKAAKAGAAAG 295
Db 267 AAAXFGAAGVLPVGGAGVPGVPGAIPIGIGIAGVGTTPAAAAAAYKAAKAGAAAG 326
QY 296 LVPGGPGFGVPGVPGAGVPGVPGAGIPVVPVPGAGIPGAAVPGVVSPEAAKAAKAA 355
Db 327 LVPGGPGFGVPGVPGAGVPGVPGAGIPVVPVPGAGIPGAAVPGVVSPEAAKAAKAA 386
QY 356 KYGARPGVGGIPVTVGAGGFPFGVPGVGGIPGVAGVPSVGGVPGVPGVGSPEA 415
Db 387 KYGARPGVGGIPVTVGAGGFPFGVPGVGGIPGVAGVPSVGGVPGVPGVGSPEA 446
QY 416 QAAAAKAAKYGVTTPAAAAAAYKAAKAGLVPGVPGVPGVPGVPGVPGVGLAPG 475
Db 447 QAAAAKAAKYGVTTPAAAAAAYKAAKAGLVPGVPGVPGVPGVPGVPGVGLAPG 506
QY 476 GVPAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 515
Db 507 GVPAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 546

RESULT 6

Q15337
ID Q15337 PRELIMINARY; PRT; 602 AA.
AC Q15337
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Elastin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97358574; PubMed=9215670;
RA Li D.Y., Toland A.E., Boak B.B., Atkinson D.L., Ensing G.J.,
RA Morris C.A., Keating M.T.;
RT "Elastin point mutations cause an obstructive vascular disease,
supravalvular aortic stenosis".
RL Hum. Mol. Genet. 6:1021-1028(1997).
DR EMBL; U93037; AAB65620.1;
DR EMBL; U93034; AAB65620.1; JOINED.
DR EMBL; U93035; AAB65620.1; JOINED.
DR EMBL; U93036; AAB65620.1; JOINED.
DR GO; GO:0005578; C:extracellular matrix; IPA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro; IPR001451; Hexapep.transf.
DR PRINTS; PR01500; TROPOLASTIN.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
FT NON_TER 1

analysis of cloned genomic and complementary DNA.";
Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684 (1987).

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RT  [2]
RN  SEQUENCE FROM N.A.
RP  MEDLINE=87274906; PubMed=3038460;
RA  Indik Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J.,
RA  Rosenbloom J., Ornstein-Goldstein N.;
RT  "Structure of the 3' region of the human elastin gene: great abundance
RT  of Alu repetitive sequences and few coding sequences.";
RL  Connect. Tissue Res. 16:197-211 (1987).
DR  EMBL; M17282; AAC98393.1; JOINED.
DR  EMBL; M16983; AAC98393.1; JOINED.
DR  EMBL; M17265; AAC98393.1; JOINED.
DR  EMBL; M17266; AAC98393.1; JOINED.
DR  EMBL; M17267; AAC98393.1; JOINED.
DR  EMBL; M17268; AAC98393.1; JOINED.
DR  EMBL; M17271; AAC98393.1; JOINED.
DR  EMBL; M17272; AAC98393.1; JOINED.
DR  EMBL; M17273; AAC98393.1; JOINED.
DR  EMBL; M17275; AAC98393.1; JOINED.
DR  EMBL; M17276; AAC98393.1; JOINED.
DR  EMBL; M17277; AAC98393.1; JOINED.
DR  EMBL; M17278; AAC98393.1; JOINED.
DR  EMBL; M17279; AAC98393.1; JOINED.
DR  EMBL; M17281; AAC98393.1; JOINED.
DR  HSP; P50099; 12FJ.
DR  GO; GO:0005578; C:extracellular matrix; NAS.
DR  GO; GO:0030023; F:extracellular matrix constituent conferring. . .; NAS.
DR  InterPro; IPR001451; Hexapep.transf.
DR  InterPro; IPR003979; tropoelastin.
DR  PRINTS; PR01500; TROPOELASTIN.
DR  PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.
SQ  SEQUENCE 687 AA; 59529 MW; 864068C4C8E3F88F-CRC64;
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Query Match          96.0%; Score 2571.5; DB 2; Length 687;
Best Local Similarity 96.3%; Pred. No. 2.5e-95;
Matches 496; Conservative 0; Mismatches 0; Indels 19; Gaps 1;

QY  1  GGVPGLPGGVPGGVFPYGGAGLGGALGGGKPLKPVPGGLAGAGLGGAGLGAFFAVT 60
Db   27  GGVPGLPGGVPGGVFPYGGAGLGGALGGGKPLKPVPGGLAGAGLGGAGLGAFFAVT 86
QY  61  FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVSAGAVVPPQAGVPGKVPVGVGL 120
Db   87  FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVSAGAVVPPQAGVPGKVPVGVGL 146
QY  121  PGVYPGGVLPGARFPGGVGLPYGTGAGVKKAPGVGGAFAGIPGVGPGGPGQPGVPLGY 180
Db   147  PGVYPGGVLPGARFPGGVGLPYGTGAGVKKAPGVGGAFAGIPGVGPGGPGQPGVPLGY 206
QY  181  PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAGKAGYPTGTGVPQAAAAAATAAKAAXF 240
Db   147  PGVYPGGVLPGARFPGGVGLPYGTGAGVKKAPGVGGAFAGIPGVGPGGPGQPGVPLGY 206
QY  241  GAGAAGVLPGVGGAGVPGVPGAGIPGIGGIAGVGTTPAAAAAATAAKAAXF 240
Db   207  PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAGKAGYPTGTGVPQAAAAAATAAKAAXF 266
QY  267  GAGAAGVLPGVGGAGVPGVPGAGIPGIGGIAGVGTTPAAAAAATAAKAAXF 300
Db   207  PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAGKAGYPTGTGVPQAAAAAATAAKAAXF 266
QY  301  PGFGPGVWGVPGAGVPGVPGAGIPVVPAGIPGAAVPGVSPVSPVSPVSPVSPVSPVSPV 360
Db   327  PGFGPGVWGVPGAGVPGVPGAGIPVVPAGIPGAAVPGVSPVSPVSPVSPVSPVSPVSPV 366
QY  361  PGVGVGGIPTYGVGGAGFPFGVGGGIPGVAGVSPVSPVSPVSPVSPVSPVSPVSPVSPV 420
Db   387  PGVGVGGIPTYGVGGAGFPFGVGGGIPGVAGVSPVSPVSPVSPVSPVSPVSPVSPVSPV 446
QY  421  AKAAYKGVGTTPAAAAAATAAKAAXFGLVPGVAGVPGVAGVPGVAGVPGVAGVPGVAGV 480
Db   447  AKAAYK-----GLVPGVAGVPGVAGVPGVAGVPGVAGVPGVAGVPGVAGVPGVAGV 487
QY  481  VGVAPGVAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 515
Db   488  VGVAPGVAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 522
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RESULT 10
Q6P0L4
ID Q6P0L4 PRELIMINARY; PRT; 658 AA.
AC Q6P0L4;

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RESULT 9
Q7Z316
ID Q7Z316 PRELIMINARY; PRT; 687 AA.
AC Q7Z316;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
DE Hypothetical protein DKFZp686O21208 (Fragment).
GN Name=DKFZp686O21208;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538199; CAD98065.1; -.
DR InterPro; IPR001451; Hexapep.transf.
DR PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.
KW Hypothetical protein.
FT NON TER
SQ SEQUENCE 687 AA; 59847 MW; 79232A191DC1F10F-CRC64;
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Query Match          93.3%; Score 2500.5; DB 2; Length 687;
Best Local Similarity 94.2%; Pred. No. 1.7e-92;
Matches 485; Conservative 0; Mismatches 1; Indels 29; Gaps 2;

QY  1  GGVPGLPGGVPGGVFPYGGAGLGGALGGGKPLKPVPGGLAGAGLGGAGLGAFFAVT 60
Db   37  GGVPGLPGGVPGGVFPY-----ALGGPGKPLKPVPGGLAGAGLGGAGLGAFFAVT 86
QY  61  FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVSAGAVVPPQAGVPGKVPVGVGL 120
Db   87  FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVSAGAVVPPQAGVPGKVPVGVGL 146
QY  121  PGVYPGGVLPGARFPGGVGLPYGTGAGVKKAPGVGGAFAGIPGVGPGGPGQPGVPLGY 180
Db   147  PGVYPGGVLPGARFPGGVGLPYGTGAGVKKAPGVGGAFAGIPGVGPGGPGQPGVPLGY 206
QY  181  PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAGKAGYPTGTGVPQAAAAAATAAKAAXF 240
Db   207  PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAGKAGYPTGTGVPQAAAAAATAAKAAXF 266
QY  241  GAGAAGVLPGVGGAGVPGVPGAGIPGIGGIAGVGTTPAAAAAATAAKAAXF 300
Db   267  GAGAAGVLPGVGGAGVPGVPGAGIPGIGGIAGVGTTPAAAAAATAAKAAXF 326
QY  301  PGFGPGVWGVPGAGVPGVPGAGIPVVPAGIPGAAVPGVSPVSPVSPVSPVSPVSPVSPV 360
Db   327  PGFGPGVWGVPGAGVPGVPGAGIPVVPAGIPGAAVPGVSPVSPVSPVSPVSPVSPVSPV 366
QY  361  PGVGVGGIPTYGVGGAGFPFGVGGGIPGVAGVSPVSPVSPVSPVSPVSPVSPVSPVSPV 420
Db   387  PGVGVGGIPTYGVGGAGFPFGVGGGIPGVAGVSPVSPVSPVSPVSPVSPVSPVSPVSPV 446
QY  421  AKAAYKGVGTTPAAAAAATAAKAAXFGLVPGVAGVPGVAGVPGVAGVPGVAGVPGVAGV 480
Db   447  AKAAYK-----GLVPGVAGVPGVAGVPGVAGVPGVAGVPGVAGVPGVAGVPGVAGV 487
QY  481  VGVAPGVAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 515
Db   488  VGVAPGVAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 522
```

RESULT 10
Q6P0L4
ID Q6P0L4 PRELIMINARY; PRT; 658 AA.
AC Q6P0L4;

DT	05-JUL-2004	(TrEMBLrel. 27, Created)	
DT	05-JUL-2004	(TrEMBLrel. 27, Last sequence update)	
DT	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)	
DE	ELN protein.		
GN	Name=ELN;		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Eye;		
RX	MEDLINE=2238257; PubMed=12477932;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,		
RA	Whiting M., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Blakesley R.W., Gough J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,		
RA	Jones S.J., Marra M.A.;		
RA	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Eye;		
RA	Strausberg R.;		
RL	Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC065566; AAH65566.1; -		
DR	InterPro; IPR001451; Hexapep trans.		
DR	InterPro; IPR003979; tropoelastin.		
DR	PRINTS; PR01500; TROPCELASTIN.		
DR	PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.		
SQ	SEQUENCE 658 AA; 56680 MW; 5DAFC00D16A2F94E CRC64;		
	Query Match 90.0%; Score 2411.5; DB 2; Length 658;		
	Best Local Similarity 93.2%; Pred. No. 5.6e-89;		
	Matches 468; Conservative 0; Mismatches 1; Indels 33; Gaps 2;		
QY	1	GGVPGAIPGVGGVPGVPGAGLGGALGGALGGKPKLPVPGGLAGAGLGAFFAVT	60
DB	27	GGVPGAIPGVGGVPGVPGAGLGGALGGALGGKPKLPVPGGLAGAGLGAFFAVT	86
QY	61	FPGALVPGGVADAAAAYKAAKAGAGLGGVPGGLGVSAGAVVPGKPKVPGVGL	120
DB	87	FPGALVPGGVADAAAAYKAAKAGAGLGGVPGGLGVSAGAVVPGKPKVPGVGL	146
QY	121	PGVPGGVLPGARFPVGGVLPVGTGAGVKPKAPGVGGAFAGIPGVGGPQGVPLGY	180
DB	147	PGVPGGVLPGARFPVGGVLPVGTGAGVKPKAPGVGGAFAGIPGVGGPQGVPLGY	206
QY	181	PIKAPKLPVGGVLPVGTGKLPVGGVGGAGAGKAGVPTGTGVPQAAAAAAXKAF	240
DB	207	PIKAPKLPVGGVLPVGTGKLPVGGVGGAGAGKAGVPTGTGVPQAAAAAAXKAF	252
QY	241	GAGAAGLVPGVGGVPGVPGVGAIPGGIAGVGTAAAAAAXKAYGAAAGLVPGG	300
DB	253	GAGAAGLVPGVGGVPGVPGVGAIPGGIAGVGTAAAAAAXKAYGAAAGLVPGG	312
QY	301	PGFPGVPGVGGVPGVPGVPGVGAIPVVPAGVPGVPGVSPVSPVSPVSPVSPV	360
DB	313	PGFPGVPGVGGVPGVPGVPGVGAIPVVPAGVPGVPGVSPVSPVSPVSPVSPV	372

296 LVPGGFGFGVGVPGAGVPGVGVPGAGIPVVPAGIPGAAVPGVSPFAAAKAAKAA 375
 Db 317 LVPGGFGFGVGVPGAGVPGVGVPGAGIPVVPAGIPGAAVPGVSPFAAAKAAKAA 376
 QY 356 KYGARPGVGVGGIPTTYGVGAGGFGFGVGVGGIPGVAGVPSVGG 399
 Db 377 KYGARPGVGVGGIPTTYGVGAGGFGFGVGVGGIPGVAGVPSVGG 420
 RESULT 14
 BAC86188 PRELIMINARY; PRT; 559 AA.
 AC BAC86188; 27, Created)
 DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
 DE CDNA FLJ43523 fis, clone PLACE500282, weakly similar to Homo sapiens
 DE elastin (supravalvular aortic stenosis, Williams-Beuren syndrome)
 DE (EIN).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primata; Catarrhini, Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP TISSUE=Placenta;
 RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
 RA Arita M., Mueashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
 RA Orsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
 RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
 RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
 RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
 RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
 RT "NDO human cDNA sequencing project.";
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK12511; BAC86188.1; -.
 SQ SEQUENCE 559 AA; 53787 MW; 20938FFEC5492A01 CRC64;
 Query Match 75.5%; Score 2023.5; DB 2; Length 559;
 Best Local Similarity 96.0%; Pred. No. 1.4e-73;
 Matches 388; Conservative 0; Mismatches 1; Indels 15; Gaps 2;
 QY 1 GGVPICAI PGVPGGVYFPAGIGALGGAGLGGPKLPVPGGLAGAGLGAFFAVT 60
 Db 27 GGVPICAI PGVPGGVYFP-----ALGGGKFLKPVPGLAGAGLGAFFAVT 76
 QY 61 FPGALVPGGVADAAAYKAAKAGAGLGGVPGVGGILGWSA-----GAVTPOGAGVKPKV 115
 Db 77 FPGALVPGGVADAAAYKAAKAGAGLGGVPGVGGILGWSAAPSVPQAVVPPQAGVKPKV 136
 QY 116 PQVGI PGVYVPGVLPGARPPGVGLPGVPTGAGVKPKAPGVGGAFAGIPGVPGPGPG 175
 Db 137 PQVGLPGVYVPGVLPGARPPGVGLPGVPTGAGVKPKAPGVGGAFAGIPGVPGPGPG 196
 QY 176 VPLGYPIKAPKLPGGVGLPYTTTKLPGYGVGGVAGAAGKAGYPTGTGVGPOAAAAA 235
 Db 197 VPLGYPIKAPKLPGGVGLPYTTTKLPGYGVGGVAGAAGKAGYPTGTGVGPOAAAAA 256
 QY 236 AAAKFGAGAAVLPVGVGAGVPGVPCALPGTGGIAGVCTPAAAAAANKAAKYCAAG 295
 Db 257 AAAKFGAGAAVLPVGVGAGVPGVPCALPGTGGIAGVCTPAAAAAANKAAKYCAAG 316
 QY 296 LVPGGFGFGVGVPGAGVPGVGVPGAGIPVVPAGIPGAAVPGVSPFAAAKAAKAA 355
 Db 317 LVPGGFGFGVGVPGAGVPGVGVPGAGIPVVPAGIPGAAVPGVSPFAAAKAAKAA 376
 QY 356 KYGARPGVGVGGIPTTYGVGAGGFGFGVGVGGIPGVAGVPSVGG 399
 Db 377 KYGARPGVGVGGIPTTYGVGAGGFGFGVGVGGIPGVAGVPSVGG 420
 RESULT 15


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AC BAC85506;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE CDNA FJ16246 fis, clone HCHON2001577, highly similar to Human elastin
DE gene.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,
RA Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
RA Masuho Y., Nagai K., Isogai T.;
RA "NEDO human cDNA sequencing project.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK122731; BAC85506.1;
SQ SEQUENCE 570 AA; 48941 MW; 3117B028D06D4F7B CRC64;

Query Match 69.8%; Score 1870; DB 2; Length 570;
Best Local Similarity 73.4%; Pred. No. 1.9e-67;
Matches 378; Conservative 1; Mismatches 0; Indels 136; Gaps 3;

QY 1 GGVPGAITGGVGGVFFPGAGLGGALGPGGKPLKPVPGGLAGLGLGAGFAFPAVT 60
DB 27 GGVPGAITGGVGGVFFPGAGLGGALGPGGKPLKPVPGGLAGLGLGAGLGA----- 77
QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVSGVAGVVPQPGAGVPGKVPVGL 120
DB 78 ----- 77
QY 121 PGVYPGVLPGARFPFGVGLFPGVPTGAGVKPKAPGVGGAFAGIPGVGPGPGQVPLGY 180
DB 78 -----GVGGAFAIPGVGPGPGQVPLGY 103
QY 181 PIKAPKLPGGVGLPYTTGKLPYGVGPGVGAAGKAGYPTGTGVPQAAAAAATAAKAF 240
DB 104 PIKAPKLP-----GVGPGVGAAGKAGYPTGTGVPQAAAAAATAAKAF 149
QY 241 GAGAAGVLPVGGAGVPGVPGALPGICGAGVGTTPAAAAAATAAKAAGVAGLVPGG 300
DB 150 GAGAAGVLPVGGAGVPGVPGALPGICGAGVGTTPAAAAAATAAKAAGVAGLVPGG 209
QY 301 PGFGPGVGVPGAGVPGVPGAGIPVVPAGIPGAAPVGVSPAAAAAATAAKAAGVAG 360
DB 210 PGFGPGVGVPGAGVPGVPGAGIPVVPAGIPGAAPVGVSPAAAAAATAAKAAGVAG 269
QY 361 PGVGVGGIPTYGVGAGGFPFGVGVGIGIPVAGVSPVGGVPGVGVGVPVGVGSPV 420
DB 270 PGVGVGGIPTYGVGAGGFPFGVGVGIGIPVAGVSPVGGVPGVGVGVPVGVGSPV 329
QY 421 AKAAKVGVTFAAAAAKAAKAAQFGLVPGVGVAGVPGVAGVPGVGLAPGVGVAPG 480
DB 330 AKAAK-----GLVPGVGVAGVPGVAGVPGVAGVPGVGLAPGVGVAPG 370
QY 481 VGVAPGVAGVPGVGGVAAAAAATAAKAAQALR 515
DB 371 VGVAPGVAGVPGVGGVAAAAAATAAKAAQALR 405

RESULT 17
ELS BOVIN
ID ELS BOVIN STANDARD; PRT; 747 AA.
AC P04985; P04986; P04987; P04988; P04989; P04990; P04991;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

```

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DE Elastin precursor (Tropoelastin).
GN Name=ELN;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Raju K., Anwar R.A.;
RA "Primary structures of bovine elastin a, b, and c deduced from the
RT sequences of cDNA clones.";
RL J. Biol. Chem. 262:5755-5762(1987).
RN [2]
RP SEQUENCE OF 1-27 FROM N.A.
RA TISSUP=Nuchal ligament;
RA MEDLINE=87194772; PubMed=3032943;
RX Yeh H., Anderson N., Ornstein-Goldstein N., Bashir M.M.,
RA Rosenbloom J.C., Abrams W.R., Indik Z., Yoon K., Parks W., Mecham R.,
RA "Structure of the bovine elastin gene and Si nuclease analysis of
RT alternative splicing of elastin mRNA in the bovine nuchal ligament.";
RL Biochemistry 28:2365-2370(1989).
RN [3]
RP SEQUENCE OF 1-27 FROM N.A.
RA MEDLINE=91234332; PubMed=2031719;
RX Manohar A., Shi W., Anwar R.A.;
RA "Partial characterization of bovine elastin gene; comparison with the
RT gene for human elastin.";
RL Biochem. Cell Biol. 69:185-192(1991).
RN [4]
RP DISULFIDE BOND.
RX MEDLINE=92337651; PubMed=1632791;
RA Brown P.L., Mecham L., Tisdale C., Mecham R.P.;
RA "The cysteine residues in the carboxy terminal domain of tropoelastin
RT form an intrachain disulfide bond that stabilizes a loop structure and
RL positively charged pocket.";
CC Biochem. Biophys. Res. Commun. 186:549-555(1992).
CC -I- FUNCTION: Major structural protein of tissues such as aorta and
CC nuchal ligament, which must expand rapidly and recover completely.
CC -I- SUBUNIT: The polymeric elastin chains are cross-linked together
CC into an extensible 3D network.
CC -I- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
CC -I- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=A;
CC IsoId=P04985-1; Sequence=Displayed;
CC Name=2; Synonyms=B;
CC IsoId=P04985-2; Sequence=VSP_004239;
CC Name=3; Synonyms=C;
CC IsoId=P04985-3; Sequence=VSP_004240;
CC -I- PTM: The crosslinks are made of deaminated Lys.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: J02717; AAA30503.1; --
CC EMBL: K03505; AAA30505.1; --
CC EMBL: K03506; AAA30506.1; --
CC EMBL: J02855; AAA30776.1; --
CC EMBL: M58652; AAA03519.2; --
CC PIR: A31865; EABO.
CC InterPro: IPR003979; tropoelastin.
CC PRINTS: PR01500; TROPELASTIN.
CC Alternative splicing; Connective tissue; Repeat; Signal;
CC Structural protein. 26
CC SIGNAL 1

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[illegible]

Qy		499 AAAKSAAKVAAKAQLR 515
Dd		591 PAAAKSAAKAAQAQR 607

RESULT 22

ID	ELS_RAT	STANDARD;	PRT; 864 AA.
AC	Q99372;		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	Elastin precursor (Tropoelastin) (Fragment).		
GN	Name=Eln;		
OS	Rattus norvegicus (Rat). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. ON NCBI_TaxID=10116;		
RP	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING. MEDLINE=91104868; PubMed=1702999; RX Pierce R.A., Deak S.B., Stolle C.A., Boyd C.D.; RT "Heterogeneity of rat tropoelastin mRNA revealed by cDNA cloning."; RL Biochemistry 29:9677-9693(1990). [2]		
RP	PARTIAL SEQUENCE FROM N.A. PubMed=2913947; RX Rich C.B., Foster J.A.; RT "Characterization of rat heart tropoelastin."; RL Arch. Biochem. Biophys. 268:551-558(1989). [3]		
RP	SEQUENCE OF 22-31 FROM N.A. RX Franzblau C., Pratt C.A., Farris B., Colanino N.M., Offner G.D., Mogayzel P.J. Jr., Troxler R.F.; RT "Role of tropoelastin fragmentation in elastogenesis in rat smooth muscle cells."; RL J. Biol. Chem. 264:15115-15119(1989). [4]		
RR	SEQUENCE OF 264-533 AND 558-864 FROM N.A., AND ALTERNATIVE SPLICING. MEDLINE=92241859; PubMed=1572637; RX Pierce R.A., Alatawi A., Deak S.B., Boyd C.D.; RT "Elements of the rat tropoelastin gene associated with alternative splicing."; RL Genomics 12:651-658(1992). [5]		
RR	SEQUENCE OF 781-864 FROM N.A. MEDLINE=88330868; PubMed=2971041; RX Deak S.B., Pierce R.A., Belsky S.A., Riley D.J., Boyd C.D.; RT "Rat tropoelastin is synthesized from a 3.5-kilobase mRNA."; J. Biol. Chem. 263:13504-13507(1988).		
CC	-! FUNCTION: Major structural protein of tissues such as aorta and nuchal ligament, which must expand rapidly and recover completely.		
CC	-! SUBUNIT: The polymeric elastin chains are cross-linked together into an extensible 3D network.		
CC	-! SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.		
CC	-! ALTERNATIVE PRODUCTS: Event=Alternative products; Named isoforms=8; Comment=Experimental confirmation may be lacking for some isoforms;		
CC	Name=1;		
CC	IsoId-Q99372-1; SequenceDisplayed;		
CC	Name=2;		
CC	IsoId-Q99372-2; Sequence=VSP_004244;		
CC	Name=3;		
CC	IsoId-Q99372-3; Sequence=VSP_004245;		
CC	Name=4;		
CC	IsoId-Q99372-4; Sequence=VSP_004246;		
CC	Name=5;		
CC	IsoId-Q99372-5; Sequence=VSP_004244, VSP_004245;		
CC	Name=6;		

[illegible]

DR	EMBL; M22772; AAA30501.1; JOINED.
DR	EMBL; M22773; AAA30501.1; JOINED.
DR	EMBL; M22774; AAA30501.1; JOINED.
DR	EMBL; M22775; AAA30501.1; JOINED.
DR	EMBL; M22986; AAA30501.1; JOINED.
DR	GO; GO:0005578; C:extracellular matrix; IEA.
DR	GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR	InterPro; IPR003979; tropoelastin.
DR	PRINTS; PR01500; TROP0ELASTIN.
FT	NON TER
SQ	SEQUENCE 666 AA; 56435 MW; BCB5B62632BE1B71 CRC64;
	Query Match 59.9%; Score 1606.5; DB 2; Length 666;
	Best Local Similarity 65.8%; Pred. No. 6.3e-57;
	Matches 352; Conservative 21; Mismatches 55; Indels 107; Gaps 19;
QY	28 GALPGGKPLKPVPVGLAGLAGLGAFLPAPVTPFGALVPCGVADAAAAAYK-AAKAGA-- 84
DB	1 GGLPGVKPAKPGVGVLVGPLGAGLGP-G-AFPFALVPGPGPAGAAAAYKAAAKAGAAAG 59
QY	85 -GLGGVPGVGLGVSAGAVPQ-----PGAGVKPKVPGVGLPVVPPGVLP--GARFFGV 137
DB	60 LGVGIGGGVGLGVSTGAIVPQLGAGVGAGVKPKVPGVGLPGVYPGVGLPGAGARFFGI 119
QY	138 GVLPGVPTGAGVKPKAGVGVGAFAFAGIPGVGFPGFPQGVPLGYPIKAPKLPGYGVLPTTT 197
DB	120 GVLPGVPTGAGVKPKAGGGGAFAFIPGVGFPGQPQGVPLGYPIKAPKL- ----- 170
QY	198 GKLPYGVPGGVAGAGKAGYPTGTGVGPQAAAAAATAKAATKFGNAGVLP--GVGGAG 255
DB	171 -----GVGFQ-AAAAAATAKAATKLGAGGAGVLPFGVGVGGAG 204
QY	256 VPGVPGALPGIGTAGVCTPAAAAAATAKAATKGAAAGL-----VP--GGPGFG-PGV- 307
DB	205 IPGAPCALPGIGTAGVCAPDAAAAAATAKAATKFAAGGPFPGVPGVPGVPGVPGV 264
QY	308 ---VGVPCAGVPGVPGVPGAGIP--VYPGAGIPGAAPVPGVSEAAAAKAATAKYCARPG 362
DB	265 VPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 324
QY	363 VGVGIIPTYGVAGGFPFG-----VGVGIGPVAG-VP----SVGGVPG 402
DB	325 VGIGIIPTFVPGPGFPFGIDAAAAAATAKAATKIGAGGVGALGGLVPGAPCALPVPVG 384
QY	403 VGVPGVGISPEAQAAAAAATAKYGVTPAAAAAATAKAATAAFG--LVPGVGVAPGVGA 460
DB	385 VGVVPGVGI-----PAAAAAATAKAATAAFGLALLAFAGLGVPGVGA 425
QY	461 PGVGVAPGVGLAPGVGVAPGVGVAPGVPGVAPGVPGVWAAAAKAATAKVAQAQLR 515
DB	426 PVGVVPGVGVPGVGVAPGVGLGVG-----GVIGAGVPAATAKAATAKAATAKQFR 475

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RESULT 26
QN2GG0
ID          PRELIMINARY;      PRT;   472 AA.
AC  Q8N2G0
DT  01-OCT-2002 (TREMBLrel. 22, Created)
DT  01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT  01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE  Hypothetical protein PSEC0191.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Whole embryo;
RA  Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
RA  Saito K., Yamanoto J., Wakamatsu A., Nagai T., Nakamura Y.,
RA  Nagahara K., Sugano S., Isozaki T.;
RL  Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR  EMBL: AK075494; EAC11651.1; -.

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DR	GO: 0005578; C:extracellular matrix; IEA.	
DR	GO: 0005201; F:extracellular matrix structural constituent; IEA.	
DR	InterPro: IPR001451; Hexapep trans.	
DR	InterPro: IPR003979; tropoelastin.	
DR	PRINTS: PR01500; TROPOELASTIN.	
DR	PROSITE; PS00101; HEXAPEP_TRANSPEPTIDASE; UNKNOWN_1.	
NON_TER	472 472	
FT	SEQUENCE 472 AA; 42665 MW; 8D7A0F3A9BF971F3 CRC64;	
SQ		
	Query Match 49.0%; Score 1314; DB 2; Length 472;	
	Best Local Similarity 55.1%; Pred. No. 2.2e-45;	
	Matches 284; Conservative 3; Mismatches 2; Indels 226; Gaps	
Qy	1 GGVPGAI PGGVPGGV FYPGAGLGNLGGALPGGKPLKVPGGLAGAGL GAGLGAFAV T 60	
Db	27 GGVPGAI PGGVPGGV FYPGAGLGNLGGALPGGKPLKVPGGLAGAGL GAGLGA- 81	
Qy	61 FPGALVPGGVADAAAAAYKAAKAGAGLGGVPGVGGLGVSAGAVVPPQPGAGVKPGKVGVL 120	
Db	82 -----LGGVGI----- 87	
Qy	121 PGVYPGGLVFGARFPGGVGLPGVPTGAGVKPKAPGVGGAFAGIPGVGPFPGQPGVPLGY 180	
Db	88 ----- 87	
Qy	181 PIKAPKLPGGYGLPYTTGKLPYGYCPGGVAGAAKAGAYPTGTGTGVGPQAAAAAKAAKF 240	
Db	88 -----PGGVGA-----GP----- 96	
Qy	241 GAGAAAGVLPGVGGAGVPGVPGAIPIGGIAGVGTAAAAAATAAKAAKYGAAAGLVPGG 300	
Db	97 -----AAAAAATAAKAAKYGAAAGLVPGG 119	
Qy	301 PGFPGVVGVPAGVPGVGVPGAGIPVVPAGAGIPCAAVPGVVSPEAAATAAKAAKYGAR 360	
Db	120 PGFPGVVGVPAGVPGVGVPGAGIPVVPAGAGIPCAAVPGVVSPEAAATAAKAAKYGAR 179	
Qy	361 PGVGVGGIPTTGVGAGGFPFGVGGIPGVAGVPSVGGVPGVGVPGVGVISPEAQAAAA 420	
Db	180 PGVGVGGIPTTGVGAGGFPFGVGGIPGVAGVPSVGGVPGVGVPGVGVISPEAQAAAA 239	
Qy	421 AKAARYGVGTAAAAAATAAKAAAPGLVPGVGVAPGVGVPAGVGVGLAPGVGVAPG 480	
Db	240 AKAARY-----GLVPGVGVAPGVGVPAGVGVGLAPGVGVAPG 280	
Qy	481 VGVAPGVGVAPGIPGGVAAATAAKAAKVAQAQLR 515	
Db	281 VGVAPGVGVAPGIPGGVAAATAAKAAKVAQAQLR 315	

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RESULT 27
ELS_CHICK
ID ELS_CHICK STANDARD; PRT; 750 AA.
AC P07916;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Elastin precursor (Tropoelastin) (Fragment).
GN Name=ELN;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1] _SEQUENCE FROM N.A.
RP MEDLINE=67242320; PubMed=3593675;
RX Bressan G.M., Argos P., Stanley K.K.;
RA "Repeating structure of chick tropoelastin revealed by complementary
RT DNA cloning.";
RL Biochemistry 26:1497-1503 (1987).
RN [2]
RP SEQUENCE OF 85-750 FROM N.A. (ISOFORM 2).

```


Db 566 GGLAPGVAVPGV--GGPAAAAKAAKAA 592

RESULT 28
Q9BDZ0 PRELIMINARY; PRT; 172 AA.

ID Q9BDZ0
AC Q9BDZ0; 2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Elastin (Fragment).
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=21621082; PubMed=11751201;
RA Sekhon H.S., Keller J.A., Prokocil B.J., Martin E.L., Spindel E.R.;
RL "Maternal nicotine exposure upregulates collagen gene expression in fetal monkey lung. Association with alpha7 nicotinic acetylcholine receptors.";
RT Am. J. Respir. Cell Mol. Biol. 26:31-41(2002).
RL Am. J. Respir. Cell Mol. Biol. 26:31-41(2002).
DR EMBL; AF230927; AAK14974.1; -.
FT NON TER 1
FT NON TER 172
FT NON TER 172
SQ SEQUENCE 172 AA; 15224 MW; 4980EF4C5AF3330B CRC64;

Query Match 29.8%; Score 797.5; DB 2; Length 172;
Best Local Similarity 90.1%; Pred. No. 4.3e-25;
Matches 155; Conservative 0; Mismatches 6; Indels 11; Gaps 2;

QY 33 GGKPLKPVGGLAGLAGGALGAPFAVPFPFGALVPGGVADAAAAYKAAGAGLVGPV-- 90
DB 1 GGKPLKPVGGLAGTGLGAGLGAPFAGAPFAGALVPGGVADAAAAYKAAGAGLVGPV 60

QY 91 -----GVGGLGVSAAGVVPFGAGVKPKVGVGLGVPGVVLP--GARFFGVGVLP 141
DB 61 GGIGGVGVGGVLGVSTGAVVPPQPVGAGVXPKVPGVGLPVGGVLPDGTGARFFGVGVLP 120

QY 142 GVPTGAGVKPAKAPGVCGAFAGIPGVPGPGOPGVPLGYPIKAPKLPGGYGL 193
DB 121 GVPTGAGVKPAKAPGVCGAFAGIPGVPGVQVPGVPLGYPIKAPKLPGGYGL 172

RESULT 29
Q9BIT7 PRELIMINARY; PRT; 1953 AA.

ID Q9BIT7
AC Q9BIT7; 2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 24, Last annotation update)
DE Major ampullate spidroid 2-like protein (Fragment).
OS Nephila inaurata madagascariensis.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Araneidae; Tetragnathidae; Nephila.
OX NCBI_TaxID=115969;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21179804; PubMed=11283372;
RA Gatesy J., Hayashi C., Motriuk D., Woods J., Lewis R.;
RL "Extreme diversity, conservation, and convergence of spider silk fibroin sequences.";
RT Science 291:2603-2605(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC Gatesy J.E., Hayashi C.Y.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF350276; AAK30605.1; -.
FT NON TER 1
FT NON TER 1953
FT NON TER 1953

SQ SEQUENCE 1953 AA; 159383 MW; C82B4DACD043CBD CRC64;

Query Match 22.9%; Score 614; DB 2; Length 1953;
Best Local Similarity 33.8%; Pred. No. 4.1e-17;
Matches 233; Conservative 16; Mismatches 237; Indels 204; Gaps 33;

QY 2 GVPGA-----PGGVPGVFYPGA-----GLGALGGALGPGKPLKVPVPGLAGAG 48
DB 688 GGFGAAAAAAGPGYGPGQGPGGAAAAAAGSGPGYGPGQGPGG-----PGAAAAA 741
QY 49 LG-----AGLCAPAVTFPFGALVPGGVADAAAAYKAAGAGLVGPV-- 89
DB 742 AGRGPGYGQGGPGGCAAAAAGPGYGPGQGPGGAAAAAAGSGPGYGPGQGPGG 799
QY 90 PGVGLGVSAAGVVPFGAGVKPKV----PGVGLPVGVPLGVPLGVPLGV-- 143
DB 800 PKRSAAAAAAGRGPG--GYGPGQQGPGGAAAAAAGPGYGPGQGPGGAAAAAASGR 858
QY 144 -PTGAVKFKAPGVGAFAGIPGVGPF--GP---PGVVP-LGYPIKAPKLPGYG-- 192
DB 859 GPQGGYGGQGGPGGAAAAAAGRGPGYGPGQGPGGAAAAAAGSGPGYGPGQGPGG 918
QY 193 -----LPYTTLKPLPYGYGPG-----GVAGAAGKAGYPTGTGVGPAAAAAAXK 237
DB 919 PQOQGGSGSAAAAAAGRGPGYGPGQGPGGAAAAAAGSGPGYGPGQGPGGAAAAA 978
QY 238 AKFGAGAAAGVLPVGVGAGVPGVPGALPGI-----GIAGVGTAAAAAAXKAAKY 291
DB 979 ---GSGPGYGPGQGPGGAAAAAAGRGPGYGPGQGPGGAAAAAAGSGPGYGPGQG 1035
QY 292 -----AAAGLVPGG-----PGFGGVGVGPVGA 313
DB 1036 PQOQGGPGGSGAAAAAAGRGPGYGPGQGPGGAAAAAAGSGPGYGPGQGPGG 1094
QY 314 -----GVPGVPGVPGAGIPVVPAGIPGAAVPGVWSP-----EAAAKA 350
DB 1095 AAAAAAAGRGPGYGPGQGPGGAAAAAAGRG-PGYYGPGQGPGGPGGPGGAAAA 1153
QY 351 AKAARYK-ARPGVGVGGITPYGVGAGF-----PGFGVGVGGIPG 390
DB 1154 AAGPGYGPGQGPGGAAAAAAGSGAGGPGYGPGQGPGGAAAAAAGSGPGYGPGQG 1212
QY 391 VAGVPSGVGVGVGVPGVGI-SPEAOAAAAAAXKAAKYGVGT--PAAAKA 437
DB 1213 AAAAAAGSGPGYGPGQGPGGSSAAAAAAGRGYRYPGQGPGGAAAAAAGSGPGYG 1272
QY 438 -----AAAKAAQFLVPGVAVPG-----VGVAVGVAVPGVLAFCVGV 477
DB 1273 GQGGPGGPGMAAAAAAAGRGPG--GYGPGQGPGGAAAAAAGPG--GYGPG-QQGPGAAA 1329
QY 478 APGVGVAVPGVAVPG--IGPGVAAAAKSAA 506
DB 1330 AAAAGSGPG--GYGPGQGPGGPGGAAAAA 1358

RESULT 30
Q9BIU9 PRELIMINARY; PRT; 651 AA.

ID Q9BIU9
AC Q9BIU9; 2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Flagelliform silk protein (Fragment).
GN Name=Flag;
OS Argiope trifasciata (Banded garden spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Araneidae; Argiope.
OX NCBI_TaxID=156845;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21179804; PubMed=11283372;
RA Gatesy J., Hayashi C., Motriuk D., Woods J., Lewis R.;
RL "Extreme diversity, conservation, and convergence of spider silk

```

RT fibroin sequences.10;
RL Sequence 291:2603-2605 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Gatesy J.E., Hayashi C.Y.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF350264; AAK30593.1; -.
FT NON TER
FT 1
SQ SEQUENCE 651 AA; 52360 MW; 77CEEC8757DE48DA CRC64;

Query Match      22.4%; Score 600.5; DB 2; Length 651;
Best Local Similarity 38.5%; Pred. No. 7e-17;
Matches 225; Conservative 17; Mismatches 201; Indels 141; Gaps 39;

QY      2  GVPGAI PGVPGGVFYFGAGLGAIG--GGALGP GPKLPVPVGGLAGAGLGA-----G 52
Db      2  GGPGA--GGAGAGGVGPG--GFGGPGFGGAGGPGG-----PGSPGAGGAGGAGGLYG 52

QY      53  LGAPPAVTFPGAL-----VPG--GVADAAAAA KAAKAGAGLGGV-----PGVGLGV 97
Db      53  PGGAGGLYFGGLYVPGGAGVPGAPGASGRAGGIGGAAGAGAGAGGVGPGVSGAGGAGG 112

QY      98  SAGAVVPQAGAVKPGVPGVGLPGVPGVPCAREPPGVGLPGV--PTGAGVKPKAPG 155
Db      113  SGVTVVESVSGGAGG--PGAG--GVGPGGVGPGCVPG-----GIYPGGAG--GLYGP 162

QY      156  VGNF-----AGIPGVPGFPGPOPGVPLGYPIKAPLPGGYGLPYTTGKLPYGVPG--GV 209
Db      163  AGGAFPGGAGAGPG--GPGGPGGPGGPGG-----LGGVGGAAGTGG-----GVGPGAG 210

QY      210  AGAAGKAGYPTGTGVQPAQAAAAA KAAKFGAGAGVLPFGVGAGVPGV--PGAIPIGIG 268
Db      211  VGPSGGAG-----GTGPVSVTSVSGAG--GPGAGG--PGAGGAGAGGVGPGFGPGG 262

QY      269  IAGVGTPTAAAAA KAAKYGAAGLV--PGGPG-----FGGVGVGPG-----312
Db      263  FGAAGPGGPGGPGAGGGA--CGAGGLYGPAGGLYGPGLYGPAGGAGVPGAPGASGR 320

QY      313  -----AGVPGV-----GVPGAGIPV-----VPGAGIPCAAVPVVSPAAAKAAK 353
Db      321  AGGIGGAAGAGGVGPGVSGGAGGSGVSVTESVTVGGAG--GAGAGGIGGPGSLGAGAT 378

QY      354  MAKYGARPGV---GVGGIPTYGVGAGGFPFGVGVGGIPGVAG-----VPSVG 398
Db      379  GG--FGRGGPGGPGGPGGPGRFGGAAGGAGAGGVGPGVSGAGAGGSGSVTVVESVVG 437

QY      399  GV--PGVGGVPGVGLISPEAQAAAA KAAKYGVGTPTAAAAA KAAXAQAQFGLVFGVGA 456
Db      438  GAGGPGAGGVGPGGVGPF-----GGVPGGIYGPAGGLYGPAGGA--FGSGGGAG--APG 490

QY      457  VGVAPGVGVA PGVGLAPGVGVA--PGVGVAPGVGVAPGTPGPGVA 499
Db      491  GPGGPGGPGGPG--GLGGGVGGAGTGGGVGPGV---GVGPGSGGA 530

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Search completed: November 19, 2004, 16:36:48
Job time : 108.124 secs

Result No.	Score	Query			DB	ID	Description
		Match	Length	%			
1	253	100.0	731	10	US-09-964-662-1	Sequence 1, Appl	
2	212	83.8	617	14	US-10-104-047-2915	Sequence 2915, Appl	
3	212	83.8	663	15	US-10-108-260A-2477	Sequence 2477, Appl	
4	212	83.8	692	15	US-10-210-172-40	Sequence 40, Appl	
5	212	83.8	711	15	US-10-210-172-38	Sequence 38, Appl	
6	212	83.8	730	10	US-09-961-403-8	Sequence 8, Appl	
7	149	58.9	60	8	US-08-806-029-24	Sequence 24, Appl	
8	149	58.9	64	8	US-08-806-029-18	Sequence 18, Appl	
9	149	58.9	64	14	US-10-117-931-14	Sequence 14, Appl	
10	149	58.9	244	16	US-10-800-179-27	Sequence 27, Appl	
11	149	58.9	246	16	US-10-800-179-26	Sequence 26, Appl	
12	149	58.9	246	16	US-10-800-179-28	Sequence 28, Appl	
13	149	58.9	312	8	US-08-806-029-34	Sequence 34, Appl	

Mon Nov 22 12:42:43 2004

us-09-743-818a-72.rapb

87 125.5 49.6 1210 16 US-10-720-025-25 Sequence 25, Appl
88 125.5 49.6 1250 10 US-09-807-742-1 Sequence 1, Appl
89 125.5 49.6 1255 9 US-09-837-969A-18 Sequence 18, Appl
90 125.5 49.6 1255 9 US-09-841-321A-18 Sequence 18, Appl
91 124.5 49.2 45 9 US-09-888-260-43 Sequence 43, Appl
92 124.5 49.2 45 9 US-09-888-260-44 Sequence 44, Appl
93 124.5 49.2 45 10 US-09-746-371C-39 Sequence 39, Appl
94 124.5 49.2 45 10 US-09-746-371C-40 Sequence 40, Appl
95 124.5 49.2 60 9 US-09-888-260-41 Sequence 41, Appl
96 124.5 49.2 60 9 US-09-888-260-42 Sequence 42, Appl
97 124.5 49.2 60 10 US-09-746-371C-37 Sequence 37, Appl
98 124.5 49.2 60 10 US-09-746-371C-38 Sequence 38, Appl
99 124.5 49.2 110 9 US-09-888-260-39 Sequence 39, Appl
100 124.5 49.2 110 9 US-09-888-260-40 Sequence 40, Appl

ALIGNMENTS

RESULT 1
US-09-964-662-1
; Sequence 1, Application US/09964662
; Publication No. US20030166846A1
; GENERAL INFORMATION:
; APPLICANT: PROTEIN SPECIALTIES LTD.
; APPLICANT: HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP
; TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN AND
; TITLE OF INVENTION: OTHER FIBROUS PROTEINS
; FILE REFERENCE: 041082/0112
; CURRENT APPLICATION NUMBER: US/09/964,662
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: 09/340,736
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 731
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-964-662-1

Query Match 100.0%; Score 253; DB 10; Length 731;
Best Local Similarity 100.0%; Pred. No. 4.5e-17;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGGLGVGAGVPGFAGAGDEGVRR 49
Db 516 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGGLGVGAGVPGFAGAGDEGVRR 564

RESULT 2
US-10-104-047-2915
; Sequence 2915, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2915
; LENGTH: 617
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2915

Query Match 83.8%; Score 212; DB 14; Length 617;
Best Local Similarity 100.0%; Pred. No. 4.3e-13;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGGLGVGAGVPGFAGAG 41
Db 453 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGGLGVGAGVPGFAGAG 493
RESULT 3
US-10-108-260A-2477
; Sequence 2477, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2477
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-2477

Query Match 83.8%; Score 212; DB 15; Length 663;
Best Local Similarity 100.0%; Pred. No. 4.6e-13;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGGLGVGAGVPGFAGAG 41
Db 481 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGGLGVGAGVPGFAGAG 521

RESULT 4
US-10-210-172-40
; Sequence 40, Application US/10210172
; Publication No. US20040043928A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Miller, Charles
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol
; APPLICANT: Rieger, Daniel
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Li, Li
; APPLICANT: Ji, Weizhen
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Casman, Stacie
; APPLICANT: Voss, Edward
; APPLICANT: Boldog, Ferenc
; APPLICANT: Gorman, Linda
; APPLICANT: Leite, Mario
; APPLICANT: Vernet, Corine
; APPLICANT: Anderson, David
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zhong, Mei
; APPLICANT: Gerlach, Valerie
; APPLICANT: Hjalte, Tord
; APPLICANT: Rastelli, Luca
; APPLICANT: Spytek, Kimberly
; APPLICANT: Edinger, Shlomit
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Alsobrook II, John
; APPLICANT: Lepley, Denise et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-416 A
; CURRENT APPLICATION NUMBER: US/10/210,172
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/309,501

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OM protein - protein search, using sw model

Run on: November 19, 2004, 16:06:25 ; Search time 2.20393 Seconds
(without alignments)
2139.188 Million cell updates/sec

Title: US-09-743-818A-72
Perfect score: 253
Sequence: 1 AAGAGAGIPGLGVGVGPG.....LGVGAGVPGFAGADEGVRR 49

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :
1: PIR 79:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	253	100.0	792	1 EAHU	elastin precursor,
2	193	76.3	860	1 EAMS	elastin precursor,
3	189	74.7	747	1 EABO	elastin precursor,
4	181	71.5	864	1 EART	elastin precursor,
5	168.5	66.6	770	2 S59623	tropoelastin - she
6	126.5	50.0	784	2 A26601	elastin precursor
7	125.5	49.6	907	2 A45560	elastin precursor
8	107	42.3	127	2 E82734	sporozoite surface
9	103.5	40.9	108	2 G86252	hypothetical prote
10	97	38.3	151	2 T08002	hypothetical prote
11	96	37.9	100	2 T7558	glycine-rich prote
12	96	37.9	158	2 T08957	glycine-rich prote
13	95.5	37.7	212	2 E86179	hypothetical prote
14	95	37.5	108	1 S01844	fibroin - silkworm
15	94.5	37.4	130	2 T04048	hypothetical prote
16	94.5	37.4	838	2 AC1064	outer membrane fim
17	94	37.2	129	2 T17530	glycine-rich prote
18	94	37.2	505	2 T04143	CLB1 protein - tom
19	93	36.8	185	2 JC4085	glycine-rich cutic
20	93	36.8	1901	2 F70806	hypothetical glyci
21	92	36.4	223	2 B95006	hypothetical prote
22	92	36.4	1733	1 B45344	probable nuclear a
23	92	36.4	1958	2 B40505	hypothetical prote
24	91.5	36.2	129	2 A24255	chorion class A pr
25	91	36.0	259	2 T17889	glycine-rich prote
26	91	36.0	523	2 AH2907	signal recognition
27	91	36.0	554	2 H97682	glycine-rich cell
28	90.5	35.8	162	2 S56703	hypothetical prote
29	89	35.2	143	2 S43071	hypothetical prote

30	89	35.2	171	2 T43959	hypothetical prote
31	89	35.2	510	2 T50526	CalB protein - Ara
32	88.5	35.0	208	2 S23463	cuticular protein
33	88.5	35.0	532	2 T35119	probable aminotran
34	88.5	35.0	1147	1 MWAXIB	myosin heavy chain
35	88	34.8	924	2 B41359	potassium channel
36	88	34.8	924	2 S12746	potassium channel
37	87.5	34.6	162	2 C85356	glycine-rich prote
38	87.5	34.6	3190	2 T13828	CREB-binding prote
39	87	34.4	384	1 A26099	glycine-rich cell
40	87	34.4	641	1 QOBE31	nuclear antigen EB
41	86.5	34.2	627	2 T04562	hypothetical prote
42	85	34.0	186	2 S28021	rab18 protein - Ar
43	85.5	33.8	234	2 G95989	hypothetical glyci
44	85.5	33.8	298	2 E95286	hypothetical prote
45	84.5	33.4	107	2 B85356	glycine-rich prote
46	84.5	33.4	419	2 G70602	hypothetical prote
47	84	33.2	139	2 T33968	hypothetical prote
48	84	33.2	839	2 C85046	probable reverse t
49	84	33.2	1240	2 T04193	hypothetical prote
50	82.5	32.6	129	2 T03861	glycine-rich prote
51	82	32.4	180	2 T49530	related to glycine
52	82	32.4	205	2 T07959	probable cell wall
53	82	32.4	338	1 KXNU	glycine-rich cell
54	82	32.4	486	1 KRXL	keratin 3, type I,
55	81.5	32.2	131	2 T05837	hypothetical prote
56	81.5	32.2	149	2 T18758	hypothetical prote
57	81	32.0	53	2 A42627	cement precursor p
58	81	32.0	603	2 A70770	hypothetical glyci
59	81	32.0	1215	2 T32734	myosin-IA - Acanth
60	80.5	31.8	447	2 G84687	probable disease r
61	80.5	31.8	496	2 H70839	hypothetical glyci
62	80	31.6	200	2 B86181	keratin, 64K type
63	80	31.6	419	1 KRXL2B	transcription fact
64	80	31.6	420	2 A49642	hypothetical glyci
65	80	31.6	543	2 F70726	probable retroelem
66	80	31.6	1328	2 G84519	neurogenic locus m
67	80	31.6	1596	2 A33106	glycine-rich cell
68	79.5	31.4	87	2 T14302	hypothetical glyci
69	79.5	31.4	1489	2 D70807	hypothetical prote
70	79	31.2	70	2 A83982	merozoite 45K surf
71	79	31.2	300	2 A39112	probable RNA bindi
72	79	31.2	302	2 A39615	hypothetical glyci
73	79	31.2	496	2 S68160	hypothetical prote
74	79	31.2	882	2 B70812	collagen alpha 2(I
75	79	31.2	1758	2 T29350	probable large gly
76	79	31.2	1759	2 T29351	hypothetical prote
77	79	31.2	1772	2 T36105	hypothetical prote
78	78.5	31.0	479	2 F70573	elastin - bovine (
79	78	30.8	76	2 I45885	circumsporozoite p
80	78	30.8	201	2 T00799	phosphatidylinosit
81	78	30.8	351	1 OZ2QKU	dnax-type molecula
82	78	30.8	490	2 T09084	hypothetical glyci
83	78	30.8	686	2 A49242	chorion class A pr
84	78	30.8	778	2 F70963	probable beta-1,3
85	77.5	30.6	119	1 JAAO92	glycine-rich prote
86	77.5	30.6	228	2 D86416	probable keratin i
87	77.5	30.6	396	2 T49109	polyketide synthas
88	77.5	30.6	473	4 A33652	hypothetical prote
89	77.5	30.6	1616	2 G70668	glycine-rich prote
90	77	30.4	102	2 E85189	related to Nup98-N
91	77	30.4	210	2 JQ1060	hypothetical prote
92	77	30.4	1844	2 T51890	hypothetical prote
93	76.5	30.2	191	2 T23594	hypothetical prote
94	76.5	30.2	214	2 T23593	hypothetical prote
95	76.5	30.2	255	2 B84777	glycine-rich prote
96	76.5	30.2	271	2 S34666	cytoplasmic male s
97	76.5	30.2	354	4 A27071	hypothetical prote
98	76.5	30.2	399	2 T18566	hypothetical prote
99	76.5	30.2	447	2 B96720	probable PPE prote
100	76.5	30.2	3716	2 E70969	

Mon Nov 22 12:42:44 2004

ALIGNMENTS

RESULT 1

EAHU
 elastin precursor, long splice form - human
 N:Alternate names: tropoelastin
 C:Species: Homo sapiens (man)
 C>Date: 22-Jun-1990 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C:Accession: A32707; A33705; A30524; A53891
 R:Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Sheppard, P.; Anderson, N.; Rosenbloom, J.
 Proc. Natl. Acad. Sci. U.S.A. 84, 5680-5684, 1987
 A:Title: Alternative splicing of human elastin mRNA indicated by sequence analysis of cDNA
 A:Reference number: A32707; MUID:87289668; PMID:3039501
 A:Accession: A32707
 A:Molecule type: mRNA
 A:Residues: 1-500, 507-792 <IND>
 A:Cross-references: UNIPROT:P15502; UNIPROT:Q9UMK5; GB:M16983; GB:J02948
 R:Bashir, M.M.; Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Rosenbloom, J.C.; Abrams, W.
 J. Biol. Chem. 264, 8887-8891, 1989
 A:Title: Characterization of the complete human elastin gene. Delineation of unusual features
 A:Reference number: A33705; MUID:99255358; PMID:2722804
 A:Accession: A33705
 A:Molecule type: DNA
 A:Residues: 1-27 <BAS>
 A:Cross-references: GB:J04821; NID:gl82052; PIDN:AAA52379.1; PID:g553276
 R:Fazio, M.J.; Olsen, D.R.; Kauh, E.A.; Baldwin, C.T.; Indik, Z.; Ornstein-Goldstein, N.
 J. Invest. Dermatol. 91, 458-464, 1988
 A:Title: Cloning of full-length elastin cDNAs from a human skin fibroblast recombinant cDNA library
 A:Reference number: A30524; MUID:89009960; PMID:3171221
 A:Accession: A30524
 A:Molecule type: mRNA
 A:Residues: 1-453, 483-617, 651-792 <PAZ>
 A:Cross-references: ENBL:M36860; NID:gl82061; PIDN:AAA52382.1; PID:gl82062
 A:Note: this sequence represents a composite of several splice forms
 R:Fazio, M.J.; Olsen, D.R.; Kuhlvanemi, H.; Chu, M.L.; Davidson, J.M.; Rosenbloom, J.; U
 Lab. Invest. 58, 270-277, 1988
 A:Title: Isolation and characterization of human elastin cDNAs, and age-associated variations
 A:Reference number: A53891; MUID:88156138; PMID:2831431
 A:Accession: A53891
 A:Molecule type: mRNA
 A:Residues: 164-453, 483-500, 507-617, 651-792 <PAZ>
 A:Cross-references: GB:M24782; NID:gl82063; PIDN:AAA53190.1; PID:gl82064
 C:Comment: The term tropoelastin refers to a soluble precursor form of the extracellular matrix
 C:Genetics: A53891
 A:Gene: GDB:ELN
 A:Cross-references: GDB:119107; OMIM:130160
 A:Map position: 7q11.23-7q11.23
 C:Superfamily: elastin
 C:Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:27-792/Product: elastin #status predicted <MAT>
 F:782-787/Disulfide bonds: #status predicted
 Query Match 100.0%; Score 253; DB 1; Length 792;
 Best Local Similarity 100.0%; Pred. No. 7.7e-16;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGLGGAGPGLGVGVPGLGVGAGVPGFAGAGVPGFAGAGVRR 49
 |||
 577 AAAGLGGAGPGLGVGVPGLGVGAGVPGFAGAGVPGFAGAGVRR 625

RESULT 2

EAWS
 elastin precursor - mouse
 N:Alternate names: tropoelastin
 C:Species: Mus musculus (house mouse)
 C>Date: 18-Aug-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
 C:Accession: A55721
 R:Wyder, K.S.; Sechler, J.L.; Boyd, C.D.; Passmore, H.C.
 Genomics 23, 125-131, 1994

A:Title: Use of an intron length polymorphism to localize the tropoelastin gene to mouse chromosome 12
 A:Reference number: A55721; MUID:95130069; PMID:7829060
 A:Accession: A55721
 A:Molecule type: mRNA
 A:Residues: 1-860 <WID>
 A:Cross-references: UNIPROT:P54320; GB:U08210; NID:g473273; PIDN:AAA80155.1; PID:g473274
 C:Genetics: A55721
 A:Map position: 5
 C:Superfamily: elastin
 C:Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
 F:1-27/Domain: signal sequence #status predicted <SIG>
 F:28-860/Product: elastin #status predicted <MAT>
 F:850-855/Disulfide bonds: #status predicted
 Query Match 76.3%; Score 193; DB 1; Length 860;
 Best Local Similarity 81.4%; Pred. No. 2.1e-10;
 Matches 35; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 AAAGLGGAGPGLGVGVPGLGVGAGVPGFAGAGVPGFAGAGVRR 43
 |||
 608 AAAGLGGAGVPGFAGAGVPGFAGAGVPGFAGAGVPGFAGAGVRR 650

Db

RESULT 3
 EABO
 elastin precursor, splice form a - bovine
 N:Alternate names: tropoelastin
 N:Contains: elastin precursor, splice form b; elastin precursor, splice form c
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 08-Jun-1989 #sequence_revision 28-Jul-1996 #text_change 09-Jul-2004
 C:Accession: A31865; A26728; C26728; A25886
 R:Yeh, H.; Anderson, N.; Ornstein-Goldstein, N.; Bashir, M.M.; Rosenbloom, J.C.; Abrams
 Biochemistry 28, 2365-2370, 1989
 A:Title: Structure of the bovine elastin gene and S1 nuclease analysis of alternative splicing
 A:Reference number: A31865; MUID:89274159; PMID:2543440
 A:Accession: A31865
 A:Molecule type: DNA
 A:Residues: 1-27 <YEH>
 A:Cross-references: UNIPROT:P04985; UNIPROT:Q28101; GB:J02855; NID:g340504; PIDN:AAA307
 R:Raju, K.; Anwar, R.A.; 5755-5762, 1987
 J. Biol. Chem. 262, 5755-5762, 1987
 A:Title: Primary structures of bovine elastin a, b, and c deduced from the sequences of cDNA
 A:Reference number: A92640; MUID:87194772; PMID:3032943
 A:Accession: A26728
 A:Molecule type: mRNA
 A:Residues: 1, 'RS', 4-11, 'E', 13-636, 'V', 638-747 <RAJ>
 A:Cross-references: GB:J02717; NID:gl63019; PIDN:AAA30503.1; PID:g163020
 A:Accession: B26728
 A:Molecule type: mRNA
 A:Residues: 1, 'RS', 4-11, 'E', 13-225, 240-636, 'V', 638-747 <RA2>
 A:Cross-references: GB:K03505; NID:gl63025; PIDN:AAA30505.1; PID:g163026
 A:Accession: C26728
 A:Molecule type: mRNA
 A:Residues: 1, 'RS', 4-11, 'E', 13-225, 260-636, 'V', 638-747 <RA3>
 A:Cross-references: GB:K03506; NID:gl63027; PIDN:AAA30506.1; PID:g163028
 R:Cicila, G.; May, M.; Ornstein-Goldstein, N.; Indik, Z.; Morrow, S.; Yeh, H.S.; Rosenbloom, J.
 Biochemistry 24, 3075-3080, 1985
 A:Title: Structure of the 3' portion of the bovine elastin gene
 A:Reference number: A22343; MUID:85280426; PMID:2992576
 A:Accession: A22343
 A:Molecule type: DNA
 A:Residues: 613-747 <CIC>
 A:Cross-references: GB:M20415
 R:Rosenbloom, J.
 Lab. Invest. 51, 605-623, 1984
 A:Title: Biology of disease: Elastin: Relation of protein and gene structure to diseases
 A:Reference number: I45885; MUID:85059254; PMID:6150137
 A:Accession: I45886
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 678-683, 685-747 <ROS>
 A:Cross-references: GB:M31898; NID:gl63015; PIDN:AAA96417.1; PID:g163018
 R:Brown, P.L.; Mecham, L.; Tidale, C.; Mecham, R.P.

RA Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
 RA Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
 RA Fewell G.A., Delehaunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
 RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
 RA Vanbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
 RA Ozeresky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
 RA Strong C.M., Hou S., Tomlinson C., Rohlffing T., Rock S.M.,
 RA Kozlowicz-Reilly A., Leonard S., Rohlffing T., Rock S.M.,
 RA Tin-Wollam A.M., Abbott A., Minx P., Maupin R., Strommatt C.,
 RA Latrelle P., Miller N., Johnson D., Murray J., Woessner J.P.,
 RA Wendt M.C., Yang S.P., Schultz B.R., Wallis J.W., Spieth J.,
 RA Bieri T.A., Nelson J.O., Berkowicz N., Wohlmann P.E., Cook L.L.,
 RA Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
 RA Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen E.,
 RA Gilett W., Zhou Y., James R., Phelps K., Iadonoto S., Bub K.,
 RA Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,
 RA Baertsch R.A., Brent M.R., Keibler E., Fliecek P., Bork P., Suyama M.,
 RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,
 RA Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
 RA Waterston R.H., Wilson R.K.;
 RT "The DNA sequence of human chromosome 7.";
 RL Nature 424:157-164 (2003).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP RP
 RA Du H., Rohlffing T., Strong C.;
 RT "The sequence of Homo sapiens BAC clone CTB-51J22.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN SEQUENCE FROM N.A.
 RP RP
 RA Waterston R.H.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RN SEQUENCE FROM N.A.
 RP RP
 RA Waterston R.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RN SEQUENCE FROM N.A.
 RP RP
 RA Wilson R.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC005056; AAS07435.1; --
 KW Hypothetical protein.
 SQ SEQUENCE 757 AA; 66106 MW; 2B24F955D8360738 CRC64;
 Query Match 100.0%; Score 253; DB 2; Length 757;
 Best Local Similarity 100.0%; Pred. No. 1.1e-12;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGGLGVGAGVPGFAGAGDEGVRR 49
 Db 542 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGGLGVGAGVPGFAGAGDEGVRR 590
 RESULT 4
 O15336 ID O15336 PRELIMINARY; PRT; 635 AA.
 AC O15336;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Elastin (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP RP
 RA Li D.Y., Toland A.E., Boak B.B., Atkinson D.L., Ensing G.J.,
 RA Morris C.A., Keating M.T.;
 RT "Elastin point mutations cause an obstructive vascular disease,
 RT supravalvular aortic stenosis.";
 RL Hum. Mol. Genet. 6:1021-1028 (1997).
 DR EMBL; U93037; AAB65621.1; --
 Query Match 83.8%; Score 212; DB 2; Length 258;
 Best Local Similarity 100.0%; Pred. No. 9.4e-10;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGGLGVGAGVPGFAG 41
 Db 76 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGGLGVGAGVPGFAG 116
 RESULT 6
 Q6ZJW6 ID Q6ZJW6 PRELIMINARY; PRT; 570 AA.
 AC Q6ZJW6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DR EMBL; U93034; AAB65621.1; JOINED.
 DR EMBL; U93035; AAB65621.1; JOINED.
 DR EMBL; U93036; AAB65621.1; JOINED.
 DR GO; GO:0005578; C:extracellular matrix; IEA.
 DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
 DR InterPro; IPR001451; Hexapep transf.
 DR InterPro; IPR003979; tropoelastin.
 DR PRINTS; PR01500; TROPELASTIN.
 DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
 FT NON_TER 1 635
 FT NON_TER 635
 SQ SEQUENCE 635 AA; 55279 MW; 72950C364127B2A4 CRC64;
 Query Match 96.8%; Score 245; DB 2; Length 635;
 Best Local Similarity 98.0%; Pred. No. 4.3e-12;
 Matches 48; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGGLGVGAGVPGFAGDEGVRR 49
 Db 549 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGGLGVGAGVPGFAGDEGVRR 597

RESULT 5

ID Q9UMF5 PRELIMINARY; PRT; 258 AA.
 AC Q9UMF5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Elastin (Fragment).
 GN Name=ELN;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP RP
 RX MEDLINE=96411691; PubMed=8812460;
 RA Osborne L.R., Martindale D.W., Scherer S.W., Shi X.-M., Huizenga J.,
 RA Heng H.H.Q., Costa T., Pober B., Lew L., Brinkman J., Rommens J.,
 RA Koop B.F., Tsui L.-C.;
 RT "Identification of genes from a 500-kb region at 7q11.23 that is
 RT commonly deleted in Williams syndrome patients.";
 RL Genomics 36:328-336 (1996).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP RP
 RX MEDLINE=20458868; PubMed=11003705;
 RA Martindale D.W., Wilson M.D., Wang D., Burke R.D., Chen X.,
 RA Duronio V., Koop B.F.;
 RT "Comparative genomic sequence analysis of the Williams syndrome region
 RT (LIMK1-RFC2) of human chromosome 7q11.23.";
 RL Mamm. Genome 11:890-898 (2000).
 DR EMBL; U63721; AAC13884.1; --
 DR InterPro; IPR001451; Hexapep transf.
 DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
 FT NON_TER 1 635
 FT NON_TER 635
 SQ SEQUENCE 258 AA; 21990 MW; C39BF7298D0E05D2 CRC64;
 Query Match 83.8%; Score 212; DB 2; Length 258;
 Best Local Similarity 100.0%; Pred. No. 9.4e-10;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGGLGVGAGVPGFAG 41
 Db 76 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGGLGVGAGVPGFAG 116
 RESULT 6
 Q6ZJW6 ID Q6ZJW6 PRELIMINARY; PRT; 570 AA.
 AC Q6ZJW6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

```

05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein FLJ16246.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,
RA Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
RA Masuho Y., Nagai K., Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK122731; BAC85506.1; -.
DR InterPro; IPR001451; Hexapep.transf.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOLASTIN.
DR PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.
SQ SEQUENCE 570 AA; 48941 MW; 3117B028D06D4F7B_CRC64;

Query Match 83.8%; Score 212; DB 2; Length 570;
Best Local Similarity 100.0%; Pred. No. 1.7e-09;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGLGAGIPGLGVGVGPGGLGVGAGVPGGLGVGAGVPGFGA 41
DB 406 AAAGLGAGIPGLGVGVGPGGLGVGAGVPGGLGVGAGVPGFGA 446

RESULT 7
BAC85506 PRELIMINARY; PRT; 570 AA.
AC BAC85506;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE CDNA FLJ16246 fis, clone HCHON2001577, highly similar to Human elastin
DE gene.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,
RA Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
RA Masuho Y., Nagai K., Isogai T.;
RL "NEDO human cDNA sequencing project.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK122731; BAC85506.1; -.
SQ SEQUENCE 570 AA; 48941 MW; 3117B028D06D4F7B_CRC64;

Query Match 83.8%; Score 212; DB 2; Length 570;
Best Local Similarity 100.0%; Pred. No. 1.7e-09;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGLGAGIPGLGVGVGPGGLGVGAGVPGGLGVGAGVPGFGA 41
DB 406 AAAGLGAGIPGLGVGVGPGGLGVGAGVPGGLGVGAGVPGFGA 446

RESULT 8
Q8NB14 PRELIMINARY; PRT; 643 AA.
AC Q8NB14;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein PSEC0254.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
RA Nagahari K., Sugano S., Isogai T.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK075554; BAC11696.1; -.
DR HSSP; P50099; IZFU.
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro; IPR001451; Hexapep.transf.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOLASTIN.
DR PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.
SQ SEQUENCE 643 AA; 55629 MW; FDFC042617E72A69_CRC64;

Query Match 83.8%; Score 212; DB 2; Length 643;
Best Local Similarity 100.0%; Pred. No. 1.9e-09;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGLGAGIPGLGVGVGPGGLGVGAGVPGGLGVGAGVPGFGA 41
DB 461 AAAGLGAGIPGLGVGVGPGGLGVGAGVPGGLGVGAGVPGFGA 501

RESULT 9
Q14235 PRELIMINARY; PRT; 687 AA.
AC Q14235;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Elastin.
DE Name=ELN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
RA Rosenbloom J.C., Peltonen L., Rosenbloom J.;
RT "Alternative splicing of human elastin mRNA indicated by sequence
RT analysis of cloned genomic and complementary DNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684 (1987).
RN [2]
RP SEQUENCE FROM N.A.
RA Indik Z., Yoon K., Morrow S.D., Cicilia G., Rosenbloom J.,
RA Rosenbloom J., Ornstein-Goldstein N.;
RT "Structure of the 3' region of the human elastin gene; great abundance
RT of Alu repetitive sequences and few coding sequences.";
RL Connect. Tissue Res. 16:197-211 (1987).
DR EMBL; M17282; AAC98393.1; -.
DR EMBL; M16983; AAC98393.1; JOINED.
DR EMBL; M17265; AAC98393.1; JOINED.
DR EMBL; M17266; AAC98393.1; JOINED.
DR EMBL; M17267; AAC98393.1; JOINED.
DR EMBL; M17268; AAC98393.1; JOINED.
DR EMBL; M17271; AAC98393.1; JOINED.
DR EMBL; M17272; AAC98393.1; JOINED.
DR EMBL; M17273; AAC98393.1; JOINED.
DR EMBL; M17275; AAC98393.1; JOINED.

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DR EMBL; M17276; AAC98393.1; JOINED.
 DR EMBL; M17277; AAC98393.1; JOINED.
 DR EMBL; M17278; AAC98393.1; JOINED.
 DR EMBL; M17279; AAC98393.1; JOINED.
 DR EMBL; M17281; AAC98393.1; JOINED.
 DR HSP; P50099; 12FJ.
 DR GO; GO:0005578; C:extracellular matrix; NAS.
 DR GO; GO:0030023; F:extracellular matrix constituent conferring...; NAS.
 DR InterPro; IPR001451; Hexapep transf.
 DR InterPro; IPR003979; tropoelastin.
 DR PRINTS; PR01500; TROPOELASTIN.
 DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
 SQ SEQUENCE 687 AA; 59529 MW; 8640684C859F88F CRC64;
 Query Match 83.8%; Score 212; DB 2; Length 687;
 Best Local Similarity 100.0%; Pred. No. 2e-09;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAAGLGAGIPGLGVGVGPGVGLGVGAGVPGVGLGVGAGVPGFGA 41
 DB 523 AAAGLGAGIPGLGVGVGPGVGLGVGAGVPGVGLGVGAGVPGFGA 563
 RESULT 10
 Q72316 PRELIMINARY; PRT; 687 AA.
 AC Q72316
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein DKFZp686O21208 (Fragment).
 GN Name=DKFZp686O21208;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human rectum tumor;
 RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
 RA Han M., Wiemann S.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX538199; CAD9065.1; -
 DR InterPro; IPR001451; Hexapep transf.
 DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 687 AA; 59847 MW; 79232A191DC1F10F CRC64;
 Query Match 83.8%; Score 212; DB 2; Length 687;
 Best Local Similarity 100.0%; Pred. No. 2e-09;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAAGLGAGIPGLGVGVGPGVGLGVGAGVPGVGLGVGAGVPGFGA 41
 DB 523 AAAGLGAGIPGLGVGVGPGVGLGVGAGVPGVGLGVGAGVPGFGA 563
 RESULT 11
 Q723F5 PRELIMINARY; PRT; 711 AA.
 AC Q723F5;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein DKFZp686F06102;
 GN Name=DKFZp686F06102;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Human fetal kidney;
 RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
 RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX537939; CAD97910.1; -
 DR InterPro; IPR001451; Hexapep transf.
 DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 711 AA; 61765 MW; 95B624A99B4A989B CRC64;
 Query Match 83.8%; Score 212; DB 2; Length 711;
 Best Local Similarity 100.0%; Pred. No. 2e-09;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAAGLGAGIPGLGVGVGPGVGLGVGAGVPGVGLGVGAGVPGFGA 41
 DB 547 AAAGLGAGIPGLGVGVGPGVGLGVGAGVPGVGLGVGAGVPGFGA 587
 RESULT 12
 ELS_HUMAN
 ID ELS_HUMAN STANDARD; PRT; 730 AA.
 AC F1502; Q14233; Q14238;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Elastin precursor (Tropoelastin).
 GN Name=ELN;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM B).
 RX MEDLINE=87289668; PubMed=3039501;
 RA Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,
 RA Rosenbloom J.C., Peltonen L., Rosenbloom J.;
 RT "Alternative splicing of human elastin mRNA indicated by sequence
 RT analysis of cloned genomic and complementary DNA.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684 (1987).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Skin fibroblast;
 RX MEDLINE=89009960; PubMed=3171221;
 RA Fazio M.J., Olsen D.R., Kauh E.A., Baldwin C.T., Indik Z.,
 RA Ornstein-Goldstein N., Yeh H., Rosenbloom J., Utito J.;
 RT "Cloning of full-length elastin cDNAs from a human skin fibroblast
 RT recombinant cDNA library: further elucidation of alternative splicing
 RT utilizing exon-specific oligonucleotides.";
 RL J. Invest. Dermatol. 91:458-464 (1988).
 RN [3]
 RP SEQUENCE OF 164-724 FROM N.A. (ISOFORM B).
 RC TISSUE=Placenta;
 RX MEDLINE=88156138; PubMed=2831431;
 RA Fazio M.J., Olsen D.R., Kuivaniemi H., Chu M.L., Davidson J.M.,
 RA Rosenbloom J., Utito J.;
 RT "Isolation and characterization of human elastin cDNAs, and age-
 RT associated variation in elastin gene expression in cultured skin
 RT fibroblasts.";
 RL Lab. Invest. 58:270-277 (1988).
 RN [4]
 RP SEQUENCE OF 603-730 FROM N.A.
 RC TISSUE=Hippocampus, and Placenta;
 RX MEDLINE=96291399; PubMed=8689688;
 RA Frangiskakis J.M., Ewart A.K., Morris C.A., Mervis C.B., Bertrand J.,
 RA Robinson B.F., Klein B.P., Ensing G.J., Everett L.A., Green E.D.,
 RA Proeschel C., Gutowski N.J., Noble M., Atkinson D.L., Odelberg S.J.,
 RA Keating M.T.;
 RT "LIM-kinase hemizygosity implicated in impaired visuospatial
 RT constructive cognition.";
 RL Cell 86:59-69 (1996).
 RN [5]
 RP INVOLVEMENT IN CUTIS LAXA.

RX MEDLINE=99091639; PubMed=9873040;
 RA Zhang M.-C., He L., Giro M., Yong S.L., Tiller G.E., Davidson J.M.;
 RT "Cutis laxa arising from frameshift mutations in exon 30 of the
 RT elastin gene (ELN).";
 RL J. Biol. Chem. 274:981-986(1999).
 RN [6]
 RP INVOLVEMENT IN SVAS.
 RX PubMed=10942104;
 RA Urban Z., Michels V.V., Thibodeau S.N., Davis E.C., Bonnefont J.-P.,
 RA Munich A., Eyskens B., Gewillig M., Devriendt K., Boyd C.D.;
 RA "Isolated supravalvular aortic stenosis: functional haploinsufficiency
 RT of the elastin gene as a result of nonsense-mediated decay.";
 RL Hum. Genet. 106:577-588(2000).
 CC -!- FUNCTION: Major structural protein of tissues such as aorta and
 CC nuchal ligament, which must expand rapidly and recover completely.
 CC -!- SUBUNIT: The polymeric elastin chains are cross-linked together
 CC into an extensible 3D network.
 CC -!- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;
 CC Name=1;
 CC IsoId=P15502-1; Sequence=displayed;
 CC Name=2;
 CC IsoId=P15502-2; Sequence=VSP_004243;
 CC -!- PTM: The crosslinks are made of deaminated Lys.
 CC -!- DISEASE: Defects in ELN are a cause of autosomal dominant cutis
 CC laxa [MIM:123700]. Cutis laxa is a rare connective tissue disorder
 CC characterized by loose, hyperextensible skin with decreased
 CC resilience and elasticity leading to a premature aged appearance.
 CC The skin changes are often accompanied by extracutaneous
 CC manifestations, including pulmonary emphysema, bladder
 CC diverticula, pulmonary artery stenosis and pyloric stenosis.
 CC -!- DISEASE: Haploinsufficiency of ELN may be the cause of certain
 CC cardiovascular and musculo-skeletal abnormalities observed in
 CC Williams-Beuren syndrome (WBS) [MIM:194050]. WBS is a rare
 CC developmental disorder and a contiguous gene deletion syndrome
 CC involving genes from chromosome band 7q11.23.
 CC -!- DISEASE: Defects in ELN are the cause of supravalvular aortic
 CC stenosis (SVAS) [MIM:185500]. SVAS is a congenital narrowing of
 CC the ascending aorta which can occur sporadically, as an autosomal
 CC dominant condition, or as one component of Williams-Beuren
 CC syndrome.

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EMBL; M17282; AAC98394.1; JOINED.
 EMBL; M16983; AAC98394.1; JOINED.
 EMBL; M17265; AAC98394.1; JOINED.
 EMBL; M17266; AAC98394.1; JOINED.
 EMBL; M17267; AAC98394.1; JOINED.
 EMBL; M17268; AAC98394.1; JOINED.
 EMBL; M17270; AAC98394.1; JOINED.
 EMBL; M17271; AAC98394.1; JOINED.
 EMBL; M17272; AAC98394.1; JOINED.
 EMBL; M17273; AAC98394.1; JOINED.
 EMBL; M17275; AAC98394.1; JOINED.
 EMBL; M17276; AAC98394.1; JOINED.
 EMBL; M17277; AAC98394.1; JOINED.
 EMBL; M17278; AAC98394.1; JOINED.
 EMBL; M17279; AAC98394.1; JOINED.
 EMBL; M17280; AAC98394.1; JOINED.
 EMBL; M17281; AAC98394.1; JOINED.
 EMBL; M36860; AAC52382.1; -
 EMBL; M24782; AAC53190.1; -
 EMBL; U62292; AAB17544.1; -
 EMBL; X15603; CAA33627.1; -

DR PIR: A32707; EAHU.
 DR HSSP: P50099; 1ZFU.
 DR Genew: HGNC:3327; ELM.
 DR MIM: 130160; -
 DR MIM: 123700; -
 DR MIM: 194050; -
 DR MIM: 185500; -
 DR GO: GO:0005578; C:extracellular matrix; TAS.
 DR GO: GO:0005615; C:extracellular space; TAS.
 DR GO: GO:0005201; F:extracellular matrix structural constituent; TAS.
 DR GO: GO:0008283; P:cell proliferation; TAS.
 DR GO: GO:0008015; P:circulation; TAS.
 DR GO: GO:0009887; P:organogenesis; TAS.
 DR GO: GO:0007585; P:respiratory gaseous exchange; TAS.
 DR InterPro: IPR003979; tropoelastin.
 DR PRINTS: PR01500; TROPOELASTIN.
 DR KW Alternative splicing; Connective tissue; Repeat; Signal;
 KW Structural protein; Williams-Beuren syndrome.
 FT SIGNAL 1 26 Elastin.
 FT CHAIN 27 730 By similarity.
 FT DISULFID 720 725 Missing (in isoform 2).
 FT VARSPPLIC 472 477 Missing (in isoform 2).
 FT /FTId=VSP_004243.
 FT SQ SEQUENCE 730 AA; 63260 MW; AB06D15BA567A246 CRC64;
 Query Match 83.8%; Score 212; DB 1; Length 730;
 Best Local Similarity 100.0%; Pred. No. 2.1e-09;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAAGLGGAGIPGLGVGVGPGLVGVGAGVPGVGVGAGVPGFGA 41
 DB 548 AAAGLGGAGIPGLGVGVGPGLVGVGAGVPGVGVGAGVPGFGA 588
 RESULT 13
 Q8N2G0 PRELIMINARY; PRT; 472 AA.
 AC Q8N2G0;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein PSEC0191.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCI_TaxID=9606;
 OX [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Whole embryo;
 RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
 RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
 RA Nagahari K., Sugano S., Isogai T.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK075494; BAC11651.1; -
 DR GO: GO:0005578; C:extracellular matrix structural constituent; IEA.
 DR GO: GO:0005201; F:extracellular matrix structural constituent; IEA.
 DR InterPro: IPR001451; Hexapep transf.
 DR InterPro: IPR003979; tropoelastin.
 DR PRINTS: PR01500; TROPOELASTIN
 DR PROSITE: PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
 FT NON_TER 472 472
 FT SQ SEQUENCE 472 AA; 42265 MW; 8D7A0F3A9BF971F3 CRC64;
 Query Match 82.2%; Score 208; DB 2; Length 472;
 Best Local Similarity 97.6%; Pred. No. 3.1e-09;
 Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AAAGLGGAGIPGLGVGVGPGLVGVGAGVPGVGVGAGVPGFGA 41
 DB 316 AAAGLGGAGIPGLGVGVGPGLVGVGAGVPGVGVGAGVPGFGA 356
 RESULT 14

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Q28097
ID Q28097 PRELIMINARY; PRT; 679 AA.
AC Q28097;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ELASTIN-CBRL2; NCBI gi: 163004 (fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85280426; PubMed=2992576;
RA Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow S.,
RA Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;
RT "Structure of the 3' portion of the bovine elastin gene.";
RL Biochemistry 24:3075-3080(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=8028442; PubMed=3665402;
RA Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N.,
RA Rosenbloom J.C., Cicila G., Yoon K., Rosenbloom J.;
RT "Sequence variation of bovine elastin mRNA due to alternative
RT splicing.";
RL Coll. Relat. Res. 7:235-247(1987).
DR EMBL; M19372; AAA30500.1; -.
DR EMBL; M11422; AAA30500.1; JOINED.
DR EMBL; M19366; AAA30500.1; JOINED.
DR EMBL; M19367; AAA30500.1; JOINED.
DR EMBL; M19368; AAA30500.1; JOINED.
DR EMBL; M19369; AAA30500.1; JOINED.
DR EMBL; M19370; AAA30500.1; JOINED.
DR EMBL; M19371; AAA30500.1; JOINED.
DR EMBL; M22771; AAA30500.1; JOINED.
DR EMBL; M22772; AAA30500.1; JOINED.
DR EMBL; M22773; AAA30500.1; JOINED.
DR EMBL; M22774; AAA30500.1; JOINED.
DR EMBL; M22988; AAA30500.1; JOINED.
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN.
FT NON TER 1
SQ SEQUENCE 679 AA; 57652 MW; EB3C019E3BD7618D CRC64;

Query Match 81.0%; Score 205; DB 2; Length 679;
Best Local Similarity 92.9%; Pred. No. 7.1e-09;
Matches 39; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAAGLGAGIPGLGVGVGPGVGLGVGAGVPGVPGFAG 42
Db 502 AAAGLGAGVPGVGLGVGVGPGVGLGVGAGVPGVPGFAG 543

RESULT 15
O15337
ID O15337 PRELIMINARY; PRT; 602 AA.
AC O15337;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Elastin (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97358574; PubMed=9215670;
RA Li D.Y., Toland A.E., Boak B.B., Atkinson D.L., Ensing G.J.,
RA Morris C.A., Keating M.T.;

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RT "Elastin point mutations cause an obstructive vascular disease,
RT supralvalvular aortic stenosis.";
RL Hum. Mol. Genet. 6:1021-1028(1997).
DR EMBL; U93037; AAB65620.1; -.
DR EMBL; U93034; AAB65620.1; JOINED.
DR EMBL; U93035; AAB65620.1; JOINED.
DR EMBL; U93036; AAB65620.1; JOINED.
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro; IPR001451; Hexapep transf.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN.
DR PROSITE; PS00101; HEXAPEP_TRANSFEROSES; UNKNOWN_1.
FT NON TER 1
FT NON TER 602
SQ SEQUENCE 602 AA; 51807 MW; 53B5B9A71EF04807 CRC64;

Query Match 80.6%; Score 204; DB 2; Length 602;
Best Local Similarity 97.6%; Pred. No. 7.8e-09;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAAGLGAGIPGLGVGVGPGVGLGVGAGVPGVPGFAG 41
Db 549 AAAGLGAGIPGLGVGVGPGVGLGVGAGVPGVPGFAG 589

RESULT 16
Q6P0L4
ID Q6P0L4 PRELIMINARY; PRT; 658 AA.
AC Q6P0L4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE ELN protein.
GN Name=ELN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX Strausberg R.;
RA Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065566; AAB65566.1; -.
DR InterPro; IPR001451; Hexapep transf.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN.
DR PROSITE; PS00101; HEXAPEP_TRANSFEROSES; UNKNOWN_1.

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Mon Nov 22 12:42:44 2004

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SQ SEQUENCE 658 AA; 56680 MW; 5DAFC00D16A2F94E CRC64;
Query Match 80.6%; Score 204; DB 2; Length 658;
Best Local Similarity 97.6%; Pred. No. 8.3e-09;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAGLGAGIPGLGVGVGPGVLGVGAGVPGVLGVGAGVPGFGA 41
    |||||
    494 AAAGLGAGIPGLGVGVGPGVLGVGAGVPGVLGVGAGVPGFGA 534

RESULT 17
AAH65566 PRELIMINARY; PRT; 658 AA.
ID AAH65566
AC AAH65566;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE ELN protein.
GN ELN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abranson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Lu X., Gibbs R.A.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX Strausberg R.;
RA Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065566; AAH65566.1; 5DAFC00D16A2F94E CRC64;
SQ SEQUENCE 658 AA; 56680 MW; 5DAFC00D16A2F94E CRC64;

Query Match 80.6%; Score 204; DB 2; Length 658;
Best Local Similarity 97.6%; Pred. No. 8.3e-09;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAGLGAGIPGLGVGVGPGVLGVGAGVPGVLGVGAGVPGFGA 41
    |||||
    494 AAAGLGAGIPGLGVGVGPGVLGVGAGVPGVLGVGAGVPGFGA 534

RESULT 18
Q28099 PRELIMINARY; PRT; 650 AA.
ID Q28099
AC Q28099;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Elastin-CBEL1; NCBI gi: 163003 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae;
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85280426; PubMed=2992576;
RA Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow S.,
RA Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;
RT "Structure of the 3' portion of the bovine elastin gene."
RL Biochemistry 24:3075-3080(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88028442; PubMed=3665402;
RA Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N.,
RA Rosenbloom J.C., Cicila G., Yoon K., Rosenbloom J.;
RT "Sequence variation of bovine elastin mRNA due to alternative
RT splicing."
RL Coll. Relat. Res. 7:235-247(1987).
DR EMBL; M19372; AAA30499.1; JOINED.
DR EMBL; M11422; AAA30499.1; JOINED.
DR EMBL; M19366; AAA30499.1; JOINED.
DR EMBL; M19368; AAA30499.1; JOINED.
DR EMBL; M19369; AAA30499.1; JOINED.
DR EMBL; M19370; AAA30499.1; JOINED.
DR EMBL; M19371; AAA30499.1; JOINED.
DR EMBL; M22771; AAA30499.1; JOINED.
DR EMBL; M22772; AAA30499.1; JOINED.
DR EMBL; M22773; AAA30499.1; JOINED.
DR EMBL; M22774; AAA30499.1; JOINED.
DR EMBL; M22775; AAA30499.1; JOINED.
DR EMBL; M22988; AAA30499.1; JOINED.
DR EMBL; M23010; AAA30499.1; JOINED.
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro; IPR001979; tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN.
DR NON TER 1
SQ SEQUENCE 650 AA; 55373 MW; CD21ABB3E9076AD7 CRC64;

Query Match 78.7%; Score 199; DB 2; Length 650;
Best Local Similarity 92.7%; Pred. No. 2.1e-08;
Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAAGLGAGIPGLGVGVGPGVLGVGAGVPGVLGVGAGVPGFGA 41
    |||||
    468 AAAGLGAGIPGLGVGVGPGVLGVGAGVPGVLGVGAGVPGFGA 508

RESULT 19
Q28096 PRELIMINARY; PRT; 666 AA.
ID Q28096
AC Q28096;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Elastin-CBEL3; NCBI gi: 163005 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae;
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85280426; PubMed=2992576;
RA Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow S.,
RA Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;
RT "Structure of the 3' portion of the bovine elastin gene."
RL Biochemistry 24:3075-3080(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88028442; PubMed=3665402;

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RA Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N.,
 RA Rosenbloom J.C., Cicila G., Yoon K., Rosenbloom J.;
 RT "Sequence variation of bovine elastin mRNA due to alternative
 RL splicing.";
 RL Coll. Relat. Res. 7:235-247(1987).
 DR EMBL; M19372; AAA30501.1; JOINED.
 DR EMBL; M11422; AAA30501.1; JOINED.
 DR EMBL; M19366; AAA30501.1; JOINED.
 DR EMBL; M19367; AAA30501.1; JOINED.
 DR EMBL; M19368; AAA30501.1; JOINED.
 DR EMBL; M19369; AAA30501.1; JOINED.
 DR EMBL; M19370; AAA30501.1; JOINED.
 DR EMBL; M19371; AAA30501.1; JOINED.
 DR EMBL; M22771; AAA30501.1; JOINED.
 DR EMBL; M22772; AAA30501.1; JOINED.
 DR EMBL; M22773; AAA30501.1; JOINED.
 DR EMBL; M22774; AAA30501.1; JOINED.
 DR EMBL; M22775; AAA30501.1; JOINED.
 DR EMBL; M22988; AAA30501.1; JOINED.
 DR GO; GO:0005578; C:extracellular matrix; IEA.
 DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
 DR InterPro; IPR003979; tropoelastin.
 DR PRINTS; PR01500; TROPOELASTIN.
 FT NON TER 1
 SQ SEQUENCE 666 AA; 56435 MW; BC5E62632BE1B71 CRC64;
 Query Match 78.7%; Score 199; DB 2; Length 666;
 Best Local Similarity 92.7%; Pred. No. 2.1e-08;
 Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 AAAGLGAGIPGLGVGVGPGVGLGVGAGVPGVGLGVGAGVPGFGA 41
 Db 476 AAAGLPAGVPGVGLGVGVGPGVGLGVGAGVPGVGLGVGAGVPGFGA 516
 RESULT 20
 Q28098
 ID Q28098 PRELIMINARY; PRT; 707 AA.
 AC Q28098;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Elastin; NCBI gi: 163002 (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85280426; PubMed=2992576;
 RA Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow S.,
 RA Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;
 RT "Structure of the 3' portion of the bovine elastin gene.";
 RL Biochemistry 24:3075-3080(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88028442; PubMed=3665402;
 RA Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N.,
 RA Rosenbloom J.C., Cicila G., Yoon K., Rosenbloom J.;
 RT "Sequence variation of bovine elastin mRNA due to alternative
 RL splicing.";
 RL Coll. Relat. Res. 7:235-247(1987).
 DR EMBL; M19372; AAA30498.1; JOINED.
 DR EMBL; M11422; AAA30498.1; JOINED.
 DR EMBL; M19366; AAA30498.1; JOINED.
 DR EMBL; M19367; AAA30498.1; JOINED.
 DR EMBL; M19368; AAA30498.1; JOINED.
 DR EMBL; M19369; AAA30498.1; JOINED.
 DR EMBL; M19370; AAA30498.1; JOINED.
 DR EMBL; M19371; AAA30498.1; JOINED.
 DR EMBL; M22771; AAA30498.1; JOINED.
 DR EMBL; M22772; AAA30498.1; JOINED.

DR EMBL; M22773; AAA30498.1; JOINED.
 DR EMBL; M22774; AAA30498.1; JOINED.
 DR EMBL; M22775; AAA30498.1; JOINED.
 DR EMBL; M22988; AAA30498.1; JOINED.
 DR EMBL; M23010; AAA30498.1; JOINED.
 DR GO; GO:0005578; C:extracellular matrix; IEA.
 DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
 DR InterPro; IPR003979; tropoelastin.
 DR PRINTS; PR01500; TROPOELASTIN.
 FT NON TER 1
 SQ SEQUENCE 707 AA; 60346 MW; FDPD559BAB34CE33 CRC64;
 Query Match 78.7%; Score 199; DB 2; Length 707;
 Best Local Similarity 92.7%; Pred. No. 2.2e-08;
 Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 AAAGLGAGIPGLGVGVGPGVGLGVGAGVPGVGLGVGAGVPGFGA 41
 Db 502 AAAGLPAGVPGVGLGVGVGPGVGLGVGAGVPGVGLGVGAGVPGFGA 542
 RESULT 21
 Q9ESZ9
 ID Q9ESZ9 PRELIMINARY; PRT; 810 AA.
 AC Q9ESZ9;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE ELN (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Sv;
 RA Green E.D.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF289665; AAF99336.1; -.
 DR GO; GO:0005578; C:extracellular matrix; IEA.
 DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
 DR InterPro; IPR003979; tropoelastin.
 DR PRINTS; PR01500; TROPOELASTIN.
 FT NON TER 1
 SQ SEQUENCE 810 AA; 67204 MW; 1ED61ED5AD4F40A2 CRC64;
 Query Match 76.3%; Score 193; DB 2; Length 810;
 Best Local Similarity 81.4%; Pred. No. 7.4e-08;
 Matches 35; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
 QY 1 AAAGLGAGIPGLGVGVGPGVGLGVGAGVPGVGLGVGAGVPGFGA 43
 Db 558 AAAGLGAGVPGVPGVGLGVGAGVPGVGLGVGAGVPGFGA 600
 RESULT 22
 ELS_MOUSE
 ID ELS_MOUSE STANDARD; PRT; 860 AA.
 AC P54320;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 34, Last annotation update)
 DE Elastin precursor (Tropoelastin).
 GN Name=Elm;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Lung;
 RX MEDLINE=95130069; PubMed=7829060;
 RA Wydner K.S., Sechler J.L., Boyd C.D., Passmore H.C.;

GO; GO:0007519; P:myogenesis; IMP.
GO; GO:0030833; P:regulation of actin filament polymerization; IMP.
GO; GO:0043149; P:stress fiber formation; IMP.
InterPro; IPR003979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
SEQUENCE 860 AA; 71398 MW; 7C340F2FFDC92B5 CRC64;

Query Match 76.3%; Score 193; DB 2; Length 860;
Best Local Similarity 81.4%; Pred. No. 7.7e-08;
Matches 35; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 AAAGLGAGIGPLGVGVGPGVLGVGAGVPGVLGVGAGVPGFGAGA 43
DB 608 AAAGLGAGVPGFGAGAGVPGFGAGAGVPGFGAGAGVPGFGAGA 650

RESULT 24
ELS BOVIN
ID ELS BOVIN STANDARD; PRT; 747 AA.
AC P04985; P04986; P04987; Q99421;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Elastin precursor (Tropoelastin).
GN Name=ELN;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
ON NCBI_TaxID=9913;
RX [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87194772; PubMed=3032943;
RA Raju K., Anwar R.A.;
RT "Primary structures of bovine elastin a, b, and c deduced from the
sequences of cDNA clones."
RL J. Biol. Chem. 262:5755-5762(1987).
RN [2]
RP SEQUENCE OF 1-27 FROM N.A.
RC TISSUE=Nuchal ligament;
RX MEDLINE=89274159; PubMed=2543440;
RA Yeh H., Anderson N., Ornstein-Goldstein N., Bashir M.M.,
RA Rosenbloom J.C., Abrams W.R., Indik Z., Yoon K., Parks W., Mecham R.,
RA Rosenbloom J.;
RT "Structure of the bovine elastin gene and S1 nuclease analysis of
alternative splicing of elastin mRNA in the bovine nuchal ligament."
RN Biochemistry 28:2365-2370(1989).
RX [3]
RP SEQUENCE OF 1-27 FROM N.A.
RX MEDLINE=91234332; PubMed=2031719;
RA Manohar A., Shi W., Anwar R.A.;
RT "Partial characterization of bovine elastin gene; comparison with the
gene for human elastin."
RN Biochem. Cell Biol. 69:185-192(1991).
RX [4]
RP DISULFIDE BOND.
RX MEDLINE=92337651; PubMed=1632791;
RA Brown P.L., Mecham R., Tisdale C., Mecham R.P.;
RT "The cysteine residues in the carboxy terminal domain of tropoelastin
form an intrachain disulfide bond that stabilizes a loop structure and
positively charged pocket."
RN Biochem. Biophys. Res. Commun. 186:549-555(1992).
CC -!- FUNCTION: Major structural protein of tissues such as aorta and
nuchal ligament, which must expand rapidly and recover completely.
CC -!- SUBUNIT: The polymeric elastin chains are cross-linked together
into an extensible 3D network.
CC -!- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=A;
CC IsoId=P04985-1; Sequence=Displayed;
CC Name=2; Synonyms=B;
CC IsoId=P04985-2; Sequence=VSP_004239;

Name=3; Synonyms=C;
IsoId=P04985-3; Sequence=VSP_004240;
-!- PTM: The crosslinks are made of deaminated lys.
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EMBL; J02717; AAA30503.1; -
EMBL; K03505; AAA30505.1; -
EMBL; K03506; AAA30506.1; -
EMBL; J02855; AAA30776.1; -
EMBL; M58652; AAA03519.2; -
PIR; A31865; EABO.
InterPro; IPR003979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
Alternative splicing; Connective tissue; Repeat; Signal;
Structural protein.
FT SIGNAL 1 26
FT CHAIN 27 747 Elastin.
FT DISULFID 737 742
FT MOD_RES 105 105 Allylsine.
FT MOD_RES 109 109 Allylsine.
FT MOD_RES 252 252 Allylsine.
FT MOD_RES 271 271 Allylsine.
FT MOD_RES 275 275 Allylsine.
FT MOD_RES 324 324 Allylsine.
FT MOD_RES 327 327 Allylsine.
FT MOD_RES 400 400 Allylsine.
FT MOD_RES 404 404 Allylsine.
FT MOD_RES 448 448 Allylsine.
FT MOD_RES 489 489 Allylsine.
FT MOD_RES 493 493 Allylsine.
FT MOD_RES 544 544 Allylsine.
FT MOD_RES 552 552 Allylsine.
FT MOD_RES 606 606 Allylsine.
FT MOD_RES 609 609 Allylsine.
FT MOD_RES 645 645 Allylsine.
FT MOD_RES 649 649 Allylsine.
FT MOD_RES 685 685 Allylsine.
FT MOD_RES 688 688 Allylsine.
FT VARSPPLIC 226 239 Missing (in isoform 2).
FT VARSPPLIC 226 259 /FTId=VSP_004239.
FT VARSPPLIC 226 259 /FTId=VSP_004240.
FT CONFLICT 1 3 MRS -> MAG (in Ref. 2 and 3).
FT CONFLICT 12 12 E -> G (in Ref. 2 and 3).
SQ SEQUENCE 747 AA; 64229 MW; 633C03E411643D83 CRC64;

Query Match 74.7%; Score 189; DB 1; Length 747;
Best Local Similarity 90.2%; Pred. No. 1.4e-07;
Matches 37; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAAGLGAGIGPLGVGVGPGVLGVGAGVPGVLGVGAGVPGFGAGA 41
DB 557 AAAGLGAGVPGVLGVGAGVPGVLGVGAGVPGFGAGA 597

RESULT 25
ELS RAT
ID ELS RAT STANDARD; PRT; 864 AA.
AC Q99372;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Elastin precursor (Tropoelastin) (Fragment).
GN Name=Eln;

R	EMBL; J04035; AAA42268.1;	-
R	EMBL; M86372; AAA42271.1;	-
R	EMBL; M86395; AAA42271.1;	JOINED.
R	EMBL; M86363; AAA42271.1;	JOINED.
R	EMBL; M86364; AAA42271.1;	JOINED.
R	EMBL; M86366; AAA42271.1;	JOINED.
R	EMBL; M86371; AAA42271.1;	JOINED.
R	EMBL; M86376; AAA42272.1;	-
R	EMBL; M86373; AAA42272.1;	JOINED.
R	EMBL; M86375; AAA42272.1;	JOINED.
R	PIR; A36106; EART.	
R	RGD; 67394; Eln.	
R	InterPro; IPR003979; tropoelastin.	
R	PRINTS; PR01500; TROPOELASTIN.	
KW	Alternative splicing; Connective tissue; Repeat; Signal;	
T	Structural protein.	
T	NON TER	1
T	SIGNAL	<1
T	CHAIN	22
T	DISULFID	854
T	VARSPLIC	263
T		307
T		
T	VARSPLIC	308
T		308
T		
T	VARSPLIC	809
T		823
T		
T	SEQUENCE	864 AA; 72786 MW; 456894BB09E79FD4 CRC64;
Q	Query Match	71.5%; Score 181; DB 1; Length 864;
Y	Best Local Similarity	78.3%; Pred. No. 7e-07
B	Matches	36; Conservative 1; Mismatches 7; Indels 2; Gaps 1;
D		
B		
Y	1	AAGGLGAGIPGLGVGVPGPLGVGGVGPGLGVGGVGPGLGVGGVGPFGGADRG 46 : : : : : : : : :
D	622	AAAGLGGVPGLVGGVGPFGVGAGAG--GFGAGAGVPFGGAVPG 665 : : : : : : : :
RESULT	26	
Q	PRELIMINARY;	PRT; 1092 AA.
D	Q964R2	
A	Q964R2;	
C	01-DEC-2001 (TrEMBLrel. 19, Created)	
D	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)	
T	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	
D	Sporozoite surface antigen STAG-1 (Fragment).	
E	Name=STAG-1;	
O	Theileria taurotrogi.	
O	Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;	
C	Theileria.	
O	NCBI_TaxID=27993;	
R	[1]_TaxID=27993;	
N	SEQUENCE FROM N.A.	
R	Skilton R.A., Wasawo D.P.S., Morzaria S.P.;	
L	Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.	
R	EMBL; AF275878; AAK69409.1; -	
D	InterPro; IPR008845; Sporozoite_P67.	
R	pfam; PF05642; Sporozoite_P67; 1.	
D	NON TER	1092 1092
F	FT	
S	SEQUENCE	1092 AA; 110405 MW; F2AF0B0D56BF622A CRC64;
Q	Query Match	52.0%; Score 131.5; DB 2; Length 1092;
Y	Best Local Similarity	65.9%; Pred. No. 0.0076;
B	Matches	29; Conservative 4; Mismatches 8; Indels 3; Gaps 3;
Y	6	GAGIPCLGV-GVGVPGPLGV-GAGVPCPLGV-GAGVPGFGGAGAEG 46 ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::
D	187	GVGVPGVPGVGVGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVGAAPGVG 230 ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::
RESULT	27	

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ELS_CHICK
ID ELS_CHICK STANDARD; PRT; 750 AA.
AC P07916;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Elastin precursor (tropoelastin) (Fragment).
GN Name=ELN;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87242320; PubMed=3593675;
RA Bressan G.M., Argos P., Stanley K.K.;
RT "Repeating structure of chick tropoelastin revealed by complementary
RT DNA cloning.";
RL Biochemistry 26:1497-1503(1987).
RN [2]
RP SEQUENCE OF 85-750 FROM N.A. (ISOFORM 2).
RX MEDLINE=88309083; PubMed=2841924;
RA Baule V.J., Foster J.A.;
RT "Multiple chick tropoelastin mRNAs.";
RL Biochem. Biophys. Res. Commun. 154:1054-1060(1988).
RN [3]
RP SEQUENCE OF 457-750 FROM N.A.
RC TISSUE=Aorta;
RX MEDLINE=87297534; PubMed=3502711;
RA Tokimitsu I., Tajima S., Nishikawa T., Tajima M., Fukasawa T.;
RT "Sequence analysis of elastin cDNA from chick aorta and tissue-
RT specific transcription of the elastin gene in developing chick
RT embryo.";
RL Arch. Biochem. Biophys. 256:455-461(1987).
CC -!- FUNCTION: Major structural protein of tissues such as aorta and
CC nuchal ligament, which must expand rapidly and recover completely.
CC -!- SUBUNIT: The polymeric elastin chains are cross-linked together
CC into an extensible 3D network.
CC -!- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=1;
CC IsoId=P07916-1; Sequence=Displayed;
CC Name=2; Synonyms=Embryonic;
CC IsoId=P07916-2; Sequence=VSP_004241, VSP_004242;
CC -!- PTM: The crosslinks are made of deaminated Lys.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M18633; AAA48761.1; -
DR EMBL; M21880; AAA49082.1; -
DR EMBL; M15889; AAA49108.1; -
DR PIR; A26601; A26601.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR003979; Tropoelastin.
DR Pfam; PF01391; Collagen; 1.
DR PRINTS; PR01500; TROPELASTIN
KW Alternative splicing; Connective tissue; Repeat; Signal;
KW Structural protein.
FT NON_TER 1 1
FT SIGNAL <1 24
FT CHAIN 25 750 Elastin.
FT DOMAIN 83 686 8 X tandem repeats.
FT REPEAT 83 127 1.
FT REPEAT 219 262 2.

```

```

FT REPEAT 263 318
FT REPEAT 319 393
FT REPEAT 394 482
FT REPEAT 483 554
FT REPEAT 555 619
FT REPEAT 620 686
FT DISULFID 739 745
FT MOD_RES 63
FT MOD_RES 66
FT MOD_RES 111
FT MOD_RES 115
FT MOD_RES 156
FT MOD_RES 159
FT MOD_RES 198
FT MOD_RES 200
FT MOD_RES 235
FT MOD_RES 252
FT MOD_RES 256
FT MOD_RES 297
FT MOD_RES 301
FT MOD_RES 354
FT MOD_RES 357
FT MOD_RES 427
FT MOD_RES 431
FT MOD_RES 513
FT MOD_RES 517
FT MOD_RES 520
FT MOD_RES 586
FT MOD_RES 590
FT MOD_RES 593
FT MOD_RES 655
FT MOD_RES 658
FT MOD_RES 719
FT MOD_RES 722
FT MOD_RES 743
FT MOD_RES 748
FT MOD_RES 750
FT VARSPLIC 212
FT
FT VARSPLIC 501
FT CONFLICT 536
FT CONFLICT 571
FT CONFLICT 610
FT CONFLICT 654
FT CONFLICT 667
SQ SEQUENCE 750 AA; 63697 MW; E57ECD60C6E8556F CRC64;

Query Match 50.0%; Score 126.5; DB 1; Length 750;
Best Local Similarity 68.3%; Pred. No. 0.014;
Matches 28; Conservative 4; Mismatches 6; Indels 3; Gaps 3;

OY 6 GAGIPGLGV-GVGPGLGV-GAGVPGLV-GAGVPGFAGA 43
| | | | | | | | | | | | | | | | | | | |
Db 466 GVGPGVGPGVGPGVGPGVGPGVGPGVGPGVGPG 506

RESULT 28
Q26675
ID Q26675 PRELIMINARY; PRT; 907 AA.
AC Q26675,
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Sporozoite surface antigen.
GN Name=spag-1;
OS Theileria annulata.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
OC Theileria.
OX NCBI_TaxID=5874;
RN [1]
RP SEQUENCE FROM N.A.

```

RC STRAIN=Hissar;
 RX MEDLINE=92365719; PubMed=1501630;
 RA Hall R., Hunt P.D., Carrington M., Simmons D.L., Williamson S.,
 RA Tait A.,
 RT "Mimicry of elastin repetitive motifs by Theileria annulata sporozoite
 RT surface antigen.";
 RL Mol. Biochem. Parasitol. 53:105-112(1992).
 DR EMBL; M63017; AAA30134.1; -;
 DR PIR; A33934; A33934.
 DR PIR; A45560; A45560.
 DR InterPro; IPR000600; ROK.
 DR InterPro; IPR008845; Sporozoite_p67.
 DR Pfam; PF05642; Sporozoite_p67; I.
 DR PROSITE; PS01125; ROK; UNKNOWN_1.
 SQ SEQUENCE 907 AA; 91885 MW; 589CE55C740D4835 CRC64;
 Query Match 49.6%; Score 125.5; DB 2; Length 907;
 Best Local Similarity 50.9%; Pred. No. 0.02; Indels 15; Gaps 3;
 Matches 29; Conservative 4; Mismatches 9;
 QY 6 GAGIPGLGV-GVGVPGLGV-GAGVPGLGV-----GAGVPFGAGADEGV 47
 Db 180 GVGVPGLGV-GVGVPGLGV-GAGVPGLGV-----GAGVPFGAGADEGV 236
 RESULT 29
 Q8PZF2 PRELIMINARY; PRT; 196 AA.
 AC Q8PZF2; 2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DE Hypothetical protein MM0542.
 GN OrderedLocustNames=MM0542;
 OS Methanosarcina mazei (Methanosarcina frisia).
 OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
 OC Methanosarcinaceae; Methanosarcina.
 OX NCBI_TaxID=22029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Goel / Gol / ATCC BAA-199 / DSM 3647 / OCM 88;
 RX MEDLINE=22120827; PubMed=12125824;
 RA Deppenmeter U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
 RA Martinez-Arias R., Henne A., Wieser A., Baeumer S., Jacobi C.,
 RA Brueggemann H., Lienard T., Christmann A., Boemcke M., Steckel S.,
 RA Bhattacharya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
 RA Fritz H.-J., Gottschalk G.;
 RT "The genome of Methanosarcina mazei: evidence for lateral gene
 RT transfer between Bacteria and Archaea.";
 RL J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
 DR EMBL; AE013279; AA030238.1; -;
 DR GO; GO:0005525; F:GTP binding; IEA.
 DR GO; GO:0007049; P:cell cycle; IEA.
 DR InterPro; IPR00158; FtsZ.
 DR InterPro; IPR001451; Hexapep_transf.
 DR PRINTS; PR00423; CELLDIVISFESZ.
 DR PROSITE; PS00101; HEXAPEP_TRANSFERSASES; UNKNOWN_1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 196 AA; 15462 MW; BB08A7BAC7D028B CRC64;
 Query Match 46.2%; Score 117; DB 2; Length 196;
 Best Local Similarity 57.1%; Pred. No. 0.03; Indels 8; Gaps 4;
 Matches 28; Conservative 8; Mismatches 5;
 QY 4 GLGAGIPGLGV-GVGVPGLGV-GAGVPGLGV-----PGFGAGADEGV 47
 Db 34 GVGVPGLGV-GVGVPGLGV-GAGVPGLGV-----PGFGAGADEGV 79
 RESULT 30
 Q6ZUN2 PRELIMINARY; PRT; 559 AA.
 ID Q6ZUN2
 AC Q6ZUN2

DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein FLJ43523.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
 RA Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
 RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
 RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
 RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
 RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
 RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK125511; BAC86188.1; -;
 DR InterPro; IPR003979; tropoelastin.
 DR PRINTS; PR01500; TROPOLASTIN.
 SQ SEQUENCE 559 AA; 53787 MW; 20938FFEC5492A01 CRC64;
 Query Match 45.5%; Score 115; DB 2; Length 559;
 Best Local Similarity 63.6%; Pred. No. 0.095; Indels 6; Gaps 3;
 Matches 28; Conservative 2; Mismatches 8;
 QY 1 AAAGLGAGIPGLGV-GVGVPGLGV-GAGVPGLGV-----GAGVP 38
 Db 313 AAAGLVPGGPGFGVGVPGLGV-GAGVPGLGV-----GAGVP 356
 Search completed: November 19, 2004, 16:36:50
 Job time : 11.907 secs

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OM protein - protein search, using sw model

Run on: November 19, 2004, 15:19:20 ; Search time 34.9467 Seconds
(without alignments)
1755.321 Million cell updates/sec

Title: US-09-743-818A-73
Perfect score: 872
Sequence: 1 GVRSLSPRLREGDPSSQH.....LGPFFGGACLGKACGRKRK 171

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_23Sep04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	872	100.0	171	3	AAY69137
2	872	100.0	200	2	AAY01305
3	872	100.0	216	2	AAY01310
4	872	100.0	731	3	AAY69068
5	872	100.0	731	4	AAB66657
6	872	100.0	731	6	ABU08725
7	872	100.0	731	7	ADL96420
8	872	100.0	733	2	AAR56653
9	872	100.0	733	2	AAY01301
10	872	100.0	757	7	ABG75223
11	872	100.0	757	7	ADP65160
12	855.5	98.1	730	2	AAW46315
13	725	83.1	183	2	AAY01311
14	725	83.1	183	3	AAY01304
15	725	83.1	692	7	ADP69138
16	725	83.1	698	2	AAW40134
17	725	83.1	698	2	AAY01302
18	725	83.1	730	5	AAO17360
19	725	83.1	730	8	ADQ13747
20	723	82.9	147	2	AAY01304
21	717	82.2	663	7	ADM03792
22	710.5	81.5	660	2	AAY01303
23	612	70.2	617	7	ADB64761
24	612	70.2	712	3	AAB08630
25	612	70.2	730	3	AAB08631

26	609	69.8	711	7	ADB40132
27	482	55.3	864	7	ADE56670
28	475	54.5	870	7	ADE08527
29	318	36.5	60	2	AA01306
30	280	32.1	472	1	AAB88422
31	274	31.4	294	1	AA082484
32	269.5	30.9	515	3	AA069135
33	269.5	30.9	571	3	AA069071
34	253	29.0	47	2	AA01307
35	212.5	24.4	199	6	AAB66661
36	212.5	24.4	199	6	ABU08735
37	212.5	24.4	199	7	ADL96424
38	212.5	24.4	200	4	AAB66658
39	212.5	24.4	200	6	ABU08726
40	212.5	24.4	200	7	ADL96421
41	212	24.3	201	2	AAW46316
42	206.5	23.7	366	8	ADP31574
43	206.5	23.7	384	8	ADP31575
44	206.5	23.7	906	8	ADP31573
45	204	23.4	738	2	AAW56163
46	201.5	23.1	279	8	ADP31572
47	200	22.9	681	4	AAB82610
48	199.5	22.9	691	4	AAB82609
49	199.5	22.9	291	4	AAB82608
50	199	22.8	528	4	AAB82611
51	198.5	22.8	252	8	ADP31571
52	197	22.6	951	8	ADP31413
53	195.5	22.4	235	2	AAW05704
54	195.5	22.4	235	2	AAW79126
55	195.5	22.4	261	2	AAW79137
56	195.5	22.4	534	8	ADP31164
57	195.5	22.4	537	8	ADP31163
58	195.5	22.4	641	2	AAW28843
59	195.5	22.4	641	3	AAW95856
60	195.5	22.4	641	4	AAB62332
61	195.5	22.4	641	6	ABP72663
62	195.5	22.4	641	6	ABP72663
63	195.5	22.4	641	6	ABP72663
64	195.5	22.4	641	7	ADK65581
65	195.5	22.4	641	8	ADJ57052
66	195.5	22.4	641	8	ADP12515
67	195	22.4	1002	6	AAE36885
68	194.5	22.3	651	2	AA040097
69	194.5	22.3	651	5	AAU11781
70	194.5	22.3	718	2	AAW53346
71	194.5	22.3	718	3	AAW59070
72	194	22.2	646	2	AAW27178
73	194	22.2	646	7	ADB61321
74	194	22.2	646	7	ADC35240
75	194	22.2	646	7	ADM46149
76	194	22.2	651	6	AAE36884
77	193.5	22.2	294	7	ADC35283
78	193	22.1	691	6	AAE36887
79	191	21.9	648	6	AAE36869
80	190.5	21.8	762	8	ADP31012
81	190.5	21.8	885	8	ADP31011
82	189	21.7	271	2	AAW50044
83	189	21.7	447	6	AAE36868
84	189	21.7	606	2	AAW99053
85	189	21.7	606	2	AAW40100
86	189	21.7	630	5	AAW50042
87	189	21.7	676	5	AAW50047
88	189	21.7	989	5	AAW50038
89	189	21.7	1255	5	AAW50037
90	189	21.7	1880	5	AAW50039
91	188.5	21.6	889	8	ADP31648
92	187.5	21.5	718	2	AAW4308
93	185	21.2	291	2	AAW49738
94	184	21.1	479	2	AAW49739
95	183.5	21.0	287	2	AAW49737
96	182.5	20.9	364	5	AAW50043
97	182.5	20.9	604	2	AAW99057
98	182.5	20.9	773	5	AAW50045

Accession	Protein	Length	Score	Value
AAM50046	N. clavip	777	20.9	99
Aaw49736	Protein P	281	20.9	100
AAM50046		777	182	99
Aaw49736		281	182	100

ALIGNMENTS

RESULT 1	
AA569137	AA569137 standard; protein; 171 AA.
ID	
XX	
XX	AA569137;
XX	
XX	30-MAY-2000 (first entry)
XX	
XX	Amino acid sequence of a human tropoelastin derivative.
XX	
XX	Tropoelastin; derivative; proteolysis; protease; antiwrinkle;
XX	hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;
XX	peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.
XX	
XX	Homo sapiens.
XX	
XX	WO200004043-A1.
XX	
XX	27-JAN-2000.
XX	
XX	19-JUL-1999; 99WO-AU000580.
XX	
XX	17-JUL-1998; 98AU-00004723.
XX	
XX	(UNSY) UNIV SYDNEY.
XX	
XX	Weiss AS;
XX	
XX	WPI; 2000-182399/16.
XX	
XX	New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
PT	cell growth.
PT	
XX	Disclosure. page 133-134: 136pp; English.
XX	

The present sequence represents a human tropoelastin derivative, which is representative of tropoelastin derivatives of the invention. In the tropoelastin derivatives of the invention a subsequence has been mutated so that susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is increased. The derivatives have with reduced susceptibility, and can be used where the wild-type protein would be degraded too easily, e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivatives, and other polypeptides containing tropoelastin derivative-derived protease-susceptibility sites, are useful in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents and for inducing chemotaxis. They are also useful for proliferation or growth inhibition, particularly of smooth muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets. Peptidomimetics that mimic the protease cleavage site in tropoelastin derivatives are competitive inhibitors of the protease, and are used for protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit protease activity that causes blood clotting.

```

XX      Sequence 171 AR;
SQ
Query Match      100.0%; Score 872; DB 3; Length 171;
Best Local Similarity 100.0%; Pred No. 4.5e-58;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GVRSTLSPELRGDPSSQHLPTPTSSPRVFGALAAAKKYGAAVPGVLGCLGCGVG 60
      |||
Db       1  GVRSTLSPELRGDPSSQHLPTPTSSPRVFGALAAAKKYGAAVPGVLGCLGCGVG 60

```

QY	61	IPGVVVGAGPAAAAA	AAAAA	AAQAGL	VGAAAGL	GGLGVGGLGV	PGVPGVGLG	GPAAAAA	120
Db	61	IPGVVVGAGPAAAAA	AAAAA	AAQAGL	VGAAAGL	GGLGVGGLGV	PGVPGVGLG	GPAAAAA	120
QY	121	AAKYGAAGLGGV	LGAGQ	PFLGGV	AAAPCG	FLSP	IFPGAC	GLGKACGR	171
Db	121	AAKYGAAGLGGV	LGAGQ	PFLGGV	AAAPCG	FLSP	IFPGAC	GLGKACGR	171

RESULT 2

[illegible]

New derivatives of human tropoelastin - with elastin-like or
 macromolecular binding properties, useful e.g. as surgical implants.
 Claim 15; Fig 8; 82pp; English.
 The invention relates to a derivative or variant of human tropoelastin
 (hTE) having elastin-like and/or macromolecule (specifically glycosaminoglycan (GAG))-binding properties. Cells containing vectors
 comprising the nucleic acids encoding the variants or derivatives are
 used to produce the proteins recombinantly. The tropoelastin derivatives
 or hybrid proteins containing the derivatives are useful in medical,
 pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
 wrinkle or hand lotions, also as surgical implants, foods and industrial
 products. The hybrid protein have controllable GAG-binding properties,
 depending on presence or absence of a specific fragment, designated
 peptide 26A, from hTE. The present sequence represents a human
 tropoelastin derivative. SHELDON
 100

[illegible]

1 GVRSLPEIREGDPSSQHLPTSPSSPRVPCALAAAKAAKAAKAAVPGVLGSLGALGGV 60
30 GVRNSLPEIREGDPSSQHLPTSPSSPRVFGALAAAKAAKAAVPGVLGSLGALGGV 89
61 IPGVGVAGPAAAAAKAAAKAAKAAQFGLVGAAGTGGGLGVDPGVGGLGIPAAAAAK 120
90 IPGVGVAGPAAAAAKAAAKAAKAAQFGLVGAAGTGGGLGVDPGVGGLGIPAAAAAK 149
Db

196 AAATGAAGLGGV LGGAGQFPLGGVAARPGFLSPIFPGGACLGKACGRKRK 216

61 IPGGV

61 TPGGVVGAGDPA A A A A A A K A A K A A O E C T I G A A A G T C C T A U G C T C U D C U G C T A

561 GVRB ST. S

61 TPGGVVGAGDPA A A A A A A K A A K A A O E C T I G A A A G T C C T A U G C T C U D C U G C T A

Db 561 GVRRLSPLELREGDPSSQHLPTSPSPRPVPGALAAAKAAKYGAAPVGLGALGVG 620
 QY 61 IPGGVVGAGPAAAKAAAKAAQFGLVGAAGLGLGVGGLGVGGLGGIPPPAAAK 120
 Db 621 IPGGVVGAGPAAAKAAAKAAQFGLVGAAGLGLGVGGLGVGGLGGIPPPAAAK 680
 QY 121 AAKYGAAGLGVGAGQFPLGGVAAPFGFLSPFFPGACLGKACGRKK 171
 Db 681 AAKYGAAGLGVGAGQFPLGGVAAPFGFLSPFFPGACLGKACGRKK 731

RESULT 7

ADL96420
 ID ADL96420 standard; protein; 731 AA.

AC ADL96420;
 XX
 XX 20-MAY-2004 (first entry)
 XX
 DE Human elastin protein fragment.
 XX
 KW fibrous protein; prosthesis; elastin; lamprin; spider silk protein;
 KW blood vessel; wound; burn healing; collagen.
 XX
 OS Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT Region 19..160
 FT Region /note= "region specifically claimed in claim 6"
 FT Region 188..367
 FT Region /note= "region specifically claimed in claim 6"
 FT Region 374..499
 FT Region /note= "region specifically claimed in claim 6"
 FT Region 607..717
 FT Region /note= "region specifically claimed in claim 6"

XX US2003166846-A1.

XX 04-SEP-2003.

XX 28-SEP-2001; 2001US-00964662.

XX 07-AUG-1996; 96US-0023522P.

XX 07-AUG-1997; 97US-00911364.

XX 29-JUN-1999; 99US-00340736.

XX (ROTH/) ROTHSTEIN A.

XX (KEEL/) KEELEY F.

XX (ROTH/) ROTHSTEIN S.

XX Rothstein A, Keeley F, Rothstein S;

XX WPI; 2003-898105/82.

XX Polypeptide for constructing human elastin-like prostheses such as tubes
 for blood vessel replacement and sheets for other uses such as wound or
 burn healing, comprises three beta sheets and three beta turns.

XX Claim 5; Fig 1B; 17pp; English.

XX This invention describes a polypeptide that comprises three beta
 sheet/beta turn structures and that is not a naturally occurring fibrous
 protein. The invention also describes a prosthesis comprising an animal,
 metal or synthetic material, where the surface is coated with the
 polypeptide, a cosmetic material comprising the polypeptide, an elastic
 material comprising the polypeptide, a high tensile strength material
 comprising the polypeptide, a material comprising two or more
 polypeptides selected from (a) a polypeptide consisting essentially of a
 portion of the polypeptide comprising at least three beta sheet/beta turn
 structures, (b) a polypeptide consisting essentially of a portion of the
 amino acid sequence of an animal elastin comprising at least three beta
 sheets/beta turns, (c) a polypeptide consisting essentially of a portion

CC of lamprin comprising at least three beta sheets/beta turns, and (d) a
 CC polypeptide consisting essentially of a spider silk protein comprising at
 CC least three beta sheets/beta turns, a polypeptide having the primary
 CC structure of a portion of a naturally occurring fibrous protein and a
 CC secondary structure comprising at least three beta sheets/beta turns,
 CC where each of the beta sheet/beta turn structures comprises from 3 to
 CC about 7 amino acids and the polypeptide is not a naturally occurring
 CC fibrous protein. The minimal functional unit (MFU) of the invention is
 CC useful to construct human elastin-like prostheses such as tubes for blood
 CC vessel replacement and sheets for other uses such as wound or burn
 CC healing. Alternatively the MFU can be co-aggregated with other proteins,
 CC for example collagen, to provide prosthesis material that resembles the
 CC natural structural materials of the body. The MFU based material is
 CC subject to infiltration of cells growing in the patient, including
 CC endothelial cells, and the prosthesis can become a permanent living
 CC tissue replacement. The material is more biocompatible than other elastin
 CC -containing materials proposed for prostheses.
 XX
 SQ Sequence 731 AA;

Query Match 100.0%; Score 872; DB 7; Length 731;
 Best Local Similarity 100.0%; Pred. No. 1.8e-57;
 Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVRRLSPLELREGDPSSQHLPTSPSPRPVPGALAAAKAAKYGAAPVGLGALGVG 60
 Db 561 GVRRLSPLELREGDPSSQHLPTSPSPRPVPGALAAAKAAKYGAAPVGLGALGVG 620
 QY 61 IPGGVVGAGPAAAKAAAKAAQFGLVGAAGLGLGVGGLGVGGLGGIPPPAAAK 120
 Db 621 IPGGVVGAGPAAAKAAAKAAQFGLVGAAGLGLGVGGLGVGGLGGIPPPAAAK 680
 QY 121 AAKYGAAGLGVGAGQFPLGGVAAPFGFLSPFFPGACLGKACGRKK 171
 Db 681 AAKYGAAGLGVGAGQFPLGGVAAPFGFLSPFFPGACLGKACGRKK 731

RESULT 8

AAR56653

ID AAR56653 standard; protein; 733 AA.

XX AC AAR56653;

XX 25-MAR-2003 (revised)

XX 22-MAR-1995 (first entry)

XX Synthetic human tropoelastin (SHEL).

XX Tropoelastin; pharmaceutical; surgical dressing.

XX Synthetic.

XX WO9414958-A1.

XX 07-JUL-1994.

XX 16-DEC-1993; 93WO-AU000655.

XX 22-DEC-1992; 92AU-00006520.

XX 28-JUN-1993; 93AU-00009661.

XX (UNSY) UNIV SYDNEY.

XX Weiss AS, Martin SL;

XX WPI; 1994-263633/32.

XX N-PSDB; AAQ70941.

XX Synthetic polynucleotide(s) - encode recombinant tropoelastins and
 variants.

XX Disclosure; Page 30; 77pp; English.

Mon Nov 22 12:42:44 2004

us-09-743-818a-73.rag

CC Human synthetic tropoelastin is susceptible to hydrolytic breakdown of
CC the crosslinks. Such material may be useful in e.g. surgical
CC applications, where the gradual loss of material over time is intended.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 733 AA;
Query Match 100.0%; Score 872; DB 2; Length 733;
Best Local Similarity 100.0%; Pred. No. 1.8e-57;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GVRSLSPELREGDPSSQHLPTSPSPRVPGALAAKAAKYAAVPGVLGGLGALGGVG 60
Db 563 GVRSLSPELREGDPSSQHLPTSPSPRVPGALAAKAAKYAAVPGVLGGLGALGGVG 622
QY 61 IPGVVVGAGPAAAAAATAAQAQGLVGAAGLGLGVGGVPGVGGVGGVGGVGGVGGV 120
Db 623 IPGVVVGAGPAAAAAATAAQAQGLVGAAGLGLGVGGVPGVGGVGGVGGVGGVGGV 682
QY 121 AAKYGAAGLGGVGGAGQFPLGGVAARPGFGLSPIPPGGACLGKACGRKK 171
Db 683 AAKYGAAGLGGVGGAGQFPLGGVAARPGFGLSPIPPGGACLGKACGRKK 733
RESULT 9
AAV01301
ID AAV01301 standard; protein; 733 AA.
AC AAV01301;
XX
XX 07-JUN-1999 (first entry)
DT
DE Amino acid sequence of synthetic human tropoelastin SHEL.
XX
KW Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;
KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
KW hand lotion; surgical implant; industrial product; human; SHEL.
XX
OS Synthetic.
OS Homo sapiens.
XX WO9903886-A1.
XX
XX 28-JAN-1999.
PD
PF 17-JUL-1998; 98WO-AU000564.
XX
XX 18-JUL-1997; 97AU-00008117.
PR
PA (UNSY) UNIV SYDNEY.
XX
XX Weiss AS;
PI
XX WPI; 1999-132162/11.
DR N-PSDB; AAX27704.
DR
XX New derivatives of human tropoelastin - with elastin-like or
XX macromolecular binding properties, useful e.g. as surgical implants.
PT
PT Disclosure; Fig 1; 82pp; English.
PS
XX The invention relates to a derivative or variant of human tropoelastin
XX (hTE) having elastin-like and/or macromolecule (specifically
XX glycosaminoglycan (GAG))-binding properties. Cells containing vectors
XX comprising the nucleic acids encoding the variants or derivatives are
XX used to produce the proteins recombinantly. The tropoelastin derivatives
XX or hybrid proteins containing the derivatives are useful in medical,
XX pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
XX wrinkle or hand lotions, also as surgical implants, foods and industrial
XX products. The hybrid protein have controllable GAG-binding properties,
XX depending on presence or absence of a specific fragment, designated
XX peptide 26A, from hTE. The present sequence represents the amino acid
XX sequence of the synthetic human tropoelastin SHEL

XX
SQ Sequence 733 AA;
Query Match 100.0%; Score 872; DB 2; Length 733;
Best Local Similarity 100.0%; Pred. No. 1.8e-57;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GVRSLSPELREGDPSSQHLPTSPSPRVPGALAAKAAKYAAVPGVLGGLGALGGVG 60
Db 563 GVRSLSPELREGDPSSQHLPTSPSPRVPGALAAKAAKYAAVPGVLGGLGALGGVG 622
QY 61 IPGVVVGAGPAAAAAATAAQAQGLVGAAGLGLGVGGVPGVGGVGGVGGVGGVGGV 120
Db 623 IPGVVVGAGPAAAAAATAAQAQGLVGAAGLGLGVGGVPGVGGVGGVGGVGGVGGV 682
QY 121 AAKYGAAGLGGVGGAGQFPLGGVAARPGFGLSPIPPGGACLGKACGRKK 171
Db 683 AAKYGAAGLGGVGGAGQFPLGGVAARPGFGLSPIPPGGACLGKACGRKK 733
RESULT 10
ABG75223
ID ABG75223 standard; protein; 757 AA.
XX
XX AC ABG75223;
XX
XX 12-FEB-2004 (first entry)
DT
XX Human tropoelastin protein.
DE
XX Human; tropoelastin; elastin; body vessel occlusion; stenosis;
KW vascular smooth muscle cell; elastin signaling; vasotropic.
XX
XX Homo sapiens.
OS
XX WO2003082203-A2.
PN
XX 09-OCT-2003.
PD
XX 27-MAR-2003; 2003WO-US009391.
PF
XX 27-MAR-2002; 2002US-0368084P.
PR
XX (UTAH) UNIV UTAH RES FOUND.
PA
XX Li DY, Karnik S;
PI
XX WPI; 2003-833516/77.
DR
XX Use of an agent that promotes elastin signaling in smooth muscle cells
XX for e.g. decreasing or preventing occlusion of a body vessel by smooth
XX muscle cells, treating or preventing obstructive vascular disease, or
XX preventing stenosis.
PT
XX Claim 24; Page 138-141; Opp; English.
PS
XX The present invention relates to the use of an agent that promotes
XX elastin signaling in smooth muscle cells for decreasing or preventing
XX occlusion of a body vessel by smooth muscle cells, decreasing vascular
XX obstruction, promoting actin stress fiber formation or actin
XX polymerisation, increasing F-actin ratio in a smooth muscle cell,
XX treating or preventing obstructive vascular disease (e.g. restenosis), or
XX preventing stenosis. The agent that promotes elastin signaling in smooth
XX muscle cells is useful for decreasing or preventing occlusion of a body
XX vessel by smooth muscle cells, decreasing vascular obstruction, promoting
XX actin stress fiber formation or actin polymerization, increasing F-actin
XX ratio in a smooth muscle cell, treating or preventing obstructive
XX vascular disease (e.g. restenosis following angioplasty), or preventing
XX stenosis. It is also useful in manufacturing a medicament for the
XX treatment or prevention of occlusion of a vessel. The present sequence is
XX the human tropoelastin protein as shown in the exemplification of the
XX invention
XX

```

SQ      Sequence 757 AA;
Query Match      100.0%; Score 872; DB 7; Length 757;
Best Local Similarity 100.0%; Pred. No. 1.8e-57;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GVRRLSPLELREGDPSSQHLPTSPSSPRVPGALAAAKAAKYGAAPVGLGGLGALGGVG 60
      |||
Db      587 GVRRLSPLELREGDPSSQHLPTSPSSPRVPGALAAAKAAKYGAAPVGLGGLGALGGVG 646

QY      61 IPGGVVGAGPAAAAAATAAQAQFGLVGAAGLGLGVLGVPVGGVGLGIPPPAAAAK 120
      |||
Db      647 IPGGVVGAGPAAAAAATAAQAQFGLVGAAGLGLGVLGVPVGGVGLGIPPPAAAAK 706

QY      121 AAKYGAAGLGGVGLGAGQFPLGGVAARPGFGLSPIPPGGACLCACGRK 171
      |||
Db      707 AAKYGAAGLGGVGLGAGQFPLGGVAARPGFGLSPIPPGGACLCACGRK 757

RESULT 11
ADP65160
ID      ADP65160 standard; protein; 757 AA.
XX
AC      ADP65160;
XX
DT      12-AUG-2004 (first entry)
XX
DE      Human elastin.
XX
KW      autoimmune disease; arthritis; gene expression analysis;
KW      rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
KW      antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;
KW      immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;
KW      fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
KW      immune; human.
XX
OS      Homo sapiens.
XX
PN      WO2003072827-A1.
XX
PD      04-SEP-2003.
XX
PF      31-OCT-2002; 2002WO-US035433.
XX
PR      31-OCT-2001; 2001US-0336220P.
XX
PA      (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
XX
PI      Hirsch R, Thorton SL;
XX
DR      WPI; 2003-712740/67.
XX
DR      GENBANK; NP_000492.
XX
PT      Diagnosing and analyzing autoimmune disease using gene expression
PT      profiles and microarray technology, useful for diagnosing and treating
PT      rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
PT      gout.
XX
PS      Disclosure; Page; 56pp; English.
XX
CC      The invention relates to a novel method for diagnosing and analysing
CC      autoimmune disease or arthritides. The method comprises obtaining a
CC      patient sample containing mRNA, analysing gene expression using the mRNA
CC      that results in a gene expression signature of the mRNA, and using that
CC      gene expression signature to diagnose or analyse the autoimmune disease
CC      or arthritides in the patient, where gene expression of at least 60% of
CC      the genes correlates with that of the gene signature. The invention
CC      further comprises: a treatment of rheumatoid arthritis; identification of
CC      genes for targeting in the treatment of rheumatoid arthritis in a mammal
CC      other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
CC      array or gene chip, specific for rheumatoid arthritis; diagnosis or
CC      analyses of autoimmune disease or rheumatoid arthritis; screening the
CC      efficacy of a candidate drug in vitro for the treatment of collagen-
CC      induced arthritis; and reducing the symptoms associated with collagen-
CC      induced arthritis. The compositions of the invention have the following
CC      activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
CC      antigout, antiinflammatory, dermatological, and immunomodulatory. The
CC      methods and compositions of the present invention are useful for
CC      diagnosing and treating autoimmune disease or arthritides, such as
CC      rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
CC      fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
CC      immune disease caused by an infectious agent. This sequence represents a
CC      protein sequence relating to the genes used in the analysis and treatment
CC      of autoimmune diseases or arthritides. Note: This sequence is not shown
CC      in the specification. It has been supplied in an electronic format from
CC      WIPO.
XX
SQ      Sequence 757 AA;
Query Match      100.0%; Score 872; DB 7; Length 757;
Best Local Similarity 100.0%; Pred. No. 1.8e-57;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GVRRLSPLELREGDPSSQHLPTSPSSPRVPGALAAAKAAKYGAAPVGLGGLGALGGVG 60
      |||
Db      587 GVRRLSPLELREGDPSSQHLPTSPSSPRVPGALAAAKAAKYGAAPVGLGGLGALGGVG 646

QY      61 IPGGVVGAGPAAAAAATAAQAQFGLVGAAGLGLGVLGVPVGGVGLGIPPPAAAAK 120
      |||
Db      647 IPGGVVGAGPAAAAAATAAQAQFGLVGAAGLGLGVLGVPVGGVGLGIPPPAAAAK 706

QY      121 AAKYGAAGLGGVGLGAGQFPLGGVAARPGFGLSPIPPGGACLCACGRK 171
      |||
Db      707 AAKYGAAGLGGVGLGAGQFPLGGVAARPGFGLSPIPPGGACLCACGRK 757

RESULT 12
AAW46315
ID      AAW46315 standard; protein; 730 AA.
XX
AC      AAW46315;
XX
DT      23-JUL-1998 (first entry)
XX
DE      Human elastin containing non-natural polypeptide MFU-1 sequence.
XX
KW      MFU-1; minimal functional unit; elastin; human; fibrous protein;
KW      beta-sheet; coating; wound dressing.
XX
OS      Homo sapiens.
XX
EH      Key      Location/Qualifiers
FT      Protein      374..499
FT      /note= "MFU-1 polypeptide"
XX
PN      WO9805685-A2.
XX
PD      12-FEB-1998.
XX
PF      07-AUG-1997; 97WO-CA000560.
XX
PR      07-AUG-1996; 96US-0023552P.
PR      07-AUG-1997; 97US-00911364.
XX
PA      (PROT-) PROTEIN SPECIALTIES LTD.
PA      (HOSP-) HOSPITAL FOR SICK CHILDREN.
XX
PI      Rothstein A, Keeley FW, Rothstein SJ;
XX
DR      WPI; 1998-145551/13.
XX
PT      New non-natural polypeptide with multiple beta-sheet, beta-turn
PT      structures - particularly based on human elastin. useful for coating
PT      prostheses, as wound dressings, etc., allows ingrowth of cells.
XX
PS      Claim 5; Fig 1B; 39pp; English.
```

XX This represents the human elastin sequence containing the minimal
 CC functional unit (MFU)-1 polypeptide of the invention. This MFU-1 is a
 CC polypeptide that has at least 3 beta-sheet/ beta-turn structures, but is
 CC not a naturally occurring fibrous protein. Each beta-sheet structure has
 CC 3-7 (preferably 5-7) amino acids and the MFU polypeptide may include at
 CC least 1 amino acid that can take part in crosslinking. The polypeptide
 CC can also be derived from the sequences of animal elastin, lamprin and
 CC spider silk protein. The MFU polypeptides are self-aligning peptides
 CC having the same primary structure as part of a natural fibrous protein.
 CC They are used to coat prostheses made of animal or synthetic material or
 CC metal, particularly for use as blood vessel or heart valve replacements,
 CC wound or burn dressings, or stents. They can be used in cosmetic, elastic
 CC or high-tensile strength materials, e.g. ropes or parachute cord.
 CC Prostheses based on the MFU allow penetration of endothelial cells, so
 CC become permanent, living, tissue replacements. The MFU polypeptides have
 CC better biocompatibility than known elastin-based materials. They are well
 CC defined, homogeneous material and are easier to manipulate and produce
 CC than full-length elastins. They are non-thrombogenic and non-immunogenic.
 CC Materials can be made from 2 or more different MFU polypeptides to allow
 CC properties to be tailored for particular applications, e.g. combining the
 CC high extensibility of elastin and the high tensile strength of spider
 CC silk protein

XX SQ Sequence 730 AA;
 Query Match 98.1%; Score 855.5; DB 2; Length 730;
 Best Local Similarity 99.4%; Pred. No. 3.1e-56;
 Matches 170; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 GVRSLSPFLREGDPSSQHLPTSPSPRVPFGALAAAKAAKYGAAPVGLGGLGALGVG 60
 Db 561 GVRSLSPFLREGDPSSQHLPTSPSPRVPFGALAAAKAAKYGAAPVGLGGLGALGVG 620
 QY 61 IPGGVVGAGPAAAKAAAKAAQFGLVGAAGLGLGVGGLGVGPGVGLGGLGIPPA 120
 Db 621 IPGGVVGAGPAAAKAAAKAAQFGLVGAAGLGLGVGGLGVGPGVGLGGLGIPPA 680
 QY 121 AAKYGAAGLGLGVGAGGFPPLGGVAAPFGGLSPIFGGACLGKACGRKK 171
 Db 681 AAKYGAAGLGLGVGA-QFPLGGVAAPFGGLSPIFGGACLGKACGRKK 730

RESULT 13
 AAY01311
 ID AAY01311 standard; protein; 183 AA.
 XX
 AC AAY01311;
 DT 07-JUN-1999 (first entry)
 DE Human tropoelastin derivative SHEL26-36 (excluding exon 26A product).
 KW Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;
 KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
 KW hand lotion; surgical implant; industrial product; human; SHEL; variant.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO9903886-A1.
 XX
 XX 28-JAN-1999.
 XX
 PF 17-JUL-1998; 98WO-AU000564.
 XX
 PR 18-JUL-1997; 97AU-00008117.
 XX
 PA (UNSY) UNIV SYDNEY.
 XX
 PI Weiss AS;
 XX
 XX WPI; 1999-132162/11.

XX New derivatives of human tropoelastin - with elastin-like or
 PT macromolecular binding properties, useful e.g. as surgical implants.
 XX
 XX Claim 39; Page 11; 82pp; English.
 XX
 CC The invention relates to a derivative or variant of human tropoelastin
 CC (hTE) having elastin-like and/or macromolecule (specifically
 CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors
 CC comprising the nucleic acids encoding the variants or derivatives are
 CC used to produce the proteins recombinantly. The tropoelastin derivatives
 CC or hybrid proteins containing the derivatives are useful in medical,
 CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
 CC wrinkle or hand lotions, also as surgical implants, foods and industrial
 CC products. The hybrid protein have controllable GAG-binding properties,
 CC depending on presence or absence of a specific fragment, designated
 CC peptide 26A, from hTE. The present sequence represents a human
 CC tropoelastin derivative SHEL26-36 excluding exon 26A product
 XX
 XX SQ Sequence 183 AA;
 Query Match 83.1%; Score 725; DB 2; Length 183;
 Best Local Similarity 97.3%; Pred. No. 5.4e-47;
 Matches 143; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 25 PSSPRVPFGALAAAKAAKYGAAPVGLGGLGALGVGIPGGVWAGPAAAAAKAAKAA 84
 Db 37 PFGCAVPFGALAAAKAAKYGAAPVGLGGLGALGVGIPGGVWAGPAAAAAKAAKAA 96
 QY 85 QFGLVGAAGLGLGVGGLGVGPGVGLGGLGIPPAKAAKAAKYGAAGLGVGAGGFPPLGGV 144
 Db 97 QFGLVGAAGLGLGVGGLGVGPGVGLGGLGIPPAKAAKAAKYGAAGLGVGAGGFPPLGGV 156
 QY 145 AARPGFGLSPIFGGACLGKACGRKK 171
 Db 157 AARPGFGLSPIFGGACLGKACGRKK 183

RESULT 14
 AAY69138
 ID AAY69138 standard; protein; 183 AA.
 XX
 AC AAY69138;
 DT 30-MAY-2000 (first entry)
 DE Amino acid sequence of a human tropoelastin derivative.
 KW Tropoelastin; derivative; proteolysis; protease; antiwrinkle;
 KW hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;
 KW peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.
 XX
 OS Homo sapiens.
 XX
 PN WO200004043-A1.
 XX
 PD 27-JAN-2000.
 XX
 PF 19-JUL-1999; 99WO-AU000580.
 XX
 PR 17-JUL-1998; 98AU-00004723.
 XX
 PA (UNSY) UNIV SYDNEY.
 XX
 PI Weiss AS;
 XX
 DR WPI; 2000-182399/16.
 XX
 XX New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
 PT cell growth.
 XX
 PS Disclosure; Page 134-135; 136pp; English.
 XX

The present sequence represents a human tropoelastin derivative, which is representative of tropoelastin derivatives of the invention. In the tropoelastin derivatives of the invention a subsequence has been mutated so that susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is increased. The derivatives have with reduced susceptibility to proteolysis is used where the wild-type protein would be degraded too easily, e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivatives, and other polypeptides containing tropoelastin derivative-derived protease-susceptibility sites, are useful in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents and for inducing chemotaxis. They are also useful for proliferation or growth inhibition, particularly of smooth muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets. Peptidomimetics that mimic the protease cleavage site in tropoelastin derivatives are competitive inhibitors of the protease, and are used for protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit protease activity that causes blood clotting

XX Sequence 183 AA;

Query Match 83.1%; Score 725; DB 3; Length 183;
Best Local Similarity 97.3%; Pred. No. 5.4e-47;
Matches 143; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 25 PSSRPVPGALAAKAAKAYGAAVPGVLGGLGALGGVIGPGVVGAGPAAAKAAKAAKAA 84
Db 37 PFGAVPGALAAKAAKAYGAAVPGVLGGLGALGGVIGPGVVGAGPAAAKAAKAAKAA 96

QY 85 QFGLVGAAGLGGVGGVPGVPGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGV 144
Db 97 QFGLVGAAGLGGVGGVGGVPGVPGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGV 156

QY 145 AARPGFGLSPIFFPGACLGKACGRKRK 171
Db 157 AARPGFGLSPIFFPGACLGKACGRKRK 183

RESULT 15

AD40134
ID AD40134 standard; protein; 692 AA.

AC AD40134;

DT 29-JAN-2004 (first entry)

DE Human NOV16b protein - SEQ ID 40.

XX NOVX; cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic;
KW antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic;
KW antiparkinsonian; antiasthmatic; gynaecological; cardiomyopathy;
KW atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;
KW multiple sclerosis; graft-versus-host disease; Alzheimer's; Parkinson's;
KW asthma; fertility disorder; vaccine; gene therapy; chromosome mapping;
KW tissue typing; human; NOV.

OS Homo sapiens.

XX WO2003064589-A2.

XX 07-AUG-2003.

XX 02-AUG-2002; 2002WO-US024483.

XX 02-AUG-2001; 2001US-0309501P.

XX 03-AUG-2001; 2001US-0310291P.

XX 07-AUG-2001; 2001US-0310544P.

XX 08-AUG-2001; 2001US-0310951P.

XX 09-AUG-2001; 2001US-0311292P.

XX 13-AUG-2001; 2001US-0311979P.

XX 16-AUG-2001; 2001US-0312892P.

PR 17-AUG-2001; 2001US-0313201P.
PR 17-AUG-2001; 2001US-0313415P.
PR 20-AUG-2001; 2001US-0313643P.
PR 20-AUG-2001; 2001US-0313702P.
PR 21-AUG-2001; 2001US-0314031P.
PR 23-AUG-2001; 2001US-0314466P.
PR 28-AUG-2001; 2001US-0315403P.
PR 29-AUG-2001; 2001US-0315853P.
PR 17-SEP-2001; 2001US-0322716P.
PR 21-SEP-2001; 2001US-0323994P.
PR 14-DEC-2001; 2001US-0340233P.
PR 05-FEB-2002; 2002US-0354591P.
PR 19-MAR-2002; 2002US-0365478P.
PR 19-APR-2002; 2002US-0373814P.
PR 19-APR-2002; 2002US-0373825P.
PR 19-APR-2002; 2002US-0373989P.
PR 23-APR-2002; 2002US-0374632P.
PR 07-JUN-2002; 2002US-0386971P.
PR 01-AUG-2002; 2002US-00210172.

XX (CURA-) CURAGEN CORP.

PA Kekuda R, Miller CE, Patturajan M, Pena CEA, Rieger DK,
XX Shinkets RA, Zerhusen BD, Li L, Ji W, Padigaru M, Casman SJ;

PI Voss EZ, Boldog FL, Gorman L, Leite MM, Vernet CAM, Anderson DW;
PI Guo X, Zhong M, Gerlach VL, Hjalt T, Rastelli L, Spytek KA;

PI Edinger SR, Ellerman K, Malyankar UM, Macdougall JR, Stone DU;
PI Alsobrook JP, Lepley DM, Burgess CE, Majumder K, Wolenc AR;

PI Smithson G;
XX

DR WPI: 2003-663472/62.
DR N-PSDB; ADE40133.

XX

PT New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.

XX Claim 1; SEQ ID NO 40; 560pp; English.

XX The invention relates to a novel NOVX polypeptide. The polypeptide of the
CC invention demonstrates cardiant, antiarteriosclerotic, hypotensive,
CC cytostatic, anorectic, antidiabetic, immunosuppressive, anti-HIV,
CC neuroprotective, nootropic, antiparkinsonian, antiasthmatic and
CC gynaecological activities and may be useful in diagnosing, treating or
CC preventing NOVX-associated disorders including cardiomyopathy,
CC atherosclerosis, hypertension, cancer, obesity, diabetes, AIDS, multiple
CC sclerosis, graft-versus-host disease, Alzheimer's disease, Parkinson's
CC disease, asthma or fertility disorders. Furthermore, the polypeptides may
CC be utilised as vaccines whilst the nucleic acids may be used as
CC hybridisation probes, in gene therapy, chromosome mapping, tissue typing,
CC preventive medicine and pharmacogenomics. The current sequence is that of
XX the human NOV protein of the invention.

SQ Sequence 692 AA;

Query Match 83.1%; Score 725; DB 7; Length 692;
Best Local Similarity 97.3%; Pred. No. 1.9e-46;
Matches 143; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 25 PSSRPVPGALAAKAAKAYGAAVPGVLGGLGALGGVIGPGVVGAGPAAAKAAKAAKAA 84
Db 546 PFGAVPGALAAKAAKAYGAAVPGVLGGLGALGGVIGPGVVGAGPAAAKAAKAAKAA 605

QY 85 QFGLVGAAGLGGVGGVPGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGV 144
Db 606 QFGLVGAAGLGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGV 665

QY 145 AARPGFGLSPIFFPGACLGKACGRKRK 171

Db 666 AARPGFGLSPIFFPGACLGKACGRKRK 692

AC AAY69069;


```
RESULT 18
AAO17360
ID AAO17360 standard; protein; 730 AA.
XX
AC AAO17360;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human elastin.
XX
KW Human; endometriosis; DNA chip; fibronectin; p27; reticulocalbin;
KW aldehyde dehydrogenase 6; gravin; phospholipase C epsilon; elastin;
KW insulin-like growth factor binding protein-2; alpha-2 type IV collagen;
KW transmembrane receptor PTK7; collagen type XVIII alpha 1;
KW platelet derived growth factor receptor alpha; laminin M chain;
KW subtilisin like protein PACE4; nidogen.
XX
OS Homo sapiens.
XX
PN EF1191107-A2.
XX
PD 27-MAR-2002.
XX
PF 21-AUG-2001; 2001EP-00250300.
XX
PR 25-SEP-2000; 2000DE-01048633.
XX
PA (SCHD ) SCHERING AG.
XX
PI Hess-Stumpp H, Haendler B, Kraetzschmar J, Krefte B, Winterhager E;
PI Regidor P, Scotti S;
XX
WPI; 2002-317413/36.
XX
PT In vitro diagnosis and monitoring of endometriosis, comprises detecting
PT reduced expression of specific gene products, e.g. from the fibronectin
PT gene.
XX
PS Claim 1; Page 15-16; 2lpp; German.
XX
CC The present invention relates to a method for the in vitro diagnosis of
CC endometriosis by determining the amount of gene product from at least one
CC specific gene in a patient sample and comparing this with the amount of
CC gene product in a control sample. A reduced level is indicative of
CC endometriosis. The gene products may be fibronectin, p27, reticulocalbin,
CC aldehyde dehydrogenase 6, gravin, phospholipase C epsilon, elastin,
CC insulin-like growth factor binding protein-2, alpha-2 type IV collagen,
CC transmembrane receptor PTK7, collagen type XVIII alpha 1, platelet
CC derived growth factor receptor alpha, laminin M chain, subtilisin like
CC protein PACE4 or nidogen. The method is useful for initial diagnosis of
CC endometriosis, and also for monitoring progress and treatment of the
CC disease. The present sequence is human elastin
XX
SQ Sequence 730 AA;

Query Match 83.1%; Score 725; DB 5; Length 730;
Best Local Similarity 97.3%; Pred. No. 2e-46;
Matches 143; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 25 PSSPRVPGALAAAKAAYGAAVPGVGLGALGGVIGPGVVGAGPAAAAAATAAKAA 84
DB 584 PGFGAVPGALAAAKAAYGAAVPGVGLGALGGVIGPGVVGAGPAAAAAATAAKAA 643
QY 85 QFGLVGAAGLGGVGGVGVGGLGIPPAATAAKAAYGAAAGLGGVVGAGPPLGGV 144
DB 644 QFGLVGAAGLGGVGGVGVGGLGIPPAATAAKAAYGAAAGLGGVVGAGPPLGGV 703
QY 145 AARPGFGLSPIFFPGGACLGKACGRKRK 171
DB 704 AARPGFGLSPIFFPGGACLGKACGRKRK 730

RESULT 20
AAO1304
ID AAY01304 standard; protein; 147 AA.
XX
AC AAY01304;
XX
```

```
RESULT 19
ADQ19747
ID ADQ19747 standard; protein; 730 AA.
XX
AC ADQ19747;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2566.
XX
KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
XX
OS Homo sapiens.
XX
PN WO2004048938-A2.
XX
PD 10-JUN-2004.
XX
PF 26-NOV-2003; 2003WO-US038193.
XX
PR 26-NOV-2002; 2002US-0429739P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Aziz N, Ginsburg WM, Zlotnik A;
XX
WPI; 2004-441208/41.
XX
PT Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.
XX
PS Example 2; SEQ ID NO 2566; 210pp; English.
XX
CC The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC protein of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX
SQ Sequence 730 AA;

Query Match 83.1%; Score 725; DB 8; Length 730;
Best Local Similarity 97.3%; Pred. No. 2e-46;
Matches 143; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 25 PSSPRVPGALAAAKAAYGAAVPGVGLGALGGVIGPGVVGAGPAAAAAATAAKAA 84
DB 584 PGFGAVPGALAAAKAAYGAAVPGVGLGALGGVIGPGVVGAGPAAAAAATAAKAA 643
QY 85 QFGLVGAAGLGGVGGVGVGGLGIPPAATAAKAAYGAAAGLGGVVGAGPPLGGV 144
DB 644 QFGLVGAAGLGGVGGVGVGGLGIPPAATAAKAAYGAAAGLGGVVGAGPPLGGV 703
QY 145 AARPGFGLSPIFFPGGACLGKACGRKRK 171
DB 704 AARPGFGLSPIFFPGGACLGKACGRKRK 730

RESULT 20
AAO1304
ID AAY01304 standard; protein; 147 AA.
XX
AC AAY01304;
```

DE Human protein of the invention SEQ ID NO:2477.
 XX human; gene therapy; diagnostic marker; pharmaceutical.
 KW Homo sapiens.
 DE EP1347046-A1.
 XX PN 24-SEP-2003.
 KW PD 12-APR-2002; 2002EP-00008400.
 XX PF 22-MAR-2002; 2002JP-00137785.
 XX PR (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX PA Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 XX PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 XX PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masubo Y;
 XX PI WPI: 2003-723558/69.
 XX DR N-PSDB; ADM01349.
 XX DR
 XX New polynucleotides and polypeptides are useful in gene therapy, for
 PT developing a diagnostic marker or medicines for regulating their
 PT expression and activity, or as a target of gene therapy.
 XX Claim 1; SEQ ID NO 2477; 305pp; English.
 PS The invention relates to a novel human polynucleotide and the encoded
 CC polypeptide. A polynucleotide of the invention may have a use in gene
 CC therapy. An oligonucleotide of the invention ADM06202-ADM0773 is useful
 CC as a primer for synthesizing the polynucleotide or as a probe for
 CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
 CC useful in gene therapy, for developing a diagnostic marker or medicines
 CC for regulating their expression and activity, or as a target of gene
 CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
 CC are useful as pharmaceutical agents. The present sequence represents a
 CC protein sequence of the invention.
 XX Sequence 663 AA;
 SQ
 Query Match 82.9%; Score 723; DB 2; Length 147;
 Best Local Similarity 100.0%; Pred. No. 6.2e-47;
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 30 VPGALAAKAAKYGAAVPGVLGGLGALGVGIPGGVVGAGPAAKAAKAAKAAQFGLV 89
 DB 6 VPGALAAKAAKYGAAVPGVLGGLGALGVGIPGGVVGAGPAAKAAKAAKAAQFGLV 65
 QY 90 GAAGLGLGVGGLGVGPGVGGTGGTTPPAAKAAKYGAAAGLGVGAGQFPLGGVAARPG 149
 DB 66 GAAGLGLGVGGLGVGPGVGGTGGTTPPAAKAAKYGAAAGLGVGAGQFPLGGVAARPG 125
 QY 150 FGLSPFPGGACLGKACGRKK 171
 DB 126 FGLSPFPGGACLGKACGRKK 147
 RESULT 21
 ADM03792
 ID ADM03792 standard; protein; 663 AA.
 XX
 AC ADM03792;
 XX
 DT 20-MAY-2004 (first entry)
 XX

DE Human tropoelastin derivative SHELgamma.
 XX Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;
 KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
 KW hand lotion; surgical implant; industrial product; human; SHEL; variant.
 XX Homo sapiens.
 OS Synthetic.
 XX WO9903886-A1.
 XX PN 28-JAN-1999.
 XX PD 17-JUL-1998; 98WO-AU000564.
 XX PF 18-JUL-1997; 97AU-00008117.
 XX PR (UNSY) UNIV SYDNEY.
 XX PA Weiss AS;
 XX PI WPI: 1999-132162/11.
 XX DR N-PSDB; AAX27706.
 XX DR
 XX New derivatives of human tropoelastin - with elastin-like or
 PT macromolecular binding properties, useful e.g. as surgical implants.
 PT Claim 19; Fig 7; 82pp; English.
 PS The invention relates to a derivative or variant of human tropoelastin
 CC (hTE) having elastin-like and/or macromolecule (specifically
 CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors
 CC comprising the nucleic acids encoding the variants or derivatives are
 CC used to produce the proteins recombinantly. The tropoelastin derivatives
 CC or hybrid proteins containing the derivatives are useful in medical,
 CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
 CC wrinkle or hand lotions, also as surgical implants, foods and industrial
 CC products. The hybrid protein have controllable GAG-binding properties,
 CC depending on presence or absence of a specific fragment, designated
 CC peptide 26A, from hTE. The present sequence represents a human
 CC tropoelastin derivative SHELgamma excluding the product encoded by exon
 CC 26A
 XX Sequence 147 AA;
 SQ
 Query Match 82.9%; Score 723; DB 2; Length 147;
 Best Local Similarity 100.0%; Pred. No. 6.2e-47;
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 30 VPGALAAKAAKYGAAVPGVLGGLGALGVGIPGGVVGAGPAAKAAKAAKAAQFGLV 89
 DB 6 VPGALAAKAAKYGAAVPGVLGGLGALGVGIPGGVVGAGPAAKAAKAAKAAQFGLV 65
 QY 90 GAAGLGLGVGGLGVGPGVGGTGGTTPPAAKAAKYGAAAGLGVGAGQFPLGGVAARPG 149
 DB 66 GAAGLGLGVGGLGVGPGVGGTGGTTPPAAKAAKYGAAAGLGVGAGQFPLGGVAARPG 125
 QY 150 FGLSPFPGGACLGKACGRKK 171
 DB 126 FGLSPFPGGACLGKACGRKK 147
 RESULT 21
 ADM03792
 ID ADM03792 standard; protein; 663 AA.
 XX
 AC ADM03792;
 XX
 DT 20-MAY-2004 (first entry)
 XX

DE Human protein of the invention SEQ ID NO:2477.
 XX human; gene therapy; diagnostic marker; pharmaceutical.
 KW Homo sapiens.
 DE EP1347046-A1.
 XX PN 24-SEP-2003.
 KW PD 12-APR-2002; 2002EP-00008400.
 XX PF 22-MAR-2002; 2002JP-00137785.
 XX PR (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX PA Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 XX PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 XX PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masubo Y;
 XX PI WPI: 2003-723558/69.
 XX DR N-PSDB; ADM01349.
 XX DR
 XX New polynucleotides and polypeptides are useful in gene therapy, for
 PT developing a diagnostic marker or medicines for regulating their
 PT expression and activity, or as a target of gene therapy.
 XX Claim 1; SEQ ID NO 2477; 305pp; English.
 PS The invention relates to a novel human polynucleotide and the encoded
 CC polypeptide. A polynucleotide of the invention may have a use in gene
 CC therapy. An oligonucleotide of the invention ADM06202-ADM0773 is useful
 CC as a primer for synthesizing the polynucleotide or as a probe for
 CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
 CC useful in gene therapy, for developing a diagnostic marker or medicines
 CC for regulating their expression and activity, or as a target of gene
 CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
 CC are useful as pharmaceutical agents. The present sequence represents a
 CC protein sequence of the invention.
 XX Sequence 663 AA;
 SQ
 Query Match 82.2%; Score 717; DB 7; Length 663;
 Best Local Similarity 96.6%; Pred. No. 7.2e-46;
 Matches 142; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 25 PSSPRVPGALAAKAAKYGAAVPGVLGGLGALGVGIPGGVVGAGPAAKAAKAAKAAKAA 84
 DB 517 PGFAGVPGALAAKAAKYGAAVPGVLGGLGALGVGIPGGVVGAGPAAKAAKAAKAAKAA 576
 QY 85 QFGLVGAAGLGLGVGGLGVGPGVGGTGGTTPPAAKAAKYGAAAGLGVGAGQFPLGGV 144
 DB 577 QFGLVGAAGLGLGVGGLGVGPGVGGTGGTTPPAAKAAKYGAAAGLGVGAGQFPLGGV 636
 QY 145 AARPGFGLSPFPGGACLGKACGRKK 171
 DB 637 AARPGFGLSPFPGGACLGKACGRKK 663
 RESULT 22
 AAY01303
 ID AAY01303 standard; protein; 660 AA.
 XX
 AC AAY01303;
 XX
 DT 07-JUN-1999 (first entry)
 XX
 DE Human tropoelastin derivative SHELdelta modified.
 KW Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;
 KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
 KW hand lotion; surgical implant; industrial product; human; SHEL.
 XX

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OS Homo sapiens.
OS Synthetic.
PN WO9903886-A1.
PD 28-JAN-1999.
XX
PF 17-JUL-1998; 98WO-AU000564.
XX
PR 18-JUL-1997; 97AU-00008117.
XX
PA (UNSY ) UNIV SYDNEY.
XX
PI Weiss AS;
XX
DR WPI; 1999-132162/11.
DR N-PSDB; AAX27705.
XX
XX New derivatives of human tropoelastin - with elastin-like or
PT macromolecular binding properties, useful e.g. as surgical implants.
XX
PS Claim 7; Fig 3; 82pp; English.
XX
CC The invention relates to a derivative or variant of human tropoelastin
CC (hTE) having elastin-like and/or macromolecule (specifically
CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors
CC comprising the nucleic acids encoding the variants or derivatives are
CC used to produce the proteins recombinantly. The tropoelastin derivatives
CC or hybrid proteins containing the derivatives are useful in medical,
CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
CC wrinkle or hand lotions, also as surgical implants, foods and industrial
CC products. The hybrid protein have controllable GAG-binding properties,
CC depending on presence or absence of a specific fragment, designated
CC peptide 26A, from hTE. The present sequence represents a human
CC tropoelastin derivative SHEldeltamodified
XX
SQ Sequence 660 AA;

Query Match      81.5%; Score 710.5; DB 2; Length 660;
Best Local Similarity 96.6%; Pred. No. 2.2e-45;
Matches 142; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 25 PSSRPVPGALAAAKAAYGAAPVGLGGLGAGVPGVVGAGPAAAKAAAKAA 84
Db 515 PFGAVPVGALAAAKAAYG-AVPGVLGGLGAGVPGVVGAGPAAAKAAAKAA 573
QY 85 QFGLVGAAGLGLGVGGLGVPGVGGVGGTTPPAAAKAAYGAAGLVGGAGQFPLGV 144
Db 574 QFGLVGAAGLGLGVGGLGVPGVGGVGGTTPPAAAKAAYGAAGLVGGAGQFPLGV 633
QY 145 AARPGFGLSPIPPGACILGKACGRKRK 171
Db 634 AARPGFGLSPIPPGACILGKACGRKRK 660

RESULT 23
ADB64761
ID ADB64761 standard; protein; 617 AA.
XX
AC ADB64761;
XX
XX 04-DEC-2003 (first entry)
XX
DE Human protein encoded by clone NT2RP70003110.
XX
KW Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;
KW cell regeneration; membrane protein; signal transduction-related protein;
KW transcription-related protein; osteoporosis; neurological disease;
KW cancer; tumour.
OS Homo sapiens.
PN EP1308459-A2.

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XX PD 07-MAY-2003.
XX
XX 28-MAR-2002; 2002EP-00007401.
XX
XX 05-NOV-2001; 2001JP-00379298.
XX 25-JAN-2002; 2002US-00350978.
XX (HELI-) HELIX RES INST.
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR WPI; 2003-450961/43.
DR N-PSDB; ADB62791.
XX
XX New polynucleotides and polypeptides, useful for developing a diagnostic
PT marker or medicines for regulation of their expression and activity, or
PT as targets of gene therapy.
XX
PS Claim 1; Page; 222pp; English.
XX
CC The invention discloses a polynucleotide comprising a sequence selected
CC from 1970 fully defined nucleotide sequences which encode novel
CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
CC or its partial peptide, an antibody binding to the polypeptide or peptide
CC of the polynucleotide, immunologically assaying the polypeptide or
CC peptide of the polynucleotide by contacting the polypeptide or peptide
CC with the antibody of the encoded protein, and observing the binding
CC between the two, a transformant carrying the polynucleotide in an
CC expressible manner and an antisense polynucleotide. The oligonucleotide
CC is useful as a primer for synthesising the polynucleotide, or as a probe
CC for detecting the polynucleotide. The polynucleotides and encoded
CC proteins are useful as pharmaceutical agents and many disease-related
CC genes may be included in them, for developing a diagnostic marker or
CC medicines for regulation of their expression and activity, or as targets
CC of gene therapy. The genes are involved in tissue and/or cell
CC regeneration. Membrane proteins, signal transduction-related proteins,
CC transcription-related proteins, disease-related proteins and genes
CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
CC neurological diseases, cancer, tumours. The cDNA may be used to regulate
CC the activity or expression of the encoded protein to treat diseases. The
CC sequence presented is a protein of the invention. Note: Some of the
CC sequence data for this patent is not represented in the printed
CC specification, but is based on sequence information supplied by the
CC European Patent Office.
XX
SQ Sequence 617 AA;

Query Match      70.2%; Score 612; DB 7; Length 617;
Best Local Similarity 85.0%; Pred. No. 5.3e-38;
Matches 125; Conservative 0; Mismatches 4; Indels 18; Gaps 1;

QY 25 PSSRPVPGALAAAKAAYGAAPVGLGGLGAGVPGVVGAGPAAAKAAAKAA 84
Db 489 PFGAVPVGALAAAKAAYGAAPVGLGGLGAGVPGVVGAGPAAAKAAAKAA 548
QY 85 QFGLVGAAGLGLGVGGLGVPGVGGVGGTTPPAAAKAAYGAAGLVGGAGQFPLGV 144
Db 549 QFGLVGAAGLGLGVGGLGVPGVGGVGGTTPPAAAKAAYGAAGLVGGAGQFPLGV 144
QY 145 AARPGFGLSPIPPGACILGKACGRKRK 171
Db 591 AARPGFGLSPIPPGACILGKACGRKRK 617

RESULT 24
AAB08630
ID AAB08630 standard; peptide; 712 AA.
XX
XX AAB08630;

```

DT 20-DEC-2000 (first entry)
XX Fusion protein comprising human elastin and c-myc.
DE
XX
XX Tropoelastin; elastin; elastic fibre; smooth muscle cell proliferation;
KW smooth muscle cell differentiation; smooth muscle cell migration;
KW smooth muscle cell function; atherosclerosis; restenosis; aneurysm;
KW smooth muscle cell function; atherosclerosis; restenosis; aneurysm;
KW vascular bypass graft stenosis; transplant arteriopathy; dissection;
KW SVAS; hypertension; transplant arteriopathy.
XX
XX Synthetic.
OS Homo sapiens.
OS Unidentified.
XX
XX WO200050068-A2.
XX
XX 31-AUG-2000.
XX
XX 28-FEB-2000; 2000WO-US002526.
XX
XX 26-FEB-1999; 99US-00258217.
XX
XX (UTAH) UNIV UTAH RES FOUND.
XX
XX Keating MT, Li DY;
XX
XX WPI; 2000-533134/48.
XX
XX Elastin based compositions useful for treating atherosclerosis,
PT restenosis, vascular bypass graft stenosis, transplant arteriopathy,
PT aneurysm, dissection SVAS and/or hypertension.
XX
XX Example 3; Page 48; 79pp; English.
XX
XX The present sequence represents a fusion protein, comprising human
CC elastin and c-myc, preceded by a His tag. The protein is used in
CC compositions of the invention. The specification describes elastin based
CC compositions that are potent regulators of smooth muscle cell
CC proliferation, differentiation and migration in vivo. The elastin-based
CC tropoelastins (or fragments of them) which have biological activities
CC comprising: inhibiting the proliferation of smooth muscle cells in vivo;
CC stimulating the differentiation of smooth muscle cells in vivo; and
CC regulating the migration of smooth muscle cells in vivo. The compositions
CC may be used for the prophylaxis or treatment of a disorder characterized
CC by diminished capacity to regulate smooth muscle cell function such as
CC atherosclerosis, restenosis, vascular bypass graft stenosis, transplant
CC arteriopathy, aneurysm and/or dissection. Disorders which may be treated
CC also include SVAS (undefined), hypertension, and transplant arteriopathy
XX
XX Sequence 730 AA;
Query Match 70.2%; Score 612; DB 3; Length 730;
Best Local Similarity 85.0%; Pred. No. 6.2e-36;
Matches 125; Conservative 0; Mismatches 4; Indels 18; Gaps 1;
QY 25 PSSPRVPGALAAAKAAYGAAPVGLGGLGALGVGIPGVGAGPAAAAAAXAAKAA 84
DB 593 PGFAGVPGALAAAKAAYGAAPVGLGGLGALGVGIPGVGAGPAAAAAAXAAKAA 652
QY 85 QFGLVGAAGLGLGVGGLGVGIPGVGAGPAAAAAAXAAKAAKYGAGLVGGAGPPLGGV 144
DB 653 QFGLVGAAGLGLGVGGLGVGIPGVGAGPAAAAAAXAAKAAKYGAGLVGGAGPPLGGV 694
QY 145 AARPGFGLSPFPGGACLGKACGRKK 171
DB 695 AARPGFGLSPFPGGACLGKACGRKK 721
RESULT 26
ID AAB08631 standard; peptide; 730 AA.
XX AAB08631;
XX

XX
DT 20-DEC-2000 (first entry)
DE
XX
XX Amino acid sequence of a human elastin polypeptide.
KW Tropoelastin; elastin; elastic fibre; smooth muscle cell proliferation;
KW smooth muscle cell differentiation; smooth muscle cell migration;
KW smooth muscle cell function; atherosclerosis; restenosis; aneurysm;
KW smooth muscle cell function; atherosclerosis; restenosis; aneurysm;
KW vascular bypass graft stenosis; transplant arteriopathy; dissection;
KW SVAS; hypertension; transplant arteriopathy.
XX
XX Homo sapiens.
XX
XX WO200050068-A2.
XX
XX 31-AUG-2000.
XX
XX 28-FEB-2000; 2000WO-US002526.
XX
XX 26-FEB-1999; 99US-00258217.
XX
XX (UTAH) UNIV UTAH RES FOUND.
XX
XX Keating MT, Li DY;
XX
XX WPI; 2000-533134/48.
XX
XX Elastin based compositions useful for treating atherosclerosis,
PT restenosis, vascular bypass graft stenosis, transplant arteriopathy,
PT aneurysm, dissection SVAS and/or hypertension.
XX
XX Example 3; Page 46; 79pp; English.
XX
XX The present sequence represents a human elastin. Peptides derived from
CC elastin are used in compositions of the invention. The specification
CC describes elastin based compositions that are potent regulators of smooth
CC muscle cell proliferation, differentiation and migration in vivo. The
CC elastin-based compositions comprise at least one elastic fibre, elastins,
CC tropoelastins (or fragments of them) which have biological activities
CC comprising: inhibiting the proliferation of smooth muscle cells in vivo;
CC stimulating the differentiation of smooth muscle cells in vivo; and
CC regulating the migration of smooth muscle cells in vivo. The compositions
CC may be used for the prophylaxis or treatment of a disorder characterized
CC by diminished capacity to regulate smooth muscle cell function such as
CC atherosclerosis, restenosis, vascular bypass graft stenosis, transplant
CC arteriopathy, aneurysm and/or dissection. Disorders which may be treated
CC also include SVAS (undefined), hypertension, and transplant arteriopathy
XX
XX Sequence 712 AA;
Query Match 70.2%; Score 612; DB 3; Length 712;
Best Local Similarity 85.0%; Pred. No. 6.1e-38;
Matches 125; Conservative 0; Mismatches 4; Indels 18; Gaps 1;
QY 25 PSSPRVPGALAAAKAAYGAAPVGLGGLGALGVGIPGVGAGPAAAAAAXAAKAA 84
DB 584 PGFAGVPGALAAAKAAYGAAPVGLGGLGALGVGIPGVGAGPAAAAAAXAAKAA 643
QY 85 QFGLVGAAGLGLGVGGLGVGIPGVGAGPAAAAAAXAAKAAKYGAGLVGGAGPPLGGV 144
DB 644 QFGLVGAAGLGLGVGGLGVGIPGVGAGPAAAAAAXAAKAAKYGAGLVGGAGPPLGGV 685
QY 145 AARPGFGLSPFPGGACLGKACGRKK 171
DB 686 AARPGFGLSPFPGGACLGKACGRKK 712
RESULT 25
ID AAB08631 standard; peptide; 730 AA.
XX AAB08631;
XX

CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 864 AA;
Query Match 55.3%; Score 482; DB 7; Length 864;
Best Local Similarity 55.4%; Pred. No. 4.3e-28;
Matches 113; Conservative 8; Mismatches 19; Indels 64; Gaps 7;
QY 30 VPGNLAARAAKAYCAA---VPGVLGGLGAGGV-----GIPGGVVGAGPAAAAA 75
DB 663 VPGSLAARAAKAYGAAGLGGPGGLGGPGGLGGPGGGPGGLGGVGGVAGGAP-AAA 721
QY 76 AAKAAKAAQGLVGAAGL-----GGLGVGGGLG---VPGVGGGLGIP 114
DB 722 AAKAAKAAQGLGAGGLGAGGLGAGGLGAGGLGAGGLGAGGLGAGGVIPGAVGLGGS 781
QY 115 PAAAKAAKAYGAAGLGGVGGAGGFPGLGGVAAAPGGLSPFP----- 157
DB 782 PAAAKAAKAYGAAGLGGVL--GARPPGGGVAARFGLSPFYPGGGAGGLGVGKPKPY 840
QY 158 -----GGACLGKACGRKK 171
DB 841 GGALGALGYQGGGCGKSKGRKK 864

RESULT 28
ADE08527
ID ADE08527 standard; protein; 870 AA.
XX ADE08527;
AC
XX 29-JAN-2004 (first entry)
DT
XX Novel protein (useful for identifying genetic disorders) #682.
DE
XX novel gene; novel protein; tissue marker; molecular weight marker;
KW chromosome marker; genetic disorder.
XX Unidentified.
OS
XX WO2003054152-A2.
PN
XX 03-JUL-2003.
PD
XX 10-DEC-2002; 2002WO-US039555.
PF
XX 10-DEC-2001; 2001US-0339739P.
PR
XX 11-DEC-2001; 2001US-0339453P.
PR
XX 14-MAR-2002; 2002US-0365091P.
PR
XX 14-MAR-2002; 2002US-0365384P.
PR
XX 12-APR-2002; 2002US-0372381P.
PR
XX 12-APR-2002; 2002US-0372615P.
PR
XX 22-APR-2002; 2002US-00128558.
PR

24-APR-2002; 2002US-0376045P.

PR (HYSE-) HYSEQ INC.
XX
XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RI, Wang Z;
PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
XX
XX WPI; 2003-569235/53.
DR N-PSDB; ADE07616.

XX New polynucleotides, useful for expressing recombinant proteins for
PT analysis, characterization or therapeutic use, or as markers for tissues
PT in which the corresponding protein is preferentially expressed.

XX Claim 20; SEQ ID NO 1593; 1177pp; English.

XX The invention comprises the amino acid and coding sequences of novel
CC proteins. The DNA and protein sequences of the invention are useful as:
CC markers for tissues in which the corresponding protein is preferentially
CC expressed; as molecular weight markers on gels; as chromosome markers or
CC tags; to identify chromosomes or to map related gene positions; and to
CC compare with endogenous DNA sequences in patients to identify potential
CC genetic disorders. The present amino acid sequence represents a protein
CC of the invention.

XX SQ Sequence 870 AA;

Query Match 54.5%; Score 475; DB 7; Length 870;
Best Local Similarity 53.5%; Pred. No. 1.5e-27;
Matches 114; Conservative 3; Mismatches 14; Indels 82; Gaps 5;
QY 25 PSSPRVPGALAAKAAKY----- 42
DB 649 PGFANVPGALAAKAAKYGILPPRASPDVAVPQPHLALWQCLARPTLSVAPEFLASC 708

QY 43 -----GAAVPGVLGGLGAGGVIPGGVVGAGPAAAAKAAKAA 83
DB 709 EQRWVEVDSRDPPTTSRAGAAVPGVLGGLGAGGVIPGGVVGAGPAAAAKAAKAA 768
QY 84 AQFG-----LVGAAGLGLGVGGLGVPGVGGGLGTPPAAAKAAKYGAAGLGGVGGAGQF 139
DB 769 AQFGEHWVEVGAAA-----RPPGQGPAPAAAKAAKYGAAGLGGVGGAGQF 816
QY 140 PLGGVAAAPPGGLSPFPFGG---ACLGKACGRK 169
DB 817 PLGGVAAAPPGGLSPFPFGSELVPC--ASCGQR 847

RESULT 29
AAV01306
ID AAV01306 standard; protein; 60 AA.
XX
XX AAV01306;
AC
XX 07-JUN-1999 (first entry)
DT
XX Human tropoelastin derivative SHEL31-36.
DE

XX Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;
KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
KW hand lotion; surgical implant; industrial product; human; SHEL; variant.
XX Homo sapiens.
OS Synthetic.
OS
XX WO9903886-A1.
PN
XX 28-JAN-1999.
PD
XX 17-JUL-1998; 98WO-AU000564.
PF
XX 18-JUL-1997; 97AU-00008117.
PR

```

XX PA (UNSY ) UNIV SYDNEY.
XX PI Weiss AS;
XX DR WPI; 1999-132162/11.
XX XX
XX PT New derivatives of human tropoelastin - with elastin-like or
XX PT macromolecular binding properties, useful e.g. as surgical implants.
XX XX
XX PS Claim 23; Page 10; 82pp; English.
XX XX
XX CC The invention relates to a derivative or variant of human tropoelastin
XX CC (hTE) having elastin-like and/or macromolecule (specifically
XX CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors
XX CC comprising the nucleic acids encoding the variants or derivatives are
XX CC used to produce the proteins recombinantly. The tropoelastin derivatives
XX CC or hybrid proteins containing the derivatives are useful in medical,
XX CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
XX CC wrinkle or hand lotions, also as surgical implants, foods and industrial
XX CC products. The hybrid protein have controllable GAG-binding properties,
XX CC depending on presence or absence of a specific fragment, designated
XX CC peptide 26A, from hTE. The present sequence represents a human
XX CC tropoelastin derivative SHEL31-36
XX XX
XX SQ Sequence 60 AA;
XX
Query Match 36.5%; Score 318; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 7.4e-17;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 112 GTPPAAAAKAAKYAGAGLVGGAGQFPLGGVAARPFGFLSPIPPGGACLGKACGRKK 171
Db |||||
1 GTPPAAAAKAAKYAGAGLVGGAGQFPLGGVAARPFGFLSPIPPGGACLGKACGRKK 60
XX
RESULT 30
AAB88422
ID AAB88422 standard; protein; 472 AA.
XX
AC AAB88422;
XX
DT 23-MAY-2001 (first entry)
XX
XX Human membrane or secretory protein clone PSEC0191.
XX
DE Human; secretory protein; membrane protein; vaccine; gene therapy;
XX
KW rheumatoid arthritis; diabetes.
XX
OS Homo sapiens.
XX
FN EP1067182-A2.
XX
PD 10-JAN-2001.
XX
PF 07-JUL-2000; 2000EP-00114090.
XX
FR 08-JUL-1999; 99JP-00194179.
XX
PR 11-JAN-2000; 2000JP-00118775.
XX
PR 02-MAY-2000; 2000JP-00183766.
XX
XX
PA (HELI-) HELIX RES INST.
XX
XX
PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
XX
DR WPI; 2001-093989/11.
XX
DR N-FSDB; AAF93849.
XX
XX
XX Nucleic acids encoding secretory proteins/membrane proteins, useful in
XX PT gene therapy or as candidate target molecules in drug development.
XX
PS Claim 1; SEQ ID NO 212; 609pp + Sequence Listing; English.
XX

```

```

CC This invention relates to nucleic acid sequences AAF93744 - AAF93916
CC which encode human secretory or membrane proteins represented by AAB88317
CC - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and
CC AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the
CC invention. The invention also includes methods for the production of
CC antibodies directed against the proteins, and cDNA sequences, which can
CC be used in vaccines. The polynucleotide sequences can be used in gene
CC therapy. The polynucleotide sequences and the proteins they encode may be
CC used in the prevention, treatment and diagnosis of diseases associated
CC with inappropriate secretory protein/membrane protein expression. The
CC nucleic acids and complementary sequences may also be used as DNA probes
CC in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect
CC and quantitate the presence of similar nucleic acid sequences in samples.
CC They may also be used to study the expression and function of secretory
CC proteins/membrane polypeptides and their role in metabolism. The
CC polypeptides may be used as antigens in the production of antibodies
CC against them and in assays to identify modulators (agonists and
CC antagonists) of expression and activity. The antibodies and antagonists
CC may also be used as therapeutic agents to down regulate expression and
CC activity. The antibodies may also be used as diagnostic agents for
CC detecting the presence of the polypeptides in samples (e.g. by enzyme
CC linked immunosorbant assay (ELISA)). Examples of diseases which may be
CC treated include rheumatoid arthritis and diabetes
XX
XX SQ Sequence 472 AA;
XX
Query Match 32.1%; Score 280; DB 4; Length 472;
Best Local Similarity 34.7%; Pred. No. 3.7e-13;
Matches 90; Conservative 13; Mismatches 28; Indels 128; Gaps 12;
XX
QY 25 PSSPRVPGGALAAKAAKYGAAPVGVGLGGLGALGGVIGPGVVGAGPAAAA 74
Db |||||
62 PLKP-VPGGLAGA-----GLGAGLGLGGVIGPGVVGAGPAAAAA 110
QY 75 -----AAAKAA 80
Db |||||
111 AAAGLVPGGPGFGPGVGVPGAGVPGVPGAGIPVPGAGIPGAAPGVGSPAAAAKAA 170
QY 81 AKAAQFGLVGAAGLGL-----GVGGL-----GVPGVG-----GLGGIP----- 114
Db |||||
171 AKAAKYGARPGVGVGGIPTYGVGAGGFGFGVGVGGIPGVAGVPGVGVGGVPGVGI 230
QY 115 -----PAAAAKAAKYG-----AAGLG-----GVLGGAGQFPLGGVAARPFGFLSP 154
Db |||||
231 SPEAQAATAAAKAAKYGLVPGVGVAPGVGVAAPGVGVAAPGVGLAP--GVGVAPGVGVA 288
QY 155 -----IFPGG-ACLGKACGR 168
Db |||||
289 VAPGIGPGGVAAAAKSAK 307
XX
Search completed: November 19, 2004, 16:28:45
Job time : 37.9467 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2004, 16:37:11 ; Search time 27.9275 Seconds
(without alignments)
2168.321 Million cell updates/sec

Title: US-09-743-818a-73

Perfect score: 872

Sequence: 1 GVRRLSPRLRGDPSSQH.....LSPIPGGACLGKACGRKK 171

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	872	100.0	731	10	US-09-964-662-1
2	725	83.1	692	15	US-10-210-172-40
3	725	83.1	730	10	US-09-961-403-8
4	717	82.2	663	15	US-10-108-260A-2477
5	612	70.2	617	14	US-10-104-047-2915
6	609	69.8	711	15	US-10-210-172-38
7	216.5	24.8	144	15	US-10-424-539-269890
8	212.5	24.4	199	10	US-09-964-662-11
9	212.5	24.4	200	10	US-09-964-662-2
10	195.5	22.4	641	14	US-10-138-098-52
11	195.5	22.4	641	14	US-10-294-804-4
12	195.5	22.4	641	14	US-10-225-838B-22
13	195.5	22.4	641	16	US-10-732-694-11
					Sequence 1, Appli
					Sequence 40, Appl
					Sequence 8, Appli
					Sequence 2477, Ap
					Sequence 3815, Ap
					Sequence 2915, Ap
					Sequence 269890,
					Sequence 11, Appl
					Sequence 2, Appli
					Sequence 52, Appl
					Sequence 4, Appli
					Sequence 22, Appl
					Sequence 11, Appl

651	9	US-09-861-597-1	Sequence 1, Appli
651	14	US-10-414-760-1	Sequence 1, Appli
646	16	US-10-406-832-27	Sequence 27, Appl
606	9	US-09-861-597-4	Sequence 4, Appli
606	9	US-09-861-597-6	Sequence 6, Appli
606	9	US-09-861-597-8	Sequence 8, Appli
809	14	US-10-414-760-13	Sequence 13, Appl
818	14	US-10-414-760-22	Sequence 22, Appl
1617	14	US-10-414-760-14	Sequence 14, Appl
1626	14	US-10-414-760-24	Sequence 24, Appl
696	8	US-08-806-029-36	Sequence 36, Appl
696	15	US-10-441-965-23	Sequence 23, Appl
750	8	US-08-806-029-25	Sequence 25, Appl
246	16	US-10-800-179-26	Sequence 26, Appl
696	15	US-10-441-965-21	Sequence 21, Appl
832	8	US-08-806-029-27	Sequence 27, Appl
1465	14	US-10-096-986-74	Sequence 74, Appl
520	17	US-10-479-638-21	Sequence 21, Appl
246	16	US-10-800-179-28	Sequence 28, Appl
244	16	US-10-800-179-27	Sequence 27, Appl
768	8	US-08-806-029-35	Sequence 35, Appl
884	14	US-10-117-931-15	Sequence 15, Appl
312	8	US-08-806-029-34	Sequence 34, Appl
378	14	US-10-117-931-26	Sequence 26, Appl
1002	14	US-10-117-931-25	Sequence 25, Appl
1536	17	US-10-479-638-54	Sequence 54, Appl
2304	17	US-10-479-638-53	Sequence 53, Appl
486	16	US-10-437-963-117435	Sequence 117435,
936	8	US-08-806-029-26	Sequence 26, Appl
884	16	US-10-800-179-25	Sequence 25, Appl
889	8	US-08-806-029-19	Sequence 19, Appl
618	15	US-10-282-122A-64608	Sequence 64608, A
965	16	US-10-800-179-31	Sequence 31, Appl
667	15	US-10-282-122A-64494	Sequence 64494, A
603	15	US-10-282-122A-64537	Sequence 64537, A
615	15	US-10-282-122A-64576	Sequence 64576, A
1038	16	US-10-800-179-30	Sequence 30, Appl
936	14	US-10-117-931-30	Sequence 30, Appl
988	8	US-08-806-029-28	Sequence 28, Appl
1470	14	US-10-184-644-479	Sequence 479, App
1470	14	US-10-184-634-479	Sequence 479, App
274	16	US-10-437-963-116008	Sequence 116008, A
396	15	US-10-425-114-49974	Sequence 49974, A
447	16	US-10-437-963-149959	Sequence 149959,
448	17	US-10-435-115-192158	Sequence 192158,
966	14	US-10-117-931-34	Sequence 34, Appl
1968	14	US-10-123-155-163	Sequence 163, App
1968	14	US-10-146-731-163	Sequence 163, App
1968	14	US-10-140-472-163	Sequence 163, App
1968	14	US-10-141-761-163	Sequence 163, App
1968	14	US-10-142-885-163	Sequence 163, App
1968	14	US-10-158-790-163	Sequence 163, App
1968	14	US-10-137-871-163	Sequence 163, App
1968	14	US-10-140-923-163	Sequence 163, App
1968	14	US-10-141-756-163	Sequence 163, App
1968	14	US-10-141-759-163	Sequence 163, App
1968	14	US-10-140-805-163	Sequence 163, App
1968	14	US-10-140-864-163	Sequence 163, App
1968	15	US-10-142-426-163	Sequence 163, App
256	10	US-09-820-843A-18	Sequence 18, Appl
259	9	US-09-861-597-2	Sequence 2, Appli
624	17	US-10-479-638-12	Sequence 12, Appl
827	16	US-10-406-832-28	Sequence 28, Appl
637	15	US-10-282-122A-64362	Sequence 64362, A
1381	15	US-10-282-122A-64895	Sequence 64895, A
2368	14	US-10-123-155-423	Sequence 423, App
2368	14	US-10-146-731-423	Sequence 423, App
2368	14	US-10-140-472-423	Sequence 423, App
2368	14	US-10-141-761-423	Sequence 423, App
2368	14	US-10-142-885-423	Sequence 423, App
2368	14	US-10-158-790-423	Sequence 423, App
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87      167      19.2      2368      14      US-10-141-756-423      Sequence 423, App
88      167      19.2      2368      14      US-10-141-753-423      Sequence 423, App
89      167      19.2      2368      14      US-10-140-805-423      Sequence 423, App
90      167      19.2      2368      14      US-10-140-864-423      Sequence 423, App
91      167      19.2      2368      15      US-10-142-426-423      Sequence 423, App
92      165.5      19.0      525      15      US-10-282-122A-64763      Sequence 64763, A
93      165.5      19.0      1670      14      US-10-123-155-325      Sequence 325, App
94      165.5      19.0      1670      14      US-10-146-731-325      Sequence 325, App
95      165.5      19.0      1670      14      US-10-140-472-325      Sequence 325, App
96      165.5      19.0      1670      14      US-10-141-761-325      Sequence 325, App
97      165.5      19.0      1670      14      US-10-142-885-325      Sequence 325, App
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100     165.5      19.0      1670      14      US-10-140-923-325      Sequence 325, App
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ALIGNMENTS

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RESULT 1
US-09-964-662-1
; Sequence 1, Application US/09964662
; Publication No. US20030166846A1
; GENERAL INFORMATION:
; APPLICANT: PROTEIN SPECIALTIES LTD
; TITLE OF INVENTION: HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP
; TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN AND
; FILE REFERENCE: 041082/0112
; CURRENT APPLICATION NUMBER: US/09/964,662
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: 09/340,736
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 731
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-964-662-1

Query Match      100.0%; Score 872; DB 10; Length 731;
Best Local Similarity 100.0%; Pred. No. 3e-55;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1      GVRRLSPRLREGDPSSQHLPTSPSSPRVPGALAAKAAKYGAAPVGVGLGALGVG 60
Db      561     GVRRLSPRLREGDPSSQHLPTSPSSPRVPGALAAKAAKYGAAPVGVGLGALGVG 620

Qy      61      IPGVGVGAPAAAATAKAAKAAQFGLVGAAGLGLGVGPGVGVGLGIPPAATAK 120
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Qy      121     AAKYGAAGLGVGLGAGOFFLGGVAARPFGLSPIFFPGACLGKACGRKK 171
Db      681     AAKYGAAGLGVGLGAGOFFLGGVAARPFGLSPIFFPGACLGKACGRKK 731
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RESULT 2
US-10-210-172-40
; Sequence 40, Application US/10210172
; Publication No. US20040043928A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Miller, Charles
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol
; APPLICANT: Rieger, Daniel
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Li, Li
; APPLICANT: Ji, Weizhen
; APPLICANT: Padigaru, Muralidhara
```

```
; APPLICANT: Casman, Stacie
; APPLICANT: Voss, Edward
; APPLICANT: Boldog, Ferenc
; APPLICANT: Gorman, Linda
; APPLICANT: Leite, Mario
; APPLICANT: Leite, Corine
; APPLICANT: Vernet, Corine
; APPLICANT: Anderson, David
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zhong, Mei
; APPLICANT: Gerlach, Valerie
; APPLICANT: Hjalte, Tord
; APPLICANT: Rastelli, Luca
; APPLICANT: Spytek, Kimberly
; APPLICANT: Edinger, Shlomit
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Alsobrook II, John
; APPLICANT: Lepley, Denise et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-416 A
; CURRENT APPLICATION NUMBER: US/10/210,172
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/309,501
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/323,994
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/373,814
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/310,291
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/310,951
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/310,544
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: 60/311,292
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/311,979
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/313,201
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/312,892
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 327
; SOFTWARE: CuraSeqlist version 0.1
; SEQ ID NO 40
; LENGTH: 692
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-210-172-40

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Best Local Similarity 97.3%; Pred. No. 1.3e-44;
Matches 143; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      25      PSSPRVPCALAAKAAKYGAAPVGVGLGALGVGIPGVVGVGAPAAAATAKAAKAA 84
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Qy      85      QFGLVGAAGLGLGVGLGVGPGVGLGIPPAATAKAAKYGAAGLGVGLGAGOFFLGGV 144
Db      606     QFGLVGAAGLGLGVGLGVGPGVGLGIPPAATAKAAKYGAAGLGVGLGAGOFFLGGV 665

Qy      145     AARPFGLSPIFFPGACLGKACGRKK 171
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RESULT 3
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; Sequence 8, Application US/09961403
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GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2004, 16:06:25 ; Search time 7.69127 Seconds
(without alignments)
2139.198 Million cell updates/sec

Title: US-09-743-818A-73
Perfect score: 872
Sequence: 1 GVRSLSPRLREGDPSSSQH.....LSPIFFGGACLGKACGRKRK 171

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	872	100.0	792	1 EAHU	elastin precursor,
2	509	58.4	770	2 S59623	tropoelastin - she
3	489.5	56.1	860	1 EAMS	elastin precursor
4	486	55.7	747	1 EABO	elastin precursor
5	482	55.3	864	1 EART	elastin precursor
6	290.5	33.3	784	2 A26601	elastin precursor
7	195.5	22.4	641	1 QQBE31	nuclear antigen EB
8	194.5	22.3	718	2 A36068	major amputate fi
9	191	21.9	268	2 B81615	fibroin heavy chai
10	190	21.8	767	2 E70895	hypothetical glyci
11	184	21.1	783	2 T35389	probable serine-th
12	181	20.8	162	2 S56703	glycine-rich cell
13	178.5	20.5	741	2 G70917	hypothetical glyci
14	178.5	20.5	1329	2 E70917	hypothetical glyci
15	175.5	20.1	1901	2 F70806	hypothetical glyci
16	173.5	19.9	158	2 T08957	glycine-rich prote
17	172.5	19.8	1489	2 D70807	hypothetical glyci
18	172	19.7	749	2 A70812	hypothetical glyci
19	171.5	19.7	618	2 A70989	hypothetical glyci
20	171	19.6	667	2 A70893	hypothetical glyci
21	170.5	19.6	603	2 A70770	hypothetical glyci
22	170.5	19.6	615	2 A70589	hypothetical glyci
23	170	19.5	212	2 E86179	hypothetical glyci
24	170	19.5	882	2 B70812	hypothetical prote
25	169.5	19.4	2639	2 T31328	hypothetical glyci
26	168	19.3	907	2 A45560	fibroin - Chinese
27	167	19.2	256	2 A70514	sporozoite surface
28	167	19.2	627	2 A44112	hypothetical glyci
29	167	19.2	837	2 E70835	spidroin 2, dragli
30	167	19.2	142	16.3	hypothetical glyci
31	165.5	19.0	525	2 E70806	hypothetical glyci
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33	163.5	18.8	801	2 F70963	hypothetical glyci
34	163.5	18.8	957	2 F70824	hypothetical glyci
35	163.5	18.8	1660	2 A70869	hypothetical glyci
36	162.5	18.6	515	2 H70663	hypothetical glyci
37	161.5	18.5	384	1 A26099	glycine-rich cell
38	161.5	18.5	491	2 D70916	hypothetical glyci
39	161	18.5	498	2 H70720	hypothetical glyci
40	161	18.5	914	2 H70987	hypothetical glyci
41	160	18.3	783	2 E70824	hypothetical glyci
42	159.5	18.3	1538	2 H70846	hypothetical glyci
43	159	18.2	606	2 H70816	hypothetical glyci
44	159	18.2	1306	2 A70934	hypothetical glyci
45	157.5	18.1	419	2 G70602	hypothetical glyci
46	157	18.0	584	2 F70804	hypothetical prote
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48	156.5	17.9	439	2 D70954	hypothetical glyci
49	156	17.9	496	2 H70839	hypothetical glyci
50	155.5	17.8	245	2 F70787	hypothetical glyci
51	154	17.7	812	2 S31521	collagen COLF1 - f
52	154	17.7	1669	1 CGMS4B	collagen alpha 1(I)
53	153.5	17.6	479	2 F70573	hypothetical prote
54	153.5	17.6	591	2 B70523	hypothetical glyci
55	153	17.5	562	2 B70953	hypothetical glyci
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57	152	17.4	743	1 S23779	hypothetical glyci
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62	150.5	17.3	1414	1 S23809	collagen alpha 1(I)
63	149.5	17.1	673	1 CGBO6C	collagen alpha 1(I)
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65	149.5	17.1	730	2 A36226	collagen alpha 1 c
66	149.5	17.1	744	2 S15435	collagen alpha 1(I)
67	149.5	17.1	923	2 E70820	hypothetical glyci
68	149	17.1	754	2 A5267	collagen alpha 5(I)
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70	148.5	17.0	1418	2 E70983	collagen alpha 1(I)
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73	147	16.9	201	2 T00799	hypothetical prote
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77	146.5	16.8	112	2 JQ1063	glycine-rich prote
78	146.5	16.8	301	2 B31219	collagen 2 - Caeno
79	146.5	16.8	532	2 F70580	hypothetical glyci
80	146.5	16.8	1487	1 CGHU6C	collagen alpha 1(I)
81	146	16.7	87	2 T14302	collagen-rich cell
82	146	16.7	402	1 CGBO2S	collagen alpha 2(I)
83	145.5	16.7	356	2 S16907	collagen alpha 1(I)
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91	144.5	16.6	457	2 H70820	hypothetical glyci
92	144.5	16.6	588	2 F70971	hypothetical glyci
93	144.5	16.6	635	2 A57131	collagen alpha 2(I)
94	144.5	16.6	839	2 F75518	hypothetical prote
95	144	16.5	461	2 F70571	hypothetical glyci
96	143.5	16.5	361	2 G70682	hypothetical glyci
97	143.5	16.5	401	1 QZQAC	circumsporozoite p
98	142.5	16.3	744	1 A34246	collagen alpha 1(I)
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us-09-743-818a-73.rpr

ALIGNMENTS

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		N;Alternate names: tropoelastin	
		C;Species: Homo sapiens (man)	
		C;Date: 22-Jun-1990 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004	
		C;Accession: A32707; A33705; A30524; A53891	
		R;Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Sheppard, P.; Anderson, N.; Rosenbloom, J.	
		Proc. Natl. Acad. Sci. U.S.A. 84, 5680-5684, 1987	
		A;Title: Alternative splicing of human elastin mRNA indicated by sequence analysis of cDNA	
		A;Reference number: A32707; MUID:87289668; PMID:3039501	
		A;Accession: A32707	
		A;Molecule type: mRNA	
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		A;Cross-references: UNIPROT:P15502; UNIPROT:Q9UMK5; GB:M16983; GB:J02948	
		R;Bashir, M.M.; Indik, Z.; Yeh, H.; Ornstein-Goldstein, N.; Rosenbloom, J.C.; Abrams, W.	
		J. Biol. Chem. 264, 8887-8891, 1989	
		A;Title: Characterization of the complete human elastin gene. Delineation of unusual features	
		A;Reference number: A33705; MUID:89255358; PMID:2722804	
		A;Accession: A33705	
		A;Molecule type: DNA	
		A;Residues: 1-27 <BAS>	
		A;Cross-references: GB:J04821; NID:g182052; PIDN:AAA52379.1; PID:g553276	
		R;Fazio, M.J.; Olsen, D.R.; Kauh, E.A.; Baldwin, C.T.; Indik, Z.; Ornstein-Goldstein, N.	
		J. Invest. Dermatol. 91, 458-464, 1988	
		A;Title: Cloning of full-length elastin cDNAs from a human skin fibroblast recombinant cell	
		A;Reference number: A30524; MUID:89009960; PMID:3171221	
		A;Accession: A30524	
		A;Molecule type: mRNA	
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		A;Cross-references: EMBL:M36860; NID:g182061; PIDN:AAA52382.1; PID:g182062	
		A;Note: this sequence represents a composite of several splice forms	
		R;Fazio, M.J.; Olsen, D.R.; Kuivaniemi, H.; Chu, M.L.; Davidson, J.M.; Rosenbloom, J.; U	
		Lab. Invest. 58, 270-277, 1988	
		A;Title: Isolation and characterization of human elastin cDNAs, and age-associated variations	
		A;Reference number: A53891; MUID:88156138; PMID:2831431	
		A;Accession: A53891	
		A;Molecule type: mRNA	
		A;Residues: 164-453,483-500,507-617,651-792 <FAZ>	
		A;Cross-references: GB:M24782; NID:g182063; PIDN:AAA53190.1; PID:g182064	
		C;Comment: The term tropoelastin refers to a soluble precursor form of the extracellular	
		line oxidase activity.	
		C;Genetics:	
		A;Gene: GDB:ELN	
		A;Cross-references: GDB:119107; OMIM:130160	
		A;Map position: 7q11.23-7q11.23	
		C;Superfamily: elastin	
		C;Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine	
		F;1-26/Domain: signal sequence #status predicted <SIG>	
		F;27-792/Product: elastin #status predicted <MAT>	
		F;782-787/Disulfide bonds: #status predicted	
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		Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
		QY 1 GVRSLSPELREGDPSSQHLPTSPSPRVPGALAAAKAAKYGAAPVGLGALGGVG 60	
		Db 622 GVRSLSPELREGDPSSQHLPTSPSPRVPGALAAAKAAKYGAAPVGLGALGGVG 681	
		QY 61 IPGVWVGAPAAAAAATAAATAAQAQGLVGAAGLGGVGLGVPVGGVGGIPPPAAAK 120	
		Db 682 IPGVWVGAPAAAAAATAAATAAQAQGLVGAAGLGGVGLGVPVGGVGGIPPPAAAK 741	
		QY 121 AAKYGAAGLGGVGGAGFPVGGVAAAPFGVGLSPFPFGACLCGKACGKRK 171	
		Db 742 AAKYGAAGLGGVGGAGFPVGGVAAAPFGVGLSPFPFGACLCGKACGKRK 792	
RESULT 2			

us-09-743-818a-73.rpr

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2004, 15:22:20 ; Search time 34.5734 Seconds
(without alignments)
2845.805 Million cell updates/sec

Title: US-09-743-818a-73

Perfect score: 872

Sequence: 1 GVRRLSPRLREGDRPSSSH.....LSPIPPGGACLGKACGRKRK 171

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt 02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	872	100.0	757	2	Q14234 homo sapien
2	872	100.0	757	2	Q75MU5
3	872	100.0	757	2	AAS07435
4	725	83.1	258	2	Q9UMF5
5	725	83.1	730	1	ELIS HUMAN
6	720	82.6	643	2	Q8NB14
7	612	70.2	570	2	Q6ZMJ6
8	612	70.2	570	2	BAC85506
9	612	70.2	658	2	Q6POL4
10	612	70.2	658	2	AAH65566
11	612	70.2	687	2	Q14235
12	608	69.7	687	2	Q7Z316
13	605	69.4	711	2	Q7Z3F5
14	531.5	61.0	707	2	Q28098
15	489.5	56.1	810	2	Q9ESZ9
16	489.5	56.1	860	1	ELIS MOUSE
17	489.5	56.1	860	2	Q8C9L8
18	485	55.6	666	2	Q28096
19	482	55.3	864	1	ELIS_RAT
20	477	54.7	747	1	ELIS_BOVIN
21	442	50.7	679	2	Q28097
22	436	50.0	650	2	Q28099
23	295.5	33.9	750	1	ELIS_CHICK
24	295	33.8	100	1	ELIS_SHEEP
25	280	32.1	472	2	Q8N2G0
26	273.5	31.4	602	2	O15337
27	273.5	31.4	635	2	O15336
28	269	30.8	559	2	Q6ZUN2
29	269	30.8	559	2	BAC86188
30	213.5	24.5	1468	2	Q9GUB5
31	204	23.4	738	2	O02402

32	201	23.1	644	2	Q8WSW4
33	199	22.8	544	2	O46171
34	195.5	22.4	641	1	EBN1_EBV
35	195.5	22.4	641	2	Q777E1
36	195.5	22.4	641	2	CAD53427
37	195	22.4	443	2	Q9GUB4
38	195	22.4	1002	2	Q9BIU8
39	194.5	22.3	747	1	SPDI_NBPCL
40	194	22.2	617	2	O46172
41	194	22.2	651	2	Q9BIU9
42	193.5	22.2	294	2	Q16986
43	193	22.1	691	2	Q9BIU3
44	191	21.9	268	2	O7M468
45	191	21.9	648	2	Q9BIU7
46	190	21.8	767	2	Q79FT0
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48	190	21.8	774	2	Q7U0P7
49	189.5	21.7	172	2	Q9BDZ0
50	189	21.7	447	2	Q9BIU1
51	187.5	21.5	69	2	Q28101
52	187.5	21.5	1460	2	Q7TWC3
53	185	21.2	524	2	Q817U1
54	184	21.1	783	2	Q9XAI1
55	183.5	21.0	988	2	O17434
56	182	20.9	563	2	Q6J6N0
57	182	20.9	563	2	AAI36347
58	182	20.9	904	2	Q76271
59	181	20.8	162	2	Q39691
60	180.5	20.7	349	2	Q9BIU0
61	178.5	20.5	738	2	O8VK15
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64	178.5	20.5	795	2	Q7U020
65	178.5	20.5	1329	2	Q79FP2
66	178.5	20.5	1329	2	CAE55390
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68	177	20.3	905	2	Q8MW55
69	176.5	20.2	233	2	Q9BIT6
70	176.5	20.2	253	2	Q9BIT4
71	176.5	20.2	922	2	Q8MW53
72	175.5	20.1	1715	2	Q8VIZ0
73	175.5	20.1	1901	1	PG54_MYCTU
74	174.5	20.0	342	2	Q9BIU1
75	174.5	20.0	922	2	O4367
76	174	20.0	373	2	Q9BIT9
77	174	20.0	603	2	Q7U079
78	174	20.0	1360	2	Q7TWC4
79	174	20.0	1408	2	Q7U022
80	173.5	19.9	158	2	Q9SZD2
81	173	19.8	486	2	Q9AR23
82	172.5	19.8	360	2	Q9BIU0
83	172.5	19.8	1489	2	Q6MMW6
84	172.5	19.8	1489	2	CAE55607
85	172	19.7	749	2	Q7D974
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ALIGNMENTS


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ID AAS07435 PRELIMINARY; PRT; 757 AA.
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DT 02-MAR-2004 (TREMELrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMELrel. 27, Last annotation update)
DE Hypothetical protein ELN.
GN ELN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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RP SEQUENCE FROM N.A.
RX MEDLINE=22737999; PubMed=12853948;
RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
RA Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
RA Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
RA Vanbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
RA Ozersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
RA Strong C.M., Hou S., Tonlinson C., Dauphin-Kohlberg S.,
RA Kozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
RA Tin-Wollam A.M., Abbott A., Minx P., Maupin R., Strowmatt C.,
RA Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,
RA Wendt M.C., Yang S.P., Schultz B.R., Wallis J.W., Spieth J.,
RA Bieri T.A., Nelson J.O., Berkowicz N., Mohldmann P.E., Cook L.L.,
RA Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
RA Gilfulton S.W., Chissoe S.B., Marra M.A., Raymond C., Haugen E.,
RA Lettitt W., Zhou Y., James R., Phelps K., Iadamoto S., Bubb K.,
RA Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,
RA Baertsch R.A., Brent M.R., Keibler E., Flicek P., Bork P., Suyana M.,
RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,
RA Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
RA Waterston R.H., Wilson R.K.;
RT "The DNA sequence of human chromosome 7.";
RL Nature 424:157-164(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Du H., Rohlfing T., Strong C.;
RT "The sequence of Homo sapiens BAC clone CTB-51J22.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Waterston R.H.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
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RA Wilson R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
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DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
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GN Name=ELN;
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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RX MEDLINE=96411691; PubMed=8812460;
RA Osborne L.R., Martindale D.W., Scherer S.W., Shi X.-M., Huizenga J.,
RA Heng H.H.Q., Costa T., Fober B., Lew L., Brinkman J., Rommens J.,
RA Koop B.F., Tsui L.-C.;
RT "Identification of genes from a 500-kb region at 7q11.23 that is
RT commonly deleted in Williams syndrome patients.";
RL Genomics 36:328-336(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20458868; PubMed=11003705;
RA Martindale D.W., Wilson M.D., Wang D., Burke R.D., Chen X.,
RA Duronio V., Koop B.F.;
RT "Comparative genomic sequence analysis of the Williams syndrome region
RT (LIMK1-RPC2) of human chromosome 7q11.23.";
RL Mamm. Genome 11:890-898(2000).
DR EMBL; U63721; AAC13884.1; -.
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Best Local Similarity 97.3%; Pred. No. 4e-33;
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DB 112 PFGVAVPGALAAAKYGAAPVGLGALGVGIPGGVAGPAAAAAAXAAKAA 171
QY 85 QFGLVGAAGLGLGVGPGVGLGIPGAPAAAKYGAAGLGVGAGGQPLGGV 144
DB 172 QFGLVGAAGLGLGVGPGVGLGIPGAPAAAKYGAAGLGVGAGGQPLGGV 231
QY 145 AARPGFLSPFPGGACLGKACGRKK 171
DB 232 AARPGFLSPFPGGACLGKACGRKK 258
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AC P15502; Q14233; Q14238;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
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GN Name=ELN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM B).
RX MEDLINE=87289668; PubMed=3039501;
RA Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Anderson N.,

```

developmental disorder and a contiguous gene deletion syndrome involving genes from chromosome band 7q11.23.

-!- DISEASE: Defects in ELN are the cause of supravalvular aortic stenosis (SVAS) [MIM:185500]. SVAS is a congenital narrowing of the ascending aorta which can occur sporadically, as an autosomal dominant condition, or as one component of Williams-Beuren syndrome.

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EMBL; M17282; AAC98394.1; JOINED.
 EMBL; M16983; AAC98394.1; JOINED.
 EMBL; M17265; AAC98394.1; JOINED.
 EMBL; M17266; AAC98394.1; JOINED.
 EMBL; M17267; AAC98394.1; JOINED.
 EMBL; M17268; AAC98394.1; JOINED.
 EMBL; M17270; AAC98394.1; JOINED.
 EMBL; M17271; AAC98394.1; JOINED.
 EMBL; M17272; AAC98394.1; JOINED.
 EMBL; M17273; AAC98394.1; JOINED.
 EMBL; M17275; AAC98394.1; JOINED.
 EMBL; M17276; AAC98394.1; JOINED.
 EMBL; M17277; AAC98394.1; JOINED.
 EMBL; M17278; AAC98394.1; JOINED.
 EMBL; M17279; AAC98394.1; JOINED.
 EMBL; M17280; AAC98394.1; JOINED.
 EMBL; M17281; AAC98394.1; JOINED.
 EMBL; M36860; AAA52382.1; -.
 EMBL; M24782; AAA53190.1; -.
 EMBL; U62292; AAB17544.1; -.
 EMBL; X15603; CAA33627.1; -.
 PIR; A32707; EAHU.
 HSSP; P50059; 1ZFU.
 Genew; HGNC:3327; ELN.
 MIM; 130160; -.
 MIM; 123700; -.
 MIM; 194050; -.
 MIM; 185500; -.
 GO; GO:0005578; C:extracellular matrix; TAS.
 GO; GO:0005615; C:extracellular space; TAS.
 GO; GO:0005201; F:extracellular matrix structural constituent; TAS.
 GO; GO:0008283; P:cell proliferation; TAS.
 GO; GO:0008015; P:circulation; TAS.
 GO; GO:0009887; P:organogenesis; TAS.
 GO; GO:0007585; P:respiratory gaseous exchange; TAS.
 InterPro; IPR003979; tropoelastin.
 PRINTS; PR01500; TROP0ELASTIN.
 KW Alternative splicing; Connective tissue; Repeat; Signal;
 Structural protein; Williams-Beuren syndrome.
 FT SIGNAL 1 26
 FT CHAIN 27 730
 FT DISULFID 720 725
 FT VARSPPLIC 472 477
 FT /FTId=VSP 004243.
 SQ SEQUENCE 730 AA; 63260 MW; AB06D15BA567AE46 CRC64;
 Query Match 83.1%; Score 725; DB 1; Length 730;
 Best Local Similarity 97.3%; Pred. No. 8.2e-33;
 Matches 143; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 25 PSSRPVPGALAAKAAKYGAAPVGLGGLGALGVGIPGGVVGAGPAAAKAAKAAKAA 84
 Db 584 PEGAVPGALAAKAAKYGAAPVGLGGLGALGVGIPGGVVGAGPAAAKAAKAAKAA 643
 QY 85 QFGLVGAAGLGGVGLGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGV 144
 Db 644 QFGVGAAGLGGVGLGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGV 703

RA	Wagatsuna
RA	Sugiyama
RA	Masuhara

Green E.D.;
Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.


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QY      144 VAARPFGFGLSPI-----PPGGACLGKACGRKK 171
DB      628 GAGGELGVGCKPKPPFGGALGALGFPGGACLGKSCGRKK 666

RESULT 19
ELS_RAT ID_ELS RAT STANDARD; PRT; 864 AA.
AC Q99372;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DD Elastin precursor (Tropoelastin) (Fragment).
GN Name=Eln;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=91104868; PubMed=1702999;
FA Pierce R.A., Deak S.B., Stolle C.A., Boyd C.D.;
ET "Heterogeneity of rat tropoelastin mRNA revealed by
RL Biochemistry 29:9677-9683(1990)."
RN [2]
RP PARTIAL SEQUENCE FROM N.A.
RX PubMed=2913947;
RA Rich C.B., Foster J.A.;
ET "Characterization of rat heart tropoelastin.";
RL Arch. Biochem. Biophys. 268:551-558(1989)."
RN [3]
RP SEQUENCE OF 22-31 FROM N.A.
RX PubMed=2768256;
FA Franzblau C., Pratt C.A., Faris B., Colanino N.M.,
RA Mogayzel P.J. Jr., Troxler R.F.;
ET "Role of tropoelastin fragmentation in elastogenesis in
RL muscle cells.";
RN J. Biol. Chem. 264:15115-15119(1989)."
RN [4]
RP SEQUENCE OF 264-533 AND 558-864 FROM N.A., AND ALTE
RX MEDLINE=92241859; PubMed=1572637;
FA Pierce R.A., Alatawi A., Deak S.B., Boyd C.D.;
ET "Elements of the rat tropoelastin gene associated w
RL splicing.";
RN Genomics 12:651-658(1992)."
RN [5]
RP SEQUENCE OF 781-864 FROM N.A.
RX MEDLINE=98330868; PubMed=2971041;
FA Deak S.B., Pierce R.A., Belsky S.A., Riley D.J., Boy
RL "Rat tropoelastin is synthesized from a 3.5-kilobase
RL J. Biol. Chem. 263:13504-13507(1988)."
CC -!- FUNCTION: Major structural protein of tissues su
CC nuchal ligament, which must expand rapidly and i
CC -!- SUBUNIT: The polymeric elastin chains are cross
CC into an extensible 3D network.
CC -!- SUBCELLULAR LOCATION: Extracellular matrix of e
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=8;
CC Comment=Experimental confirmation may be lack
CC isoforms;
CC Name=1;
CC IsoId=Q99372-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q99372-2; Sequence=VSP_004244;
CC Name=3;
CC IsoId=Q99372-3; Sequence=VSP_004245;
CC Name=4;
CC IsoId=Q99372-4; Sequence=VSP_004246;
CC Name=5;
CC IsoId=Q99372-5; Sequence=VSP_004244; VSP_0042
CC Name=6;
CC IsoId=Q99372-6; Sequence=VSP_004245; VSP_0042

```


[illegible]

QY 155 ----IFPGG-ACLGKACGR 168
Db 289 VAPGIGPGGVAAAASAAK 307

RESULT 26
O15337 PRELIMINARY; PRT; 602 AA.

ID O15337
AC O15337;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Elastin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97358574; PubMed=9215670;
RA Li D.Y., Toland A.E., Boak B.B., Atkinson D.L., Ensing G.J.,
RA Morris C.A., Keating M.T.;
RT "Elastin point mutations cause an obstructive vascular disease,
RT supravalvular aortic stenosis";
RL Hum. Mol. Genet. 6:1021-1028(1997).
DR EMBL; U93037; AAB65620.1; -.
DR EMBL; U93034; AAB65620.1; JOINED.
DR EMBL; U93035; AAB65620.1; JOINED.
DR EMBL; U93036; AAB65620.1; JOINED.
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro; IPR001451; Hexapep transf.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 602
SQ SEQUENCE 602 AA; 51807 MW; 53B5B9A71EF04807 CRC64;

Query Match 31.4%; Score 273.5; DB 2; Length 602;
Best Local Similarity 36.6%; Pred. No.8.2e-08;
Matches 94; Conservative 13; Mismatches 29; Indels 121; Gaps 14;

Qy 28 PRVPGAL-----AAAKAAKYGAAV-----PGVLGGIGA-LG 57
Db 255 PGVPGAIPGIGIAGVTTPAAAAAAAKAAKYGAAGLVPGFGPGVGVPGAAGVP 314
Qy 58 GVGTIPGG----VVCAG-PAMAA-----AAKAAKAAQAQGL-----VGAA 92
Db 315 GVGVPGAGIPVPCAGIPGAAPGWSPESPAKAAKAAKAYGARPGVGVPVGVGAG 374
Qy 93 GLGLGLGVGLGVPGVG-----GLGGIP-----PAAAKAAKYGAAGLVGL 134
Db 375 GFPGFGVGVGIPGVAGVPSVGVGVGPVGVGISPEAQAAAAKAAKYGAAG-AAGVLG 433
Qy 135 G-----AGQFDL-----GGVAARPFGFLS 153
Db 434 GLVFPGAAPGVPGTGVTCPTAAAAKAAKAAQFALLNLAGLVPGVVPAGVGVA 493

Qy 154 P---IFFGGACLGHKACG 167
Db 494 PGVGVAFP--VGLAPG 507

RESULT 27
O15336 PRELIMINARY; PRT; 635 AA.

ID O15336
AC O15336;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE	Elastin (Fragment).
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;	
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=97358574; PubMed=92156770;
RA	Li D.Y., Toland A.E., Boak B.B., Atkinson D.L., Ensing G.J.,
RA	Morris C.A., Keating M.T.;
RT	"Elastin point mutations cause an obstructive vascular disease,
RT	supraaortic valvular aortic stenosis."
RL	Hum. Mol. Genet. 6:1021-1028(1997).
DR	EMBL; U930337; AAB65621.1; -
DR	EMBL; U930334; AAB65621.1; JOINED.
DR	EMBL; U93035; AAB65621.1; JOINED.
DR	EMBL; U93036; AAB65621.1; JOINED.
DR	GO; GO:0005578; C:extracellular matrix; IEA.
DR	GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR	InterPro; IPR001451; Hexapep transf.
DR	InterPro; IPR003979; tropoelastin.
DR	PRINTS; PR01500; TROPOLASTIN.
DR	PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN_1.
FT	NON TER 1
FT	NON TER 635
SQ	SEQUENCE 635 AA; 55279 MW; 72950C364127B2A4 CRC64;

Query Match	31.4%; Score 273.5; DB 2; Length 635;
Best Local Similarity	36.6%; Pred.No. 8.5e-08;
Matches	94; Conservative 13; Mismatches 29; Indels 121; Gaps 14;

Qy	28	PRVPGAL-----AAAKAAKYGRAV-----PCVLGGLGA-LG 57
Dd	255	PGVPCLPTGGTGTTPAAAAAATAAKAYGAAGLVPGPGPGWVGPGAGVP 314
Qy	58	GVGIPGG----VVGAG-PAAAA-----AAKAAKAAQAQFGL-----VGAA 92
Dd	315	GVGVPGAGIFWPVGAGIPGAAPGVWSPEAAAATAAKAYGARPGVGVGGIPTYGVGAG 374
Qy	93	GLGLGVGGLGVPGVG-----GLGGTP-----PAAAAAATKAAAGLGGVLG 134
Dd	375	GFGFGVGVGIGIFGVAGVPSGVGPGVGVGISPEAQAAAAATAAKAYGAAG-AGVLG 433
Qy	135	G-----AGQPPL-----CGVAARPQFGLS 153
Dd	434	GLVPDCAVAVPVPGVPGVTPTAAAAATAAKAAQAFALLNLAGLVGVGPAVGVA 493
Qy	154	P---IPFGGACLGKACG 167
Dd	494	PGVGVA PG---VGLAPG 507

RESULT 28
Q6ZUN2
ID Q6ZUN2 PRELIMINARY; PRT; 559 AA.
AC Q6ZUN2
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ43523.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Oshina A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saïto K., Nishikawa T., Klmura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanekori Y.

Qy	153 S-----PIFGGAC 161
Dd	421 SESRECPGSWHFRSSGSC 440
RESULT 30	
Q9GUB5	
ID	PRELIMINARY; PRT: 1468 AA.
AC	Q9GUB5;
DT	01-MAR-2001 (trEMBLrel. 16, Created)
DT	01-MAR-2001 (trEMBLrel. 16, Last sequence up)
DT	01-OCT-2002 (trEMBLrel. 22, Last annotation
DE	Heavy-chain fibroin (fragment).
GN	Name=Fib-H;
CN	Galleria mellonella (Wax moth) .
OS	Eukaryota; Metazoa; Arthropoda; Hexapoda; In-
OC	Neoptera; Endopterygota; Lepidoptera; Gloss-
OC	Pyrallidae; Galleriinae; Galleria.
OX	NCBI_TaxID=7137;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Posterior silk gland;
RX	MEDLINE=22063245; PubMed=11896872;
RA	Zurovec M.; Sehna F.;
RT	"Unique molecular architecture of silk fibre
RT	Galleria mellonella.";
RT	PMID=12722629; 226472002)

```

FT      NON_TER      1468
SQ      SEQUENCE     1468 AA; 122704 MW;  2DA59E1181BB3DDF CRC64;

Query Match      24.5%; Score 213.5; DB 2; Length 1468;
Best Local Similarity 39.1%; Pred. No. 0.00033;
Matches 63; Conservative 17; Mismatches 42; Indels 39; Gaps 6;

QY      32  GALAAAKAAKYGAAPGV-----LGLGALGGVGIPG-----GVVGAGPAAAAAKAA 79
DB      351  GP1GATSTAGLGGVGAAGASGLGLGGAGASAGSAGAGLGGIGAGGSGSSAASA 410
QY      80  AAKAAQFGLV-----GAAGLGLGVGGLGVPGVGGGLGGIPPAAKAA 122
DB      411  ASGASGAEVIVIDRRSAAASAAASGASGLGLGGLGPGYGGG1GLNGVSSASAL--- 467
QY      123  KYGAAGLGGVLGGAGQFFLGGVGAARPGFLSPIPPGAC1G 163
DB      468  ---GAGLGGV-GTAGASGLGGLG---GAGVSAVGPAGAGLG 501

Search completed: November 19, 2004, 16:36:52
Job time : 36.5734 secs

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1 AAAGLCAGTCLGVGVCPLGVGAGVPGIGVAGVPGCGAVPGGALAAKAAKYGAAPG 60 QY
 |||||
 1 AAAGLCAGTCLGVGVCPLGVGAGVPGIGVAGVPGCGAVPGGALAAKAAKYGAAPG 60 Db
 |||||
 61 VLGGGLGALGGVGI PGGVVGGAPAAAAKAAKAAKQFGLVGAGLGGGLGVGGVPGVG 120 QY

Db 61 VLGGGALGVGIPGGVVGAGPAAAKAAQFGLVGAAGLGGVGLGVPVG 120
QY 121 GLGGIPPAAKAAKAGAGLGGVVGAGGQFPLGGVAARPGFGLSPIFFGGACLGKACGR 180
Db 121 GLGGIPPAAKAAKAGAGLGGVVGAGGQFPLGGVAARPGFGLSPIFFGGACLGKACGR 180
QY 181 KRK 183
Db 181 KRK 183

RESULT 3

ADE40134
ID ADE40134 standard; protein; 692 AA.

XX AC ADE40134;

DT 29-JAN-2004 (first entry)

XX Human NOV16b protein - SEQ ID 40.

XX NOVX; cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic;
KW anti-diabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic;
KW antiparkinsonian; antiasthmatic; gynaecological; cardiomyopathy;
KW atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;
KW multiple sclerosis; graft-versus-host disease; Alzheimer's; Parkinson's;
KW asthma; fertility disorder; vaccine; gene therapy; chromosome mapping;
KW tissue typing; human; NOV.

XX OS Homo sapiens.

XX PN WO2003064589-A2.

XX PD 07-AUG-2003.

XX PF 02-AUG-2002; 2002WO-US024483.

XX 02-AUG-2001; 2001US-0309501P.
PR 03-AUG-2001; 2001US-0310291P.
PR 07-AUG-2001; 2001US-0310544P.
PR 08-AUG-2001; 2001US-0310951P.
PR 09-AUG-2001; 2001US-0311292P.
PR 13-AUG-2001; 2001US-0311979P.
PR 16-AUG-2001; 2001US-0312892P.
PR 17-AUG-2001; 2001US-0313201P.
PR 17-AUG-2001; 2001US-0313415P.
PR 20-AUG-2001; 2001US-0313643P.
PR 20-AUG-2001; 2001US-0313702P.
PR 21-AUG-2001; 2001US-0314031P.
PR 23-AUG-2001; 2001US-0314466P.
PR 28-AUG-2001; 2001US-0315403P.
PR 29-AUG-2001; 2001US-0315853P.
PR 17-SEP-2001; 2001US-0322716P.
PR 21-SEP-2001; 2001US-0323994P.
PR 14-DEC-2001; 2001US-0340233P.
PR 05-FEB-2002; 2002US-0354591P.
PR 19-MAR-2002; 2002US-0365478P.
PR 19-APR-2002; 2002US-0372814P.
PR 19-APR-2002; 2002US-0373825P.
PR 19-APR-2002; 2002US-0373989P.
PR 23-APR-2002; 2002US-0374632P.
PR 07-JUN-2002; 2002US-0386971P.
PR 01-AUG-2002; 2002US-00210172.

PA (CURA-) CURAGEN CORP.

XX Kekuda R, Miller CE, Patturajan M, Pena CEA, Rieger DK;
PI Shimkets RA, Zerhusen BD, Li L, Ji W, Padigar M, Casman SJ;
PI Voss EZ, Boldog FL, Gorman L, Leite MW, Vernet CAM, Anderson DW;
PI Guo X, Zhong M, Gerlach VL, Hjalt I, Rastelli L, Spytek KA;
PI Edinger SR, Ellerman K, Malyankar UM, Macdougall JR, Stone DJ;
PI Alsobrook JP, Lepley DM, Burgess CE, Majumder K, Wolenc AR;

PI Smithson G;
XX WFI; 2003-663472/62.
DR N-PSDB; ADE40133.
XX New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX Claim 1; SEQ ID NO 40; 560pp; English.

XX The invention relates to a novel NOVX polypeptide. The polypeptide of the
CC invention demonstrates cardiant, antiarteriosclerotic, hypotensive,
CC cyostatic, anorectic, antidiabetic, immunosuppressive, anti-HIV,
CC neuroprotective, nootropic, antiparkinsonian, antiasthmatic and
CC gynaecological activities and may be useful in diagnosing, treating or
CC preventing NOVX-associated disorders including cardiomyopathy,
CC atherosclerosis, hypertension, cancer, obesity, diabetes, AIDS, multiple
CC sclerosis, graft-versus-host disease, Alzheimer's disease, Parkinson's
CC disease, asthma or fertility disorders. Furthermore, the polypeptides may
CC be utilised as vaccines whilst the nucleic acids may be used as
CC hybridisation probes, in gene therapy, chromosome mapping, tissue typing,
CC preventive medicine and pharmacogenomics. The current sequence is that of
CC the human NOV protein of the invention.

XX Sequence 692 AA;

Query Match 100.0%; Score 935; DB 7; Length 692;
Best Local Similarity 100.0%; Pred. No. 9.9e-58;
Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGLGGAGIPGLGVGVPGLGVGAGVPGFGLGVGAGVPGFAGVPGALAAKAAKYGAAPVG 60

Db 510 AAAGLGGAGIPGLGVGVPGLGVGAGVPGFGLGVGAGVPGFAGVPGALAAKAAKYGAAPVG 569

QY 61 VLGGGALGVGIPGGVVGAGPAAAKAAQFGLVGAAGLGGVGLGVPVG 120

Db 570 VLGGGALGVGIPGGVVGAGPAAAKAAQFGLVGAAGLGGVGLGVPVG 629

QY 121 GLGGIPPAAKAAKAGAGLGGVVGAGGQFPLGGVAARPGFGLSPIFFGGACLGKACGR 180

Db 630 GLGGIPPAAKAAKAGAGLGGVVGAGGQFPLGGVAARPGFGLSPIFFGGACLGKACGR 689

QY 181 KRK 183

Db 690 KRK 692

RESULT 4

AAV01302

ID AAV01302 standard; protein; 698 AA.

XX AAV01302;

XX 07-JUN-1999 (first entry)

DE Human tropoelastin variant SHELdelta26A.

XX Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;
KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
KW hand lotion; surgical implant; industrial product; human; SHEL; variant.

XX OS Homo sapiens.

XX Synthetic.

XX WO9903886-A1.

XX 28-JAN-1999.

XX 17-JUL-1998; 98WO-AU0000564.

XX 18-JUL-1997; 97AU-00008117.

XX PA (UNSY) UNIV SYDNEY.
XX PI Weiss AS;
XX DR WPI; 2000-182399/16.
XX DR N-PSDB; AA261144.
XX PT New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and cell growth.
XX PT cell growth.
XX PS Disclosure; Page 110-112; 136pp; English.
XX CC The present sequence represents a human reduced tropoelastin derivative, designated SHEL-delta-26a. The sequence is produced by removing exon 26a of SHEL (SHEL not defined). The protein is representative of tropoelastin derivatives of the invention, in which a subsequence has been mutated so that susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is increased. The derivatives have with reduced susceptibility, and can be used where the wild-type protein would be degraded too easily, e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivatives, and other polypeptides containing tropoelastin derivative-derived protease-susceptibility sites, are useful in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents and for inducing chemotaxis. They are also useful for proliferation or growth inhibition, particularly of smooth muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets. Peptidomimetics that mimic the protease cleavage site in tropoelastin derivatives are competitive inhibitors of the protease, and are used for protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit protease activity that causes blood clotting

XX PA (UNSY) UNIV SYDNEY.
XX PI Weiss AS;
XX DR WPI; 1999-132162/11.
XX PT New derivatives of human tropoelastin - with elastin-like or macromolecular binding properties, useful e.g. as surgical implants.
XX PT macromolecular binding properties, useful e.g. as surgical implants.
XX PS Claim 13; Fig 2; 82pp; English.
XX CC The invention relates to a derivative or variant of human tropoelastin (hTE) having elastin-like and/or macromolecule (specifically glycosaminoglycan (GAG))-binding properties. Cells containing vectors comprising the nucleic acids encoding the variants or derivatives are used to produce the proteins recombinantly. The tropoelastin derivatives or hybrid proteins containing the derivatives are useful in medical, pharmaceutical, veterinary and cosmetic applications, e.g. as anti-wrinkle or hand lotions, also as surgical implants, foods and industrial products. The hybrid protein have controllable GAG-binding properties, depending on presence or absence of a specific fragment, designated peptide 26A, from hTE. The present sequence represents the synthetic human tropoelastin variant SHELdelta26A

Query Match 100.0%; Score 935; DB 2; Length 698;
Best Local Similarity 100.0%; Pred. No. 1e-57;
Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGLGGAGIPGLGVGVGPGVLGVGAGVPGVLGVGAGVPGFAGVPGALAAAKAAYGAAVPG 60
DB 516 AAAGLGGAGIPGLGVGVGPGVLGVGAGVPGVLGVGAGVPGFAGVPGALAAAKAAYGAAVPG 575

QY 61 VLGGGLGALGGVGPVGGVGGAPAAAATAAQAQFGLVGAAGLGLGVGLGVPGVG 120
DB 576 VLGGGLGALGGVGPVGGVGGAPAAAATAAQAQFGLVGAAGLGLGVGLGVPGVG 635

QY 121 GLGGIPPAATAAKAAYGAAAGLGGVGLGGAGQFPLGGVAARPFGLSPIPPGACLGKACGR 180
DB 636 GLGGIPPAATAAKAAYGAAAGLGGVGLGGAGQFPLGGVAARPFGLSPIPPGACLGKACGR 695

QY 181 KRK 183
DB 696 KRK 698

RESULT 5
AAAY69069 standard; protein; 698 AA.
XX AC AAAY69069;
XX DT 30-MAY-2000 (first entry)
XX DE Amino acid sequence of a human reduced tropoelastin derivative.
XX KW Tropoelastin; derivative; SHEL-delta-26a; SHEL; proteolysis; protease;
XX KW antiwrinkle; hand lotion; bulking agent; chemotaxis; proliferation;
XX KW growth inhibition; peptidomimetic; lung damage; elastin; cancer;
XX KW metastasis; blood clotting.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO200004043-A1.
XX PD 27-JAN-2000.
XX XX 19-JUL-1999; 99WO-AU000580.
XX PF 17-JUL-1998; 98AU-00004723.
XX PR

Synthetic.

WO9903886-A1.

28-JAN-1999.

17-JUL-1998; 98WO-AU000564.

18-JUL-1997; 97AU-00008117.

(UNSY) UNIV SYDNEY.

Weiss AS;

WPI; 1999-132162/11.

N-PSDB; AAX27705.

New derivatives of human tropoelastin - with elastin-like or macromolecular binding properties, useful e.g. as surgical implants.

Claim 7; Fig 3; 82pp; English.

The invention relates to a derivative or variant of human tropoelastin (hTE) having elastin-like and/or macromolecule (specifically glycosaminoglycan (GAG))-binding properties. Cells containing vectors comprising the nucleic acids encoding the variants or derivatives are used to produce the proteins recombinantly. The tropoelastin derivatives or hybrid proteins containing the derivatives are useful in medical, pharmaceutical, veterinary and cosmetic applications, e.g. as anti-wrinkle or hand lotions, also as surgical implants, foods and industrial products. The hybrid protein have controllable GAG-binding properties, depending on presence or absence of a specific fragment, designated peptide 26A, from hTE. The present sequence represents a human tropoelastin derivative SHEldeltamodified

Sequence 660 AA;

Query Match 98.4%; Score 920.5; DB 2; Length 660;
Best Local Similarity 99.5%; Pred. No. 9.9e-57;
Matches 182; Conservative 0; Mismatches 0; Indels 1; Gaps 1

QY 1 AANGLGAGTGLGVGVPGVLGVGAGVPGFAGVPFGAVPCALAAAKAAKYCAAVPG 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 479 AAGLGGAGTGLGVGVPGVLGVGAGVPGFAGVPFGAVPCALAAAKAAKYG-AVPG 537
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 VLGGGLGALGGVGIPGGVYGAGPAAAAAATAKAAKAAQFGLVGAAGLGGVLGVGPVG 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 538 VLGGGLGALGGVGIPGGVYGAGPAAAAAATAKAAKAAQFGLVGAAGLGGVLGVGPVG 597
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 121 GLGGIPPAATAKAAKYCAAGLGGVLGGAGGPPFLGGVAARPFGLSPIFFGGACLGKACGR 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 598 GLGGIPPAATAKAAKYCAAGLGGVLGGAGGPPFLGGVAARPFGLSPIFFGGACLGKACGR 657
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 181 KRK 183
| | | | |
Db 658 KRK 660
| | | | |

RESULT 10
AAY01310
ID ID AAY01310 standard; protein; 216 AA.
XX XX AAY01310;
XX XX
XX XX 07-JUN-1999 (first entry)
XX XX Human tropoelastin derivative SHEL26-36.
XX XX Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;
KW KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
KW KW hand lotion; surgical implant; industrial product; human; SHEL; variant.
XX XX Homo sapiens.

OS Synthetic.
 XX WO9903886-A1.
 PN
 XX 28-JAN-1999.
 PD
 XX 17-JUL-1998; 98WO-AU000564.
 XX PF
 XX 18-JUL-1997; 97AU-00008117.
 PR
 XX (UNSY) UNIV SYDNEY.
 PA
 XX Weiss AS;
 XX
 XX WPI; 1999-132162/11.
 DR
 XX New derivatives of human tropoelastin - with elastin-like or
 PT macromolecular binding properties, useful e.g. as surgical implants.
 XX
 XX Claim 35; Page 11; 82pp; English.
 XX
 CC The invention relates to a derivative or variant of human tropoelastin
 CC (hTE) having elastin-like and/or macromolecule (specifically
 CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors
 CC comprising the nucleic acids encoding the variants or derivatives are
 CC used to produce the proteins recombinantly. The tropoelastin derivatives
 CC or hybrid proteins containing the derivatives are useful in medical,
 CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
 CC wrinkle or hand lotions, also as surgical implants, foods and industrial
 CC products. The hybrid protein have controllable GAG-binding properties,
 CC depending on presence or absence of a specific fragment, designated
 CC peptide 26A, from hTE. The present sequence represents a human
 CC tropoelastin derivative SHEL26-36
 XX
 XX Sequence 216 AA;
 SQ

Query Match 97.2%; Score 908.5; DB 2; Length 216;
 Best Local Similarity 84.7%; Pred. No. 2.6e-56;
 Matches 183; Conservative 0; Mismatches 0; Indels 33; Gaps 1;
 QY 1 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFGA----- 41
 DB 1 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFGA----- 41
 QY 42 -----VPGALAAKAAKYGAAVPGVLGGIGALGVGAGVPGFGA----- 41
 DB 61 SSSQHLPTSPSPRVPFGALAAKAAKYGAAVPGVLGGIGALGVGAGVPGFGA----- 120
 QY 88 AAKAAKAAQFGLVGAAGLGGIGLVGVLGGIPGVPVGGIPGAAKAAKYGAAAGLGGVGG 147
 DB 121 AAKAAKAAQFGLVGAAGLGGIGLVGVLGGIPGVPVGGIPGAAKAAKYGAAAGLGGVGG 180
 QY 148 AGQPLGGVAARPGLSPFPGGACLGKACGRKK 183
 DB 181 AGQPLGGVAARPGLSPFPGGACLGKACGRKK 216

RESULT 11
 AAY69068
 ID AAY69068 standard; protein; 731 AA.
 XX
 AC AAY69068;
 XX
 XX 30-MAY-2000 (first entry)
 DT
 XX Amino acid sequence of a human tropoelastin splice form.
 DE
 XX Tropoelastin; derivative; proteolysis; protease; antiwrinkle;
 KW hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;
 KW peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.
 XX
 OS Homo sapiens.
 XX

PH Key Location/Qualifiers
 FT Cleavage-site 441..442
 FT Cleavage-site 503..504
 FT Cleavage-site 515..516
 FT Cleavage-site 564..565
 XX
 PN WO200004043-A1.
 XX
 XX 27-JAN-2000.
 PD
 XX 19-JUL-1999; 99WO-AU000580.
 PF
 XX 17-JUL-1998; 98AU-00004723.
 PR
 XX (UNSY) UNIV SYDNEY.
 PA
 XX Weiss AS;
 XX
 XX WPI; 2000-182399/16.
 DR N-PSDB; AA261146.
 DR
 XX New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
 PT cell growth.
 PT
 XX Disclosure; Page 107-109; 136pp; English.
 PS
 XX The present sequence represents a human tropoelastin splice form. The
 CC specification describes tropoelastin derivatives, in which a subsequence
 CC has been mutated so that susceptibility to proteolysis is reduced or
 CC eliminated, or a subsequence has been inserted so that susceptibility to
 CC proteolysis is increased. The derivatives have with reduced
 CC susceptibility, and can be used where the wild-type protein would be
 CC degraded too easily, e.g. in contact with serum or wound exudate. The
 CC tropoelastin derivatives provide competitive inhibition of protease
 CC activity. The tropoelastin derivatives, and other polypeptides containing
 CC tropoelastin derivative-derived protease-susceptibility sites, are useful
 CC in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand
 CC lotions), as bulking agents and for inducing chemotaxis. They are also
 CC useful for proliferation or growth inhibition, particularly of smooth
 CC muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes,
 CC chondrocytes and platelets. Peptidomimetics that mimic the protease
 CC cleavage site in tropoelastin derivatives are competitive inhibitors of
 CC the protease, and are used for protecting against lung damage caused by
 CC elastin, for inhibiting or controlling localized growth of cancers or
 CC metastases, or to limit protease activity that causes blood clotting
 XX
 XX Sequence 731 AA;
 SQ

Query Match 97.2%; Score 908.5; DB 3; Length 731;
 Best Local Similarity 84.7%; Pred. No. 7.5e-56;
 Matches 183; Conservative 0; Mismatches 0; Indels 33; Gaps 1;
 QY 1 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFGA----- 41
 DB 516 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFGA----- 575
 QY 42 -----VPGALAAKAAKYGAAVPGVLGGIGALGVGAGVPGFGA----- 87
 DB 576 SSSQHLPTSPSPRVPFGALAAKAAKYGAAVPGVLGGIGALGVGAGVPGFGA----- 635
 QY 88 AAKAAKAAQFGLVGAAGLGGIGLVGVLGGIPGVPVGGIPGAAKAAKYGAAAGLGGVGG 147
 DB 636 AAKAAKAAQFGLVGAAGLGGIGLVGVLGGIPGVPVGGIPGAAKAAKYGAAAGLGGVGG 695
 QY 148 AGQPLGGVAARPGLSPFPGGACLGKACGRKK 183
 DB 696 AGQPLGGVAARPGLSPFPGGACLGKACGRKK 731

RESULT 12
 AAB66657
 ID AAB66657 standard; protein; 731 AA.
 XX

spider silk; cord; rope; parachute; cosmetic; platelet binding inhibitor;
platelet activation inhibitor; non-thrombogenic; cell infiltration;
non-immunogenic; biocompatible; high tensile strength; elasticity;
plasticity.
Homo sapiens.
US6489446-B1.
03-DEC-2002.
29-JUN-1999; 99US-00340736.
07-AUG-1996; 96US-0023522P.
07-AUG-1997; 97US-00911364.
(HSCR-) HSC RES & DEV LP.
(PROT-) PROTEIN SPECIALTIES LTD.
Rothstein A, Keeley F, Rothstein S;
WPI; 2003-391056/37.
Novel polypeptide useful in prosthesis, has a secondary structure
characterized by three beta-sheet/beta-turn structures, and is not a
naturally occurring fibrous protein.
Claim 1; Fig 1B; 21pp; English.
The invention describes a polypeptide (I) comprising a minimal
functioning unit (MFU) which is present in the sequence of human elastin
and comprised of at least three beta-sheet/beta-turn structures, and at
least one amino acid residue that participates in cross-linking, and not
a naturally occurring fibrous protein. The MFU material can be used to
construct human elastin-like prostheses such as tubes for blood vessel
replacement, heart replacement valves and sheets for other uses such as
burns or wounds to promote healing. MFUs can be co-aggregated with other
proteins, for e.g. collagen, to provide prosthesis material that
resembles the natural structural materials of the body. MFUs modeled on
lamprin and other fibrous proteins e.g. spider silk, can be used to make
a variety of materials, for a number of different applications, for e.g.
in cords and ropes for use in parachutes and in cosmetics. Coating
synthetic prostheses with MFUs modeled on human elastin significantly
inhibits platelet binding and activation. The human-like MFU material is
more biocompatible than other elastin-containing materials. In contrast
to solubilised fragments of elastin used before, an MFU is a single
peptide of defined composition. The MFU is considerably smaller than the
parent protein, simpler in structure, easier to produce or express in
quantity, to handle in solution and to manipulate for experimental and
practical purposes. Like other elastin preparations, the MFU is non-
thrombogenic and provides a friendly environment for cell infiltration.
Being composed entirely of a human elastin sequence, MFU is non-
immunogenic, thus providing a truly biocompatible material. MFUs modeled
on lamprin and other fibrous proteins can be used to make a variety of
materials having high tensile strength, elasticity and plasticity of
their parent proteins. This is the amino acid sequence of mature human
elastin on which the MFU peptides of the invention are based

spider silk; cord; rope; parachute; cosmetic; platelet binding inhibitor;
platelet activation inhibitor; non-thrombogenic; cell infiltration;
non-immunogenic; biocompatible; high tensile strength; elasticity;
plasticity.
Homo sapiens.
US6489446-B1.
03-DEC-2002.
29-JUN-1999; 99US-00340736.
07-AUG-1996; 96US-0023522P.
07-AUG-1997; 97US-00911364.
(HSCR-) HSC RES & DEV LP.
(PROT-) PROTEIN SPECIALTIES LTD.
Rothstein A, Keeley F, Rothstein S;
WPI; 2003-391056/37.
Novel polypeptide useful in prosthesis, has a secondary structure
characterized by three beta-sheet/beta-turn structures, and is not a
naturally occurring fibrous protein.
Claim 1; Fig 1B; 21pp; English.
The invention describes a polypeptide (I) comprising a minimal
functioning unit (MFU) which is present in the sequence of human elastin
and comprised of at least three beta-sheet/beta-turn structures, and at
least one amino acid residue that participates in cross-linking, and not
a naturally occurring fibrous protein. The MFU material can be used to
construct human elastin-like prostheses such as tubes for blood vessel
replacement, heart replacement valves and sheets for other uses such as
burns or wounds to promote healing. MFUs can be co-aggregated with other
proteins, for e.g. collagen, to provide prosthesis material that
resembles the natural structural materials of the body. MFUs modeled on
lamprin and other fibrous proteins e.g. spider silk, can be used to make
a variety of materials, for a number of different applications, for e.g.
in cords and ropes for use in parachutes and in cosmetics. Coating
synthetic prostheses with MFUs modeled on human elastin significantly
inhibits platelet binding and activation. The human-like MFU material is
more biocompatible than other elastin-containing materials. In contrast
to solubilised fragments of elastin used before, an MFU is a single
peptide of defined composition. The MFU is considerably smaller than the
parent protein, simpler in structure, easier to produce or express in
quantity, to handle in solution and to manipulate for experimental and
practical purposes. Like other elastin preparations, the MFU is non-
thrombogenic and provides a friendly environment for cell infiltration.
Being composed entirely of a human elastin sequence, MFU is non-
immunogenic, thus providing a truly biocompatible material. MFUs modeled
on lamprin and other fibrous proteins can be used to make a variety of
materials having high tensile strength, elasticity and plasticity of
their parent proteins. This is the amino acid sequence of mature human
elastin on which the MFU peptides of the invention are based

CC Human synthetic tropoelastin is susceptible to hydrolytic breakdown of
CC the crosslinks. Such material may be useful in e.g. surgical
CC applications, where the gradual loss of material over time is intended.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 733 AA;

Query Match 97.2%; Score 908.5; DB 2; Length 733;
Best Local Similarity 84.7%; Pred. No. 7.5e-56;
Matches 183; Conservative 0; Mismatches 0; Indels 33; Gaps 1;
QY 1 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFCA----- 41
Db 518 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFCA----- 577
QY 42 -----VPCALAAAKAAKYGAAPVGLGALGVGVPGVGVGAGPAAAAA 87
Db 578 SSSQHLPTSPSPRVFGALAAAKAAKYGAAPVGLGALGVGVPGVGVGAGPAAAAA 637
QY 88 AAKAAAKAAQFGLVGAAGLGLGVGVPGVGVGAGLGGIPPPAAAAAKAAKYGAAGLGVVGG 147
Db 638 AAKAAAKAAQFGLVGAAGLGLGVGVPGVGVGAGLGGIPPPAAAAAKAAKYGAAGLGVVGG 697
QY 148 AGQFPLGGVAARPGFGLSPIFFPGACLGKACGRKK 183
Db 698 AGQFPLGGVAARPGFGLSPIFFPGACLGKACGRKK 733

RESULT 16
AA01301
ID AAY01301 standard; protein; 733 AA.
AC AAY01301;
XX
DT 07-JUN-1999 (first entry)
XX
DE Amino acid sequence of synthetic human tropoelastin SHEL.
XX
KW Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;
KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
KW hand lotion; surgical implant; industrial product; human; SHEL.
XX
OS Synthetic.
OS Homo sapiens.
XX WO9903886-A1.
XX 28-JAN-1999.
XX 17-JUL-1998; 98WO-AU000564.
XX 18-JUL-1997; 97AU-00008117.
XX (UNSY) UNIV SYDNEY.
XX Weiss AS;
XX WPI; 1999-132162/11.
XX DR N-PSDB; AAX27704.
XX New derivatives of human tropoelastin - with elastin-like or
PT macromolecular binding properties, useful e.g. as surgical implants.
XX
PS Disclosure; Fig 1; 82pp; English.
XX
CC The invention relates to a derivative or variant of human tropoelastin
CC (hTE) having elastin-like and/or macromolecule (specifically
CC glycosaminoglycan (GAG)) binding properties. Cells containing vectors
CC comprising the nucleic acids encoding the variants or derivatives are
CC used to produce the proteins recombinantly. The tropoelastin derivatives
CC or hybrid proteins containing the derivatives are useful in medical,
CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
CC wrinkle or hand lotions, also as surgical implants, foods and industrial

CC products. The hybrid protein have controllable GAG-binding properties,
CC depending on presence or absence of a specific fragment, designated
CC peptide 26A, from hTE. The present sequence represents the amino acid
CC sequence of the synthetic human tropoelastin SHEL
XX
SQ Sequence 733 AA;

Query Match 97.2%; Score 908.5; DB 2; Length 733;
Best Local Similarity 84.7%; Pred. No. 7.5e-56;
Matches 183; Conservative 0; Mismatches 0; Indels 33; Gaps 1;
QY 1 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFCA----- 41
Db 518 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFCA----- 577
QY 42 -----VPCALAAAKAAKYGAAPVGLGALGVGVPGVGVGAGPAAAAA 87
Db 578 SSSQHLPTSPSPRVFGALAAAKAAKYGAAPVGLGALGVGVPGVGVGAGPAAAAA 637
QY 88 AAKAAAKAAQFGLVGAAGLGLGVGVPGVGVGAGLGGIPPPAAAAAKAAKYGAAGLGVVGG 147
Db 638 AAKAAAKAAQFGLVGAAGLGLGVGVPGVGVGAGLGGIPPPAAAAAKAAKYGAAGLGVVGG 697
QY 148 AGQFPLGGVAARPGFGLSPIFFPGACLGKACGRKK 183
Db 698 AGQFPLGGVAARPGFGLSPIFFPGACLGKACGRKK 733

RESULT 17
ABG75223
ID ABG75223 standard; protein; 757 AA.
AC ABG75223;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human tropoelastin protein.
XX
KW Human; tropoelastin; elastin; body vessel occlusion; stenosis;
KW vascular smooth muscle cell; elastin signaling; vasotropic.
XX
OS Homo sapiens.
XX WO2003082203-A2.
XX 09-OCT-2003.
XX 27-MAR-2003; 2003WO-US009391.
XX 27-MAR-2002; 2002US-0368084P.
XX (UTAH) UNIV UTAH RES FOUND.
XX Li DY, Karnik S;
XX WPI; 2003-833516/77.
XX Use of an agent that promotes elastin signaling in smooth muscle cells
PT for e.g. decreasing or preventing occlusion of a body vessel by smooth
PT muscle cells, treating or preventing obstructive vascular disease, or
PT preventing stenosis.
XX
PS Claim 24; Page 138-141; Opp; English.
XX
CC The present invention relates to the use of an agent that promotes
CC elastin signaling in smooth muscle cells for decreasing or preventing
CC occlusion of a body vessel by smooth muscle cells, decreasing vascular
CC obstruction, promoting actin stress fiber formation or actin
CC polymerisation, increasing F-actin ratio in a smooth muscle cell,
CC treating or preventing obstructive vascular disease (e.g. restenosis), or
CC preventing stenosis. The agent that promotes elastin signaling in smooth
CC muscle cells is useful for decreasing or preventing occlusion of a body
CC vessel by smooth muscle cells, decreasing vascular obstruction, promoting

CC actin stress fiber formation or actin polymerization, increasing F:G
CC actin ratio in a smooth muscle cell, treating or preventing obstructive
CC vascular disease (e.g. restenosis following angioplasty), or preventing
CC stenosis. It is also useful in manufacturing a medicament for the
CC treatment or prevention of occlusion of a vessel. The present sequence is
CC the human tropoelastin protein as shown in the exemplification of the
CC invention
XX
SQ Sequence 757 AA;
Query Match 97.2%; Score 908.5; DB 7; Length 757;
Best Local Similarity 84.7%; Pred. No. 7.7e-56;
Matches 183; Conservative 0; Mismatches 0; Indels 33; Gaps 1;
QY 1 AAAGLGAGIPGLGVGVPGFGLGVGAGVPGFGLGVGAGVPGFAGADEGVRSLSPELREGDP 601
Db 542 AAAGLGAGIPGLGVGVPGFGLGVGAGVPGFGLGVGAGVPGFAGADEGVRSLSPELREGDP 601
QY 42 -----VPGALAAAKAAKYGAAPVGLGGLGALGVGIPGGVWAGPAAAAA 87
Db 602 SSSQHLPTSPSSPRVPGALAAAKAAKYGAAPVGLGGLGALGVGIPGGVWAGPAAAAA 661
QY 88 AAKAAKAAQFGLVGAAGLGGVGLGVPGVGGVGGIPPAKAAKAAKYGAAGLGGVGG 147
Db 662 AAKAAKAAQFGLVGAAGLGGVGLGVPGVGGVGGIPPAKAAKAAKYGAAGLGGVGG 147
QY 148 AQOPLGGVAARPFGFGLSPIFFGGACLGKACGRKK 183
Db 722 AQOPLGGVAARPFGFGLSPIFFGGACLGKACGRKK 757
QY 148 AQOPLGGVAARPFGFGLSPIFFGGACLGKACGRKK 183
Db 722 AQOPLGGVAARPFGFGLSPIFFGGACLGKACGRKK 757
RESULT 18
ADP65160
ID ADP65160 standard; protein; 757 AA.
AC ADP65160;
XX
XX
DE 12-AUG-2004 (first entry)
XX Human elastin.
XX autoimmune disease; arthritis; gene expression analysis;
KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
KW antiarthritis; osteopathic; antigout; antiinflammatory; dermatological;
KW immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;
KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
KW immune; human.
OS Homo sapiens.
XX
XX WO2003072827-A1.
XX
XX 04-SEP-2003.
XX
XX 31-OCT-2002; 2002WO-US035433.
XX
XX 31-OCT-2001; 2001US-0336220P.
XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
XX
XX Hirsch R, Thorton SL;
XX
XX WPI; 2003-712740/67.
XX GENBANK; NF_000492.
XX
XX Diagnosing and analyzing autoimmune disease using gene expression
XX profiles and microarray technology, useful for diagnosing and treating
XX rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
XX gout.
XX
XX Disclosure; Page; 56pp; English.
XX
XX The invention relates to a novel method for diagnosing and analysing

CC autoimmune disease or arthritides. The method comprises obtaining a
CC patient sample containing mRNA, analysing gene expression using the mRNA
CC that results in a gene expression signature of the mRNA, and using that
CC gene expression signature to diagnose or analyse the autoimmune disease
CC or arthritides in the patient, where gene expression of at least 60% of
CC the genes correlates with that of the gene signature. The invention
CC further comprises: a treatment of rheumatoid arthritis; identification of
CC genes for targeting in the treatment of rheumatoid arthritis in a mammal
CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
CC analyses of autoimmune disease or rheumatoid arthritis; screening the
CC efficacy of a candidate drug in vitro for the treatment of collagen-
CC induced arthritis; and reducing the symptoms associated with collagen-
CC induced arthritis. The compositions of the invention have the following
CC activities: immunosuppressive, antirheumatic, and immunomodulatory. The
CC antigout, antiinflammatory, dermatological, antiarthritis, osteopathic,
CC methods and compositions of the present invention are useful for
CC diagnosing and treating autoimmune disease or arthritides, such as
CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
CC immune disease caused by an infectious agent. This sequence represents a
CC protein sequence relating to the genes used in the analysis and treatment
CC of autoimmune diseases or arthritides. Note: This sequence is not shown
CC in the specification. It has been supplied in an electronic format from
CC WIPO.

XX Sequence 757 AA;

Query Match 97.2%; Score 908.5; DB 7; Length 757;
Best Local Similarity 84.7%; Pred. No. 7.7e-56;
Matches 183; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

QY 1 AAAGLGAGIPGLGVGVPGFGLGVGAGVPGFGLGVGAGVPGFAGADEGVRSLSPELREGDP 601
Db 542 AAAGLGAGIPGLGVGVPGFGLGVGAGVPGFGLGVGAGVPGFAGADEGVRSLSPELREGDP 601
QY 42 -----VPGALAAAKAAKYGAAPVGLGGLGALGVGIPGGVWAGPAAAAA 87
Db 602 SSSQHLPTSPSSPRVPGALAAAKAAKYGAAPVGLGGLGALGVGIPGGVWAGPAAAAA 661
QY 88 AAKAAKAAQFGLVGAAGLGGVGLGVPGVGGVGGIPPAKAAKAAKYGAAGLGGVGG 147
Db 662 AAKAAKAAQFGLVGAAGLGGVGLGVPGVGGVGGIPPAKAAKAAKYGAAGLGGVGG 721
QY 148 AQOPLGGVAARPFGFGLSPIFFGGACLGKACGRKK 183
Db 722 AQOPLGGVAARPFGFGLSPIFFGGACLGKACGRKK 757

RESULT 19

AAW46315
ID AAW46315 standard; protein; 730 AA.

XX AAW46315;

XX 23-JUL-1998 (first entry)

XX Human elastin containing non-natural polypeptide MFU-1 sequence.

XX MFU-1; minimal functional unit; elastin; human; fibrous protein;
XX beta-sheet; coating; wound dressing.

XX Homo sapiens.

Key Location/Qualifiers
Protein 374..499
/note= "MFU-1 polypeptide"

XX WO9805685-A2.

XX 12-FEB-1998.

XX 07-AUG-1997; 97WO-CA000560.

Db 573 GLGIPPAARAAKAAKY-----GVAARPGFGLSPIFFGACLGKACGR 614

Qy 181 KRK 183
|||
Db 615 KRK 617

RESULT 21
AAB08630
ID AAB08630 standard; peptide; 712 AA.
XX AAB08630;
AC
XX
DT 20-DEC-2000 (first entry)
XX
DE Amino acid sequence of a human elastin polypeptide.
XX
KW Tropoelastin; elastin; elastic fibre; smooth muscle cell proliferation;
KW smooth muscle cell differentiation; smooth muscle cell migration;
KW smooth muscle cell function; atherosclerosis; restenosis; aneurysm;
KW vascular bypass graft stenosis; transplant arteriopathy; dissection;
KW SVAS; hypertension; transplant arteriopathy.
XX
OS Homo sapiens.
XX WO200050068-A2.
XX
XX
PD 31-AUG-2000.
XX
XX
PF 28-FEB-2000; 2000WO-US002526.
XX
XX
PR 26-FEB-1999; 99US-00258217.
XX
XX (UTAH) UNIV UTAH RES FOUND.
PA
PI Keating MT, Li DY;
XX
XX WPI; 2000-533134/48.
XX
XX
PT Elastin based compositions useful for treating atherosclerosis,
PT restenosis, vascular bypass graft stenosis, transplant arteriopathy,
PT aneurysm, dissection SVAS and/or hypertension.
XX
PS Example 3; Page 46; 79pp; English.
XX
CC The present sequence represents a human elastin. Peptides derived from
CC elastin are used in compositions of the invention. The specification
CC describes elastin based compositions that are potent regulators of smooth
CC muscle cell proliferation, differentiation and migration in vivo. The
CC elastin-based compositions comprise at least one elastic fibre, elastins,
CC tropoelastins (or fragments of them) which have biological activities
CC comprising: inhibiting the proliferation of smooth muscle cells in vivo;
CC stimulating the differentiation of smooth muscle cells in vivo; and
CC regulating the migration of smooth muscle cells in vivo; and
CC by diminished capacity to regulate smooth muscle cell function such as
CC atherosclerosis, restenosis, vascular bypass graft stenosis, transplant
CC arteriopathy, aneurysm and/or dissection. Disorders which may be treated
CC also include SVAS (undefined), hypertension, and transplant arteriopathy
XX
SQ Sequence 712 AA;

Query Match 87.9%; Score 822; DB 3; Length 712;
Best Local Similarity 90.2%; Pred. No. 8.3e-50;
Matches 165; Conservative 0; Mismatches 0; Indels 18; Gaps 1;

Qy 1 AAAGLGAGIPGLGVGVPGFGLGVGAGVPGFGLGVGAGVPGFGLGVGAGVPGFGLGVGAGVPG 60
|||
Db 548 AAAGLGAGIPGLGVGVPGFGLGVGAGVPGFGLGVGAGVPGFGLGVGAGVPGFGLGVGAGVPG 607

Qy 61 VLGLGALGGVIGPGVVVGGCPAAARAAKAAKAAQFGLVGAAGLGLGVGGLGVPGVG 120
|||
Db 608 VLGLGALGGVIGPGVVVGGCPAAARAAKAAKAAQFGLVGAAGLGLGVGGLGVPGVG 667

Qy 121 GLGIPPAARAAKAAKYGAAGLGGVGGAGQFPLGGVAARPGFGLSPIFFGACLGKACGR 180
|||
Db 668 GLGIPPAARAAKAAKY-----GVAARPGFGLSPIFFGACLGKACGR 709

Qy 181 KRK 183
|||
Db 710 KRK 712

RESULT 22
AAB08631
ID AAB08631 standard; peptide; 730 AA.
XX AAB08631;
AC
XX 20-DEC-2000 (first entry)
DT
XX Fusion protein comprising human elastin and c-myc.
DE
XX Tropoelastin; elastin; elastic fibre; smooth muscle cell proliferation;
KW smooth muscle cell differentiation; smooth muscle cell migration;
KW smooth muscle cell function; atherosclerosis; restenosis; aneurysm;
KW vascular bypass graft stenosis; transplant arteriopathy; dissection;
KW SVAS; hypertension; transplant arteriopathy.
XX
XX Synthetic.
OS Homo sapiens.
OS Unidentified.
XX
XX WO200050068-A2.
XX
XX 31-AUG-2000.
XX
XX 28-FEB-2000; 2000WO-US002526.
XX
XX 26-FEB-1999; 99US-00258217.
XX
XX (UTAH) UNIV UTAH RES FOUND.
PA
PI Keating MT, Li DY;
XX
XX WPI; 2000-533134/48.
XX
XX Elastin based compositions useful for treating atherosclerosis,
PT restenosis, vascular bypass graft stenosis, transplant arteriopathy,
PT aneurysm, dissection SVAS and/or hypertension.
XX
PS Example 3; Page 48; 79pp; English.
XX
CC The present sequence represents a fusion protein, comprising human
CC elastin and c-myc, preceded by a His tag. The protein is used in
CC compositions of the invention. The specification describes elastin based
CC compositions that are potent regulators of smooth muscle cell
CC proliferation, differentiation and migration in vivo. The elastin-based
CC compositions comprise at least one elastic fibre, elastins, tropoelastins
CC (or fragments of them) which have biological activities comprising:
CC inhibiting the proliferation of smooth muscle cells in vivo; stimulating
CC the differentiation of smooth muscle cells in vivo; and regulating the
CC migration of smooth muscle cells in vivo. The compositions may be used
CC for the prophylaxis or treatment of a disorder characterized by
CC diminished capacity to regulate smooth muscle cell function such as
CC atherosclerosis, restenosis, vascular bypass graft stenosis, transplant
CC arteriopathy, aneurysm and/or dissection. Disorders which may be treated
CC also include SVAS (undefined), hypertension, and transplant arteriopathy
XX
SQ Sequence 730 AA;

Query Match 87.9%; Score 822; DB 3; Length 730;
Best Local Similarity 90.2%; Pred. No. 8.5e-50;
Matches 165; Conservative 0; Mismatches 0; Indels 18; Gaps 1;

Qy 1 AAAGLGAGIPGLGVGVPGFGLGVGAGVPGFGLGVGAGVPGFGLGVGAGVPGFGLGVGAGVPG 60


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XX 17-JUL-1998; 98WO-AU000564.
XX 18-JUL-1997; 97AU-00008117.
XX (UNSY ) UNIV SYDNEY.
XX Weiss AS;
XX WPI; 1999-132162/11.
XX N-PSDB; AAX27707.
XX New derivatives of human tropoelastin - with elastin-like or
XX PT macromolecular binding properties, useful e.g. as surgical implants.
XX PS Claim 15; Fig 8; 82pp; English.
XX CC The invention relates to a derivative or variant of human tropoelastin
XX CC (hTE) having elastin-like and/or macromolecule (specifically
XX CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors
XX CC comprising the nucleic acids encoding the variants or derivatives are
XX CC used to produce the proteins recombinantly. The tropoelastin derivatives
XX CC or hybrid proteins containing the derivatives are useful in medical,
XX CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
XX CC wrinkle or hand lotions, also as surgical implants, foods and industrial
XX CC products. The hybrid protein have controllable GAG-binding properties,
XX CC depending on presence or absence of a specific fragment, designated
XX CC peptide 26A, from hTE. The present sequence represents a human
XX CC tropoelastin derivative SHELgamma
XX SQ Sequence 200 AA;
Query Match 85.7%; Score 801; DB 2; Length 200;
Best Local Similarity 82.2%; Pred No. 8.3e-49;
Matches 162; Conservative 1; Mismatches 10; Indels 24; Gaps 1;
QY 11 GLGVGVPGVLGVGAGVPLGVGA-----GVPGFAGVPGAL 46
Db 4 GALVGLGVPLGVGAGVPGFAGAGDEGVRRLSPELREGDPSSQHLPTSPSPVPGAL 63
QY 47 AAAAAYGAAVPGVLGGLGALGGVIGPVGAGPAAAAAAYGAAAGL 106
Db 64 AAAAAYGAAVPGVLGGLGALGGVIGPVGAGPAAAAAAYGAAAGL 123
QY 107 GGLGVGLGVPGVGLGGLGIPAAAAAAYGAAAGLGGVIGAGOPPLGGVAARPFGGLSP 166
Db 124 GGLGVGLGVPGVGLGGLGIPAAAAAAYGAAAGLGGVIGAGOPPLGGVAARPFGGLSP 183
QY 167 IFPGGACLGKACGRKRK 183
Db 184 IFPGGACLGKACGRKRK 200
RESULT 25
RAY01304
ID AAY01304 standard; protein; 147 AA.
XX AC AAY01304;
XX XX 07-JUN-1999 (first entry)
XX DE Human tropoelastin derivative SHELgamma.
XX KW Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;
XX KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
XX KW hand lotion; surgical implant; industrial product; human; SHEL; variant.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN W0903886-A1.
XX XX 28-JAN-1999.

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XX 17-JUL-1998; 98WO-AU000564.
XX 18-JUL-1997; 97AU-00008117.
XX (UNSY ) UNIV SYDNEY.
XX Weiss AS;
XX WPI; 1999-132162/11.
XX N-PSDB; AAX27706.
XX New derivatives of human tropoelastin - with elastin-like or
XX PT macromolecular binding properties, useful e.g. as surgical implants.
XX PS Claim 19; Fig 7; 82pp; English.
XX CC The invention relates to a derivative or variant of human tropoelastin
XX CC (hTE) having elastin-like and/or macromolecule (specifically
XX CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors
XX CC comprising the nucleic acids encoding the variants or derivatives are
XX CC used to produce the proteins recombinantly. The tropoelastin derivatives
XX CC or hybrid proteins containing the derivatives are useful in medical,
XX CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
XX CC wrinkle or hand lotions, also as surgical implants, foods and industrial
XX CC products. The hybrid protein have controllable GAG-binding properties,
XX CC depending on presence or absence of a specific fragment, designated
XX CC peptide 26A, from hTE. The present sequence represents a human
XX CC tropoelastin derivative SHELgamma excluding the product encoded by exon
XX CC 26A
XX SQ Sequence 147 AA;
Query Match 78.0%; Score 729; DB 2; Length 147;
Best Local Similarity 99.3%; Pred No. 7.1e-44;
Matches 143; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 40 GAVPGALAAAKAAYGAAVPGVLGGLGALGGVIGPVGAGPAAAAAAYGAAAGL 99
Db 4 GGVPGALAAAKAAYGAAVPGVLGGLGALGGVIGPVGAGPAAAAAAYGAAAGL 63
QY 100 LVGAAGLGGVGLGVPGVGLGGLGIPAAAAAAYGAAAGLGGVIGAGOPPLGGVAAR 159
Db 64 LVGAAGLGGVGLGVPGVGLGGLGIPAAAAAAYGAAAGLGGVIGAGOPPLGGVAAR 123
QY 160 PFGLSPITFPFGACLGKACGRKRK 183
Db 124 PFGLSPITFPFGACLGKACGRKRK 147
RESULT 26
RAY69137
ID AAY69137 standard; protein; 171 AA.
XX AC AAY69137;
XX XX 30-MAY-2000 (first entry)
XX DE Amino acid sequence of a human tropoelastin derivative.
XX KW Tropoelastin; derivative; proteolysis; protease; antiwrinkle;
XX KW hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;
XX KW peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.
XX OS Homo sapiens.
XX OS W0200004043-A1.
XX XX 27-JAN-2000.
XX XX 19-JUL-1999; 99WO-AU000580.
XX XX 17-JUL-1998; 98AU-00004723.

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DB	799	VL-GARPPFGGVAARPGFGLSPIYVGGAGGLGVGGKPKPYGGALGALGYGGGCGFGK	857
QY	177	ACGRKRK	183
	:		
Db	858	SCGRKRK	864
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XX	AC	AAP82484;	
XX	DT	24-OCT-2003 (revised)	
XX	DT	25-MAR-2003 (revised)	
XX	DT	31-OCT-1990 (first entry)	
XX	DE	Tropoelastin.	
XX	KW	Chicken; tropoelastin; platelet aggregation; arteriosclerosis.	
XX	OS	Gallus gallus.	
XX	Key	Location/Qualifiers	
FT	Region	3. .32	
FT		/label= repeat_region	
FT		/rpt_type= tandem	
FT		/rpt_unit= RU1:VPGVG	
FT	Region	53. _64	
FT		/label= repeat_unit	
FT		/rpt_type= direct	
FT	Region	92. .96	
FT		/rpt_unit= RU2:AAAAAKAAAKAAK	
FT	Region	99. .103	
FT		/label= RU1	
FT	Region	113. .123	
FT		/label= RU1	
FT	Region	126. .137	
FT		/label= RU2	
FT	Region	173. .182	
FT		/label= rpt_region	
FT		/rpt_type= tandem	
FT		/rpt_unit= RU1 (x2)	
XX	PN	JP63014694-A.	
XX	PD	21-JAN-1988.	
XX	PF	08-JUL-1986; 86JP-00158655.	
XX	PR	08-JUL-1986; 86JP-00158655.	
XX	PA	(SHIS) SHISEIDO CO LTD.	
XX	PA	(KAOS) KAO CORP.	
XX	WI	WPI; 1988-059829/09.	
XX	PS	N-PSDB; AAN82138.	
XX	PT	CDNA fragment encoding trophy-elastin - has inhibiting activity towards	
XX	PT	platelet aggregation and is useful for prophylaxis of arteriosclerosis.	
XX	PS	Claim 1; Fig 1; 5pp; Japanese.	
XX	CC	The cDNA was sequenced from a clone prepd. from mRNA isolated from	
XX	CC	chicken aorta tissue. It can be used to produce tropoelastin which is a	
XX	CC	precursor of elastin which does not have desmosine, isodesmosine and	
XX	CC	lysnyl-leucine residues and isn't cross-linked. (Updated on 25-MAR-2003	
XX	CC	to correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)	
XX	SQ	Sequence 294 AA;	
Query Match		40.7%;	Score 381; DB 1; Length 294;

result No.	Score	Query §		DB	ID	Description
		Match	Length			
1	935	100.0	692	15	US-10-210-172-40	Sequence 40, Appl
2	935	100.0	730	10	US-09-961-403-8	Sequence 8, Appli
3	927	99.1	663	15	US-10-108-260A-2477	Sequence 2477, Ap
4	908.5	97.2	731	10	US-09-964-663-1	Sequence 1, Appli
5	822	87.9	617	14	US-10-104-047-2915	Sequence 2915, Ap
6	819	87.6	711	15	US-10-210-172-38	Sequence 38, Appl
7	307.5	32.9	696	8	US-08-806-029-36	Sequence 36, Appl
8	307.5	32.9	696	15	US-10-441-965-23	Sequence 23, Appl
9	307.5	32.9	750	8	US-08-806-029-25	Sequence 25, Appl
10	304.5	32.6	696	15	US-10-441-965-21	Sequence 21, Appl
11	304.5	32.6	1465	14	US-10-096-986-74	Sequence 74, Appl
12	301.5	32.2	312	8	US-08-806-029-34	Sequence 34, Appl
13	301.5	32.2	378	14	US-10-117-931-26	Sequence 26, Appl

Db	516	AAAGL	GAGTGGG	VPGVGLGVGAGVPGLVGACGVPFGAGACDEGVRSLSPELREGDP	578
Qy	42	-----	-VPGALAAKAKYGAAYPGVLGGI	-----	
Db	576	SSSQHLPSTPSRPRVPGGALAAKAKYGAAYPGVLGGI	GLGVGIPGGVWAGPAAAAA	635	
Qy	88	AAKAAAQAQFGLVCAAGLGGIVGGLGVPGVGGIGGIPPAAAAKAAKYGAAGLGVLGG	147		
Db	636	AAKAAAQAQFGLVCAAGLGGIVGGLGVPGVGGIGGIPPAAAAKAAKYGAAGLGVLGG	147		
Qy	148	AQQPLGVVAARPQGFLSPIFFGGACLGKACGRKRK	183		
Db	696	AQQPLGVVAARPQGFLSPIFFGGACLGKACGRKRK	731		
RESULT 5					
US-10-104-047-2915					
; Sequence 2915, Application US/10104047					
; Publication No. US20030236392A1					
; GENERAL INFORMATION:					
; APPLICANT: HELIX RESEARCH INSTITUTE					
; TITLE OF INVENTION: NO. US20030236392alel full length cDNA					
; FILE REFERENCE: HI-A0105					
; CURRENT APPLICATION NUMBER: US/10/104,047					
; PRIOR FILING DATE: 2002-03-25					
; PRIOR FILING DATE:					
; NUMBER OF SEQ ID NOS: 4096					
; SOFTWARE: PatentIn Ver. 2.1					
; SEQ ID NO 2915					
; LENGTH: 617					
; TYPE: PRT					
; ORGANISM: Homo sapiens					
US-10-104-047-2915					
Query Match 87.9%; Score 822; DB 14; Length 617;					
Best Local Similarity 90.2%; Pred. No. 1e-47;					
Matches 165; Conservative 0; Mismatches 0; Indels 18; Gaps 1;					
Qy	1	AAAGL	GAGTGGG	VPGVGLGVGAGVPGLVGACGVPFGAGACDEGVRSLSPELREGDP	578
Db	453	AAAGL	GAGTGGG	VPGVGLGVGAGVPGLVGACGVPFGAGACDEGVRSLSPELREGDP	578
Qy	61	VLGGI	GALGVGI	PPGGVVGAGPAAAAKAAKAAQFGLVGAAGLGGIVGGLGVPGVG	120
Db	513	VLGGI	GALGVGI	PPGGVVGAGPAAAAKAAKAAQFGLVGAAGLGGIVGGLGVPGVG	572
Qy	121	GLGGI	PPAAAAKAAKYGAAGLGGIVGAGQFPLGGVVAARPQFGLSPIFFGGACLGKACGR	180	
Db	573	GLGGI	PPAAAAKAAKYGAAGLGGIVGAGQFPLGGVVAARPQFGLSPIFFGGACLGKACGR	614	
Qy	181	KRK	183		
Db	615	KRK	617		
RESULT 6					
US-10-210-172-38					
; Sequence 38, Application US/10210172					
; Publication No. US20040043928A1					
; GENERAL INFORMATION:					
; APPLICANT: Kekuda, Ramesh					
; APPLICANT: Miller, Charles					
; APPLICANT: Patturajan, Meera					
; APPLICANT: Pena, Carol					
; APPLICANT: Rieger, Daniel					
; APPLICANT: Shimkets, Richard					
; APPLICANT: Zerhusen, Bryan					
; APPLICANT: Li, Li					
; APPLICANT: Ji, Weizhen					
; APPLICANT: Padigaru, Muralidhara					
; APPLICANT: Casman, Stacie					

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OM protein - protein search, using sw model

Run on: November 19, 2004, 16:06:25 ; Search time 8.231 Seconds
(without alignments)
2139.188 Million cell updates/sec

Title: US-09-743-818A-74
Perfect score: 935
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR 79: *
1: Pirl: *
2: Pirl: *
3: Pirl: *
4: Pirl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	908.5	97.2	792	1 EAHU	elastin precursor,
2	672	71.9	747	1 EABO	elastin precursor,
3	657	70.3	860	1 EAMS	elastin precursor,
4	655.5	70.1	770	2 S59623	tropoelastin - she
5	640	68.4	864	1 EART	elastin precursor
6	382.5	40.9	784	2 A26601	elastin precursor
7	265	28.3	641	1 QQBE31	nuclear antigen EB
8	243.5	26.0	718	2 A36068	major ampullate fi
9	232	24.8	767	2 F70895	hypothetical glyci
10	226	24.2	907	2 A45560	sporozoite surface
11	216	23.1	882	2 B70812	hypothetical glyci
12	214.5	22.9	212	2 E86179	hypothetical glyci
13	213.5	22.8	2639	2 T31328	hypothetical prote
14	212	22.7	783	2 F70824	fibroin - Chinese
15	212	22.7	1901	2 F70806	hypothetical glyci
16	211	22.6	479	2 F70573	hypothetical glyci
17	211	22.6	741	2 G70917	hypothetical prote
18	211	22.6	1329	2 F70917	hypothetical glyci
19	210.5	22.5	498	2 C70720	hypothetical glyci
20	209	22.4	749	2 A70812	hypothetical glyci
21	209	22.4	1489	2 D70807	hypothetical glyci
22	207.5	22.2	603	2 A70770	hypothetical glyci
23	207	22.1	268	2 B61615	hypothetical glyci
24	206	22.0	1381	2 F70806	hypothetical glyci
25	205.5	22.0	778	2 D70863	hypothetical glyci
26	205	21.9	525	2 F70878	hypothetical glyci
27	203.5	21.8	384	1 A26099	hypothetical glyci
28	203.5	21.8	618	2 A70989	hypothetical glyci
29	203.5	21.8	801	2 F70824	hypothetical glyci

30	203	21.7	496	2	H70839	hypothetical glyci
31	203	21.7	837	2	E70835	hypothetical glyci
32	202	21.6	1660	2	A70869	hypothetical glyci
33	200	21.4	162	2	S56703	glycine-rich cell
34	200	21.4	1306	2	A70934	hypothetical glyci
35	199	21.3	923	2	E70820	hypothetical glyci
36	197	21.1	447	2	G84687	hypothetical glyci
37	196.5	21.0	408	2	S57483	probable disease r
38	196	21.0	1538	2	H70846	glycin-rich protei
39	195.5	20.9	635	2	A57131	hypothetical glyci
40	195	20.9	1733	1	B45344	collagen alpha 2(V
41	195	20.9	1958	2	B40505	probable nuclear a
42	194.5	20.8	314	2	H70987	hypothetical prote
43	194.5	20.8	957	2	D70835	hypothetical glyci
44	193.5	20.7	396	2	T49109	hypothetical glyci
45	193.5	20.7	419	2	G70602	glycine-rich prote
46	193.5	20.7	667	2	A70893	hypothetical prote
47	192.5	20.6	1079	2	B70807	hypothetical glyci
48	192	20.5	158	2	T08957	hypothetical glyci
49	192	20.5	615	2	H70589	glycine-rich prote
50	191.5	20.5	338	1	KNMU	hypothetical glyci
51	191.5	20.5	783	2	T35389	probable serine-th
52	191	20.4	439	2	D70954	hypothetical glyci
53	190.5	20.4	608	2	T05442	glycine-rich prote
54	190.5	20.4	743	1	S23779	collagen alpha 1(V
55	190	20.3	487	2	E70983	hypothetical glyci
56	190	20.3	694	2	F70868	hypothetical glyci
57	189.5	20.3	744	2	S15435	collagen alpha 1(V
58	189	20.2	576	2	A70900	hypothetical glyci
59	189	20.2	627	2	A44112	spidroin 2, dragli
60	188.5	20.2	562	2	B70953	hypothetical glyci
61	188.5	20.2	1758	2	T29350	hypothetical prote
62	188.5	20.2	1759	2	T29351	collagen alpha 2(I
63	187	20.0	255	2	B84777	hypothetical prote
64	187	20.0	584	2	G70804	hypothetical glyci
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66	185.5	19.8	744	1	A34246	collagen alpha 1(V
67	185.5	19.8	744	1	S23298	collagen alpha 1(V
68	185	19.8	245	2	F70787	hypothetical glyci
69	184.5	19.7	1373	1	A43291	collagen alpha 2(I
70	184	19.7	402	1	CG802S	collagen alpha 2(I
71	184	19.7	491	2	D70916	hypothetical glyci
72	184	19.7	594	2	G70545	hypothetical glyci
73	184	19.7	606	2	H70816	hypothetical glyci
74	184	19.7	1763	2	S16366	collagen alpha 2(I
75	183.5	19.6	173	2	JQ1064	glycine-rich prote
76	183.5	19.6	256	2	A70514	hypothetical glyci
77	182.5	19.5	1669	1	CGHU4B	collagen alpha 1(I
78	182	19.5	463	2	B70893	hypothetical glyci
79	182	19.5	591	2	B70523	hypothetical glyci
80	182	19.5	853	2	A70896	hypothetical glyci
81	181	19.4	201	2	T00799	hypothetical prote
82	181	19.4	220	2	T14441	glycine-rich prote
83	181	19.4	469	2	A24450	collagen alpha 2(V
84	180.5	19.3	361	2	G70682	hypothetical glyci
85	180.5	19.3	731	2	C70974	hypothetical glyci
86	180	19.3	298	2	E95286	hypothetical prote
87	180	19.3	2038	2	A43742	female sterile hom
88	178.5	19.1	1669	1	CGMS4B	collagen alpha 1(I
89	178	18.9	532	2	F70580	hypothetical glyci
90	177	18.9	291	1	S31415	glycine-rich prote
91	177	18.9	484	2	G70846	hypothetical glyci
92	176.5	18.9	401	1	OZZQAC	hypothetical glyci
93	176.5	18.9	588	2	F70971	circumsporozoite p
94	176	18.8	271	2	S34666	hypothetical glyci
95	174.5	18.7	210	2	JQ1060	glycine-rich prote
96	174.5	18.7	461	2	F70571	glycine-rich prote
97	174	18.6	674	2	S23297	hypothetical glyci
98	174	18.6	1466	1	CGHU7L	collagen alpha 1(X
99	173.5	18.6	1011	2	F70620	collagen alpha 1(I
100	173.5	18.6	1366	1	CGHU2S	hypothetical glyci
						collagen alpha 2(I

RESULT 7
Q6ZMJ6 PRELIMINARY; PRT; 570 AA.
ID Q6ZMJ6
AC Q6ZMJ6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ16246.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RA Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,
RA Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saïto K., Nishikawa T., Kimura K.,
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
RA Masuho Y., Nagai K., Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AK122731; BAC85506.1; -.
DR InterPro; IPR001451; Hexapep transf.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOELASTIN.
DR PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN 1.
SQ SEQUENCE 570 AA; 48941 MW; 3117B028D06DAF7B CRC64;
Query Match 87.9%; Score 822; DB 2; Length 570;
Best Local Similarity 90.2%; Pred. No. 1.7e-35;
Matches 165; Conservative 0; Mismatches 0; Indels 18; Gaps 1
Qy 1 AAAGLGAGIGPLGVGVGPGVLGVGGVPGLVGGAGVPGLVGGAVPGALAAKAAKYGAAPVG 60
Dd 406 AAAGLGAGIGPLGVGVGPGVLGVGGVPGLVGGAGVPGLVGGAVPGALAAKAAKYGAAPVG 465
Qy 61 VLGLGALGVGIPGVVVGGAPAAAAAAXAAAQAQFLYCAAGLGGVLGVGGILGVPGVG 120
Dd 466 VLGLGALGVGIPGVVVGGAPAAAAAAXAAAQAQFLYCAAGLGGVLGVGGILGVPGVG 525
Qy 121 GLGIIPPAAXAAKYGAAGLGGVLGGAGQPFLGGVAARPFGLSPIPPGGACLKACGR 180
Dd 526 GLGIIPPAAXAAKY-----GVAARPGFGLSPIPPGGACLKACGR 567
Qy 181 KRK 183
Dd 568 KRK 570
RESULT 8
BAC85506 PRELIMINARY; PRT; 570 AA.
ID BAC85506
AC BAC85506;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE CDNA FLJ16246 fis, clone HCION2001577, highly similar to Human elastin gene.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RA Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,
RA Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saïto K., Nishikawa T., Kimura K.,

DR HSP; P50039; 1ZFU.
DR CO; GO:0005578; C.extracellular matrix; NAS.
DR GO; GO:0030023; F.extracellular matrix constituent conferring...; NAS.
DR InterPro; IPR001451; Hexapep.transf.
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROP0ELASTIN.
DR PROSITE; PRO0101; HEXAPEP TRANSFERASES; UNKNOWN 1.
DR PROSITE; 687 AA; 59529 MW; 864068C4C8E9F8F CRC64;
DR SEQUENCE

[illegible]

Qy	181	KK	183
Dp	685	KK	687

RESULT 10	
Q7Z316	PRELIMINARY; PRT; 687 AA.
ID	Q7Z316
AC	Q7Z316;
DT	01-OCT-2003 (TrEMBLrel. 25, Created)
DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Hypothetical protein DKFP686O21208 (Fragment).
GN	Name=DKFP686O21208;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	T1SSU=Human rectum tumor;
RA	Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA	Han M., Wiemann S.;
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR	EMBL; BX538139; CAD98065.1; -
DR	InterPro; IPR000451; Hexapep_transf.
DR	PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
KW	Hypothetical protein.
FT	NON TER 1
SC	SEQUENCE 687 AA: 59847 MW: 73232A191DC1F10F CRC64:

KR	PROSLI; ESDVQVR; RMAN DL _TANGLICLIPDSEY; GAGGAL
DW	Hypothetical protein.
FT	NON TER ¹
SF	SEQUENCE 687 AA; 95847 MW; 792322A191DC1F10F CRC64;
QT	
Query Match	87.5%; Score 818; DB 2; Length 687;
Best Local Similarity	89.6%; Pred. No. 3.le-35;
Matches 164;	Conservative 0; Mismatches 1; Indels 18; Gaps 1;
QY	1 AAGLGAGIGPLGVGVGPGLGVGAGVPGFLGVGAGVPFGAVPGLAAAKAAKYGAAPVG 60
DB	523 AAAGLGAGIGPLGVGVGPGLGVGAGVPGFLGVGAGVPFGAVPGLAAAKAAKYGAAPVG 582
QY	61 VLGGHGLALGGVIGPGVVYGAGPAAAAAKAAKAAQFGLVGAAGLGLGVGCLGVPGVG 120
DB	583 VLGGHGLALGGVIGPGVVYGAGPAAAAATAKAANKAAQFGLVGAAGLGLGVGCLGVPGVG 642
QY	121 GLGGTPPAAKAAKYAGNGLGVGGAGQFPFLGGVAARPFGFLSPIPPGACLGKACGR 180
DB	643 GLGGTPPAAKAAKYI-----GVAARPGFLSPIPPGACLGKACGR 684
QY	181 KRK 183

RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,	
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,	
RA	Villallon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Fatey J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,	
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,	
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.B.,	
RA	Jones S.J., Marra M.A.;	
RT	"Generation and initial analysis of more than 15,000 full-length human	
RT	and mouse cDNA sequences.";	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	
RL	[2]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Eye;	
RA	Strausberg R.;	
RL	Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; BC065566; AAH65566.1; -	
DR	InterPro; IPR001451; Hexapep.transf.	
DR	InterPro; IPR003979; tropoelastin.	
DR	PRINTS; PR01500; TROP0ELASTIN	
DR	PROSITE; PS00101; HEXAPEP-TRANSFASERES; UNKNOWN 1.	
SQ	SEQUENCE 658 AA; 56680 MW; 5DAFC00D16A2F94E_CRC64;	
Query Match	87.1%; Score 814; DB 2; Length 658;	
Best Local Similarity	89.6%; Pred. No. 4.9e-35;	
Matches 164; Conservative	0; Mismatches 1; Indels 18; Gaps	
Qy	1 AAGLGAGTIGLVGVGVPGVLGVGAGVPGFPGVAGVPGALAAAKAAYGAAPG	
Db	494 AAGLGAGTIGLVGVGVPGVLGVGAGVPGFPGVAGVPGALAAAKAAYGAAPG	
Qy	61 VLGGALGAGVGPVGGVVGAGPAAAKAAAKAQAQFLVGAAGLGGVLGVPGVGVG	
Db	554 VLGGALGAGVGPVGGVVGAGPAAAKAAAKAQAQFLVGAAGLGGVLGVPGVGVG	
Qy	121 GLGGIPPAAKAAKAYGAAGLGGVLGGAGGFFLGGVAARPGFLSPFFGGACLGKACGR	
Db	614 GLGGIPPAAKAAKAY-----GVNARPGFLSPFFGGACLGKACGR	
Qy	181 KRK 183	
Db	656 KRK 658	
RESULT 13		
ID	AAH65566	
AC	AAH65566 PRELIMINARY; PRT; 658 AA.	
DT	02-WAR-2004 (TReMBLrel. 27, Created)	
DT	02-WAR-2004 (TReMBLrel. 27, Last sequence update)	
DE	02-WAR-2004 (TReMBLrel. 27, Last annotation update)	
DE	ELN protein.	
GN	ELN.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OC	NCBI_TaxID=9606;	
RP	[1]_TaxID=9606;	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Eye;	
RC	TISSUE=Eye;	
RX	MEDLINE=22389257; PubMed=12477932;	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	
RA	Altshul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,	
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,	
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	

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RESULT 14
Q28098          PRELIMINARY;      PRT;   707 AA.
AC Q28098;
AT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-JUN-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Elastin; NCBI gi: 153002 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_taxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85280426; PubMed=2992576;
RA Cicila G., May M., Ornstein-Goldstein N., Indik Z., Morrow S.,
RA Yeh H.S., Rosenbloom J., Boyd C., Rosenbloom J., Yoon K.;
RT "Structure of the 3' portion of the bovine elastin gene.";
RL Biochemistry 24:3075-3080(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88028442; PubMed=3665402;
RA Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N.,
RA Rosenbloom J.C., Cicila G., Yoon K., Rosenbloom J.;
RT "Sequence variation of bovine elastin mRNA due to alternative
RT splicing.";
RL Coll. Relat. Res. 7:235-247(1987).
DR EMBL; M19372; AAA30498.1; --
DR EMBL; M11422; AAA30498.1; JOINED.
DR EMBL; M19366; AAA30498.1; JOINED.
DR EMBL; M19367; AAA30498.1; JOINED.
DR EMBL; M19368; AAA30498.1; JOINED.

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RESULT 15

[illegible]

1	CONFLICT	3	MRS -> MAG (in Ref. 2 and 3).
12	CONFLICT	12	E -> G (in Ref. 2 and 3).
747	SEQUENCE	747	AA; 64229 MW; 633C03E411643D83CRC64;

Query Match	70.9%;	Score	663;	DB 1;	Length	747;
Best local Similarity	72.3%;	Pred. No.	3.6e-27;			4;
Matches 141;	Conservative	8;	Mismatches	30;	Indels	16;
					Gaps	
QY	1	AAAGLCAGIPGLGVGVPGLGVGAGVPGGLGVGAGVPGFAGVFGAALAAAACAAYGAAPVG	60			
DDb	557	AAAGLPAGVPGLVGAGVPGGLGVGAGVPGFAGVFGTTLAAAKAFGGPVG	616			
QY	61	VLGGLGALGGVGPVGCVGAGPAAAAAKAAKAAAOFLGVGAAGLGGGLGVGGLG-VPGV	119			
Ddb	617	ALGGVGDLLGAGCPGGVAGVWP-AAAAAKAAKAAQAQFGL---GGVGGLGVGGLGAVPGA	672			
QY	120	GGCGGIPPAATAKAAYGAAGLVGGAGQPPLGGVAARPFGLSPI-----F	168			
Ddb	673	VSLGVGVSPAAAANKAFGAAGLGGVLGACGPPFIFGGAGGLGVGGKKPKFFGGALGALGF	732			
QY	169	PGGACLGKACGRKRK	183			
Ddb	733	PGGACLGKSCGRKRK	747			
RESULT 17						
Q9ESZ9		PRELIMINARY;	PRT;	810 AA.		
ID	Q9ESZ9					
AC	Q9ESZ9;					
DT	01-WAR-2001 (T=EMBLrel. 16, Created)					
DT	01-MAR-2001 (T=EMBLrel. 16, Last sequence update)					
DT	01-JUN-2003 (T=EMBLrel. 24, Last annotation update)					
DE	ELN (Fragment).					
OS	Mus musculus (Mouse).					
OOC	Eukaryota; Metazoa;					
OOC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.					
OX	NCBI_TaxID=10090;					
[1]						
RN	SEQUENCE FROM N.A.					
RP	STRAIN=129/Sv;					
RC	Green E.D.;					
RL	Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.					
DR	EMBL; AF289665; AAF99336.1;					
DR	GO; GO:0005578; C:extracellular matrix; IEA.					
DR	GO; GO:0005201; F:extracellular matrix structural constituent; IEA.					
DR	InterPro; IPR003979; tropoelastin.					
DR	PRINTS; PR01500; TROP0ELASTIN.					
FT	NON TER					
[1]						
Q9ESZ9	810 AA. 67204 MW. 1ED61ED5AD4F40A2 CRC64;					

[illegible]

RESULT 18

Q8C9L8

ID Q8C9L8 PRELIMINARY; PRT; 860 AA.

AC Q8C9L8;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Mus musculus c3oneA630042119 product:elastin, full insert sequence

DE library, clone:A630042119 product:elastin, full insert sequence

DE (Elastin).

DE Name=El;

GN Name=El;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;

RN [1]

RN SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Thymus;

RX MEDLINE=99279253; PubMed=10349636;

RA Carninci P.; Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning.";

RL Meth. Enzymol. 303:19-44(1999).

RN [2]

RN SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Thymus;

RX MEDLINE=21085660; PubMed=11217851;

RA RIKEN FANTOM Consortium;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

RN [3]

RN SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Thymus;

RA The FANTOM Consortium;

RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

RN [4]

RN SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Thymus;

RX MEDLINE=20499374; PubMed=11042159;

RA Carninci P.; Shibata Y.; Hayatsu M.; Sugahara Y.; Shibata K.; Itoh M.,

RA Konno H.; Okazaki Y.; Muramatsu M.; Hayashizaki Y.;

RT "Normalization and subtraction of cap-trapper-selected cDNAs to

RT Prepare full-length cDNA libraries for rapid discovery of new genes.";

RL Genome Res. 10:1617-1630(2000).

RN [5]

RN SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Thymus;

RX MEDLINE=20530913; PubMed=11078661;

RA Shibata K.; Itoh M.; Aizawa K.; Nagaoka S.; Sasaki N.; Carninci P.,

RA Konno H.; Akiyama J.; Nishi K.; Kitsuunai T.; Tashiro H.; Itoh M.,

RA Sumi N.; Ishii Y.; Nakamura S.; Hazama M.; Nishine T.; Harada A.,

RA Yamamoto R.; Matsumoto H.; Sakaguchi S.; Ikegami T.; Kashiwagi K.,

RA Fujiwaka S.; Inoue K.; Togawa Y.; Izawa M.; Ohara E.; Watahiki M.,

RA Yoneda Y.; Ishikawa T.; Ozawa K.; Tanaka T.; Matsura S.; Kawai J.,

RA Okazaki Y.; Muramatsu M.; Inoue Y.; Kira A.; Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format

RT sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771(2000).

RN [6]

RN SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Thymus;

RA Adachi J.; Aizawa K.; Akimura T.; Arakawa T.; Bono H.; Carninci P.,

RA Fukuda S.; Furuno M.; Hanagaki T.; Hara A.; Hashizume W.,

RA Hayashida K.; Hayatsu M.; Hiramoto K.; Hiraoka T.; Hirozane T.,

RA Hori F.; Imotani K.; Ishii Y.; Itoh M.; Kagawa I.; Kasukawa T.,

RA Katoh H.; Kawai J.; Kojima Y.; Kondo S.; Konno H.; Koyama S.,

RA Kurihara C.; Matsuyama T.; Miyazaki A.; Murata M.; Nakamura M.,

RA Nishi K.; Nomura K.; Numazaki R.; Ohno M.; Ohsato N.; Okazaki Y.,

RA Saito R.; Saitoh H.; Sakai C.; Sakai K.; Sakazume N.; Sano H.,

RA Sasaki D.; Shibata K.; Shinagawa A.; Shiraki T.; Sogabe Y.; Tagami M.,

RA Tagawa A.; Takahashi F.; Takaku-Akahira S.; Takeda Y.; Tanaka T.,

RA Tomaru A.; Toyota T.; Yasunishi A.; Muramatsu M.; Hayashizaki Y.;

EMBL; M60647; AAA42269.1; --
DR EMBL; J04035; AAA42268.1; --
DR EMBL; M86372; AAA42271.1; --
DR EMBL; M86355; AAA42271.1; JOINED.
DR EMBL; M86363; AAA42271.1; JOINED.
DR EMBL; M86364; AAA42271.1; JOINED.
DR EMBL; M86366; AAA42271.1; JOINED.
DR EMBL; M86371; AAA42271.1; JOINED.
DR EMBL; M86376; AAA42272.1; --
DR EMBL; M86373; AAA42272.1; JOINED.
DR EMBL; M86375; AAA42272.1; JOINED.
DR PIR; A36106; EART.
DR RGD; 67394; Eln
DR InterPro; IPR003979; tropoelastin.
DR PRINTS; PR01500; TROPOLASTIN.
DR KW Alternative splicing; Connective tissue; Repeat; Signal;
KW Structural protein.
FT NON TER 1 1
FT SIGNAL <1 21
FT CHAIN 22 864
FT DISULFID 854 859
FT VARSPLIC 263 307
FT FT
FT FT
FT FT
FT VARSPLIC 308 308
FT FT
FT FT
FT VARSPLIC 809 823
FT FT
FT FT
FT SEQUENCE 864 AA; 72786 MW; 456894BB09E79FD4 CRC64;
QY Query Match 68.4%; Score 640; DB 1; Length 864;
DB Best Local Similarity 59.1%; Pred. No. 6.2e-26;
Matches 146; Conservative 9; Mismatches 24; Indels 68; Gaps 9
QY 1 AAAGLGAGIGGLGVGVPGLGVGAGVPGLVGAGVPGF--GAVPGALAAAKAAYGAA- 57
DB 622 AAAGLGAGVPLGVGAGVPGFGAG--GFGAGAGVPGFAGVPGSLAASKAAYGAAG 679
QY 58 ---VPGVLGGLGALGGV-----GIPGVVGAGPAAAAAATAKAAQAQFLGVGA 104
DB 680 GLGGPGLGGPGLGGPGGPGGPGGLGVGPGVAGGAF-AATAAATAKAAQAQYLGGAG 738
QY 105 GI-----GGLGVGCLG---VPGVGGGLGIPPAAAAKAAYGAAGLGG 143
DB 739 GLGAGGLGAGGLGAGGLGAGGLGAGGAGVPGAVGLGVSPAAAKAAYGAAGLGG 798
QY 144 VLGGAGQPLGVAARPFGILSPIFP-----GGACILGK 176
DB 799 VL-GARPPGGVAARPFGILSPIYPGGGAGGLGVGKKPKPYGGALGALGYQGCGCFGK 857
QY 177 ACGRKRK 183
DB 858 SCGRKRK 864
RESULT 21
Q28099 ID Q28099 PRELIMINARY; PRT; 650 AA.
AC Q28099;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE Elastin-CBELL; NCBI gi: 163003 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_Taxid=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=65280426; PubMed=2992576;

Biochemistry 24:3075-3080(1985).
[2]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=88028442; PubMed=3665402;
RA Yeh H., Ornstein-Goldstein N., Indik Z., Sheppard P., Anderson N.,
RA Rosenbloom J.C., Cilla G., Yoon K., Rosenbloom J.;
RT "sequence variation of bovine elastin mRNA due to alternative
RT splicing";
RL Coll. Relat. Res. 7:235-247(1987).
DR EMBL; M19372; AAA30500.1; -
DR EMBL; M11422; AAA30500.1; JOINED.
DR EMBL; M19366; AAA30500.1; JOINED.
DR EMBL; M19367; AAA30500.1; JOINED.
DR EMBL; M19368; AAA30500.1; JOINED.
DR EMBL; M19369; AAA30500.1; JOINED.
DR EMBL; M19370; AAA30500.1; JOINED.
DR EMBL; M19371; AAA30500.1; JOINED.
DR EMBL; M22771; AAA30500.1; JOINED.
DR EMBL; M22772; AAA30500.1; JOINED.
DR EMBL; M22773; AAA30500.1; JOINED.
DR EMBL; M22774; AAA30500.1; JOINED.
DR EMBL; M22988; AAA30500.1; JOINED.
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro; IPR003979; tropoelastin.
FT PRINTS; PR01500; TROPOELASTIN.
FT NON TER 1
SQ SEQUENCE 679 AA; 57652 MW; EB3C019E3BD7618D CRC64;

Query Match 66.6%; Score 622.5; DB 2; Length 679;
Best Local Similarity 68.2%; Pred. No. 4.3e-25;
Matches 133; Conservative 8; Mismatches 25; Indels 29; Gap

QY 1 AAAGLGAGTICLVGVGVVGLGVGAGVPGVLGVGAGVPFGAVPGALAAAKAYGAIV
Db ||||| :||| :||||| :||||| :||||| :||||| :||||| :||||| :||| :
QY 502 AAAGLPAVGVLGVGVGVVGLGVGAGVPGVLGVGAGVPGALAAAKAYGAIV
Db ||||| :||| :||||| :||||| :||||| :||||| :||||| :||||| :||| :
QY 61 VLGGIAGLGGVGIPIGGVGVGAGPAAATAAKAAKAAQAQGLVGAAGLGGVGGIG-V
Db ||||| :||| :||||| :||||| :||||| :||||| :||||| :||||| :||| :
QY 549 ALGGVDLGGAGIPGGVAGVGP-AAATAAKAAKAAQAQFGL---GGVGLGVGGIGV
Db ||||| :||| :||||| :||||| :||||| :||||| :||||| :||||| :||| :
QY 120 GGLGGIPPAAAAKAARYGAAGLGGVILGGAGOPPLGGVAARPFGLSPI-----
Db ||||| :||| :||||| :||||| :||||| :||||| :||||| :||||| :||| :
QY 605 VGLGVSVAAAAKAARKFAAGLGGVILGGAGQPFPFGGAGGLGVGKKPKPPGGALGAI
Db ||||| :||| :||||| :||||| :||||| :||||| :||||| :||||| :||| :
QY 169 PGACLGKACGRKRK 183
Db ||||| :||| :||||| :||||| :||||| :||||| :||||| :||||| :||| :
QY 665 PGACLGKSCGRKRK 679

RESULT 23
ELS_CHICK
ID AC ELUS_CHICK STANDARD; PRT; 750 AA.
DT DT 01-AUG-1988 (Rel. 08, Created)
DT DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE DE Elastin precursor (Tropoelastin) (Fragment).
GN Name=EIM;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87242320; PubMed=3593675;
RA Bressan G.M., Argos P., Stanley K.K.;
RT "Repeating structure of chick tropoelastin revealed by complementary
RT DNA cloning."
RL Biochemistry 26:1497-1503(1987).
RN [2]
RP SEQUENCE OF 85-750 FROM N.A. (ISOFORM 2)

Db 467 AKAAQFALLNLAGLVPGVGAP--GVGVAFGVGAFGVGLAPG---GVGVAFG 513

RESULT 26

ID	OL5336	PRELIMINARY;	PRT;	635 AA.
AC	OL5336;			
DT	01-JAN-1998 (TReMBLrel. 05, Created)			
DT	01-JAN-1998 (TReMBLrel. 05, Last sequence update)			
DT	01-MAR-2004 (TReMBLrel. 26, Last annotation update)			
DE	Elastin (Fragment)			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97358574; PubMed=9215670;			
RA	Li D.Y., Toland A.E., Boak B.B., Atkinson D.L., Ensing G.J.,			
RA	Morris C.A., Keating M.T.;			
RT	"Elastin point mutations cause an obstructive vascular disease,			
RT	supravalvular aortic stenosis";			
RL	Hum. Mol. Genet. 6:1021-1028(1997).			
DR	EMBL; U93037; AAB65621.1; -			
DR	EMBL; U93034; AAB65621.1; JOINED.			
DR	EMBL; U93035; AAB65621.1; JOINED.			
DR	EMBL; U93036; AAB65621.1; JOINED.			
DR	GO; GO:0005578; C:extracellular matrix; IEA.			
DR	GO; GO:0005201; F:extracellular matrix structural constituent; IEA.			
DR	InterPro; IPR001451; Hexapep.transf.			
DR	InterPro; IPR003979; tropoelastin.			
DR	PRINTS; PR01500; TROP0ELASTIN.			
DR	PROSITE; PS00101; HEXAPEP_TRANSF0ERASES; UNKNOWN_1.			
FT	NON_TER 1			
FT	NON_TER 635			
FT	SEQUENCE 635 AA; 55279 MW; 72950C364127B2A4 CRC64;			
SQ				
Query Match	37.6%;	Score 351.5;	DB 2;	Length 635;
Best Local Similarity	46.1%;	Pred No. 4.7e-11;		
Matches 107;	Conservative 18;	Mismatches 46;	Indels 61;	Gay
QY 1	AAAGLGAGTGLGVG--VGVPGLGV--GAGVPLGV-----GAGVPFGAVPG-----			
Db	290 AAAGLVPGPGFGGVGVPGAGVGVPGAGIPVVPAGIFG-AAVPGVSPAA			
QY 48	AAAKYGAAPGV-----LGLGALGV-----GIP--GGV			
Db	349 AAKAYTGAR--PGVGVGGIPTVYGAGGFGFGVGGIFGVAGVPSVGVPGVGVGV			
QY 81	GPAKAAAKAAKAAQFLVGMAGLGLGLGVG--VPGVGLGGIP--PA-----			
Db	408 GISPEAQA--AAKAAKYGAGAGVGLGLVPGAPGVPGVGGVGTPTPAAAGV			
QY 131	AKAAKYGAGLGGVVGAGQFPLGGVAARFGLSP---IPFGACGLKACG 179			
Db	467 AKAAQFALLNLAGLVPGVGAP--GVGVAFGVGAFGVGLAPG---GVGVAFG 513			
RESULT 27				
Q6ZUN2				
ID	Q6ZUN2	PRELIMINARY;	PRT;	559 AA.
AC	Q6ZUN2;			
DT	05-JUL-2004 (TReMBLrel. 27, Created)			
DT	05-JUL-2004 (TReMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TReMBLrel. 27, Last annotation update)			
DE	Hypothetical protein FLJ43523.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	TISSUE=Placenta;			

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RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.,
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK125511; BAC86188.1; -.
DR InterPro; IPR003979; troponelastin.
DR PRINTS; PRO1500; TROPOELASTIN.
DR SEQUENCE 559 AA; 53787 MW; 20938FFEC5492A01 CRC64;

Query Match 32.9%; Score 307.5; DB 2; Length 559;
Best Local Similarity 39.6%; Pred. No. 8.3e-09;
Matches 107; Conservative 14; Mismatches 48; Indels 101; Gaps 17;

QY 2 AAGLG---AGIPGLGV-----GVGP-----GLGVGAGVPG 29
Db 174 APGVGAFAGIPGVGPGFGPGVPLGYPIKAPKLPFGYGLPYTTGKLPYGVGPG-GVAG 232
QY 30 LGVAGVGP---GFGAVPGALAAK-AAKYGAAPVGLGGLGALGVGIP-----GGVVG 79
Db 233 AAGKAGYPTGTGVPQAAAAAAXKAGAGVLPVGGAGVPGVPGAIPGIGGIAG 292
QY 80 AGPAAAAAAXKAAKAAQFGLVGAAGL-----GGLGVGGLGVPGVG--GLG-----123
Db 293 VGTPTAAAAAAXKAAKAYG--AAAGLVPGGPGFGVPGVPGAGVPGAGIPVVP 350
QY 124 --GIPPA-----AAKAAKYGA--AGLGGV--LG-GAGQRP-----LG 154
Db 351 GAGIPGAAPGVVSPAAAAKAAKAYGARGPVGVGGIPTYGVGAGGFPFGVGVGGIP 410
QY 155 GVAARPGFGLS-----PIPPGGAC 173
Db 411 GVAGVPGVGGSRRCPCGSHWFFRSGSSC 440

RESULT 29
ELS_SHEEP
ID ELS_SHEEP STANDARD; PRT; 100 AA.
AC F11547;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Elastin (Tropoelastin) (Fragment).
GN Names=ELN;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Catartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95305763; PubMed=3839997;
RA Yoon K., Davidson J.M., Boyd C., May M., Luvalle P.,
RA Ornstein-Goldstein N., Smith J., Indik Z., Ross A., Golub E.,
RA Rosenbloom J.;
RT "Analysis of the 3' region of the sheep elastin gene.";
RL Arch. Biochem. Biophys. 241:684-691(1985).
CC -!- FUNCTION: Major structural protein of tissues such as aorta and
CC nuchal ligament, which must expand rapidly and recover completely.
CC -!- SUBUNIT: The polymeric elastin chains are cross-linked together
CC into an extensible 3D network.
CC -!- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
CC -!- PTM: The crosslinks are made of deaminated Lys.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M26188; AAA31515.1; ALT_SEQ.
CC EMBL; M26189; AAA31516.1; -.
CC PIR; S59623; S59623
CC Connective tissue; Repeat; Structural protein.
CC NON TER 1
CC DISULFID 90 95 By similarity.
CC SEQUENCE 100 AA; 8662 MW; 5C680C6A5AE6786 CRC64;

Query Match 31.6%; Score 295; DB 1; Length 100;
Best Local Similarity 64.0%; Pred. No. 1.3e-08;
Matches 64; Conservative 5; Mismatches 17; Indels 14; Gaps 3;

QY 98 FGL--VGAAGLGLGVGGLG-VPGVGLGGIPPPAAAAKAAKYGAAGLGVGAGQFPPLG 154
Db 1 FGLGVGGLGVGGLGVGGLGAVPGAVGLGVSPAAAAKAAKFTGAAGLGVGAGRFFPIG 60
QY 155 GVAARPGFGLSPI-----FPGGACLGKACGRKFK 183

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Db 61 GCAGGLGVGKPKPPFGGALGALGPPGGACLGKSCGRK 100
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RESULT 30

Q9GUB5 PRELIMINARY; PRT; 1468 AA.
AC Q9GUB5;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
DE Heavy-chain fibroin (Fragment).
GN Name=Fib-H;
OS Galleria mellonella (Wax moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea;
OC Pyralidae; Galleriinae; Galleria.
OX NCBI_taxid=7137;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Posterior silk gland;
RX MEDLINE=22063245; PubMed=11886872;
RA Zurovec M., Sehna F.;
RT "Unique molecular architecture of silk fibroin in the waxmoth,
RT Galleria mellonella.";
RL J. Biol. Chem. 277:22639-22647(2002).
DR EMBL; AF095239; AAG10393.1; -.
FT NON TER 1468 1468
SQ SEQUENCE 1468 AA; 122704 MW; 2DA59E1181BB3DDF CRC64;

Query Match 28.5%; Score 266.5; DB 2; Length 1468;
Best Local Similarity 35.6%; Pred. No. 2e-06;
Matches 83; Conservative 23; Mismatches 58; Indels 69; Gaps 10;
QY 1 AAAGLGAGIPGLGVG-----VGVPGLG-----VGAGVPLGVG 33
Db 280 AAGSAGAGLGGVGGVSGSSAASAGSAGAGEVILIDRSSAASRAAAGSAGSVG-G 338
QY 34 AGVPFGAVP--GALAAAKAAYGAAVPGV---LGLGLGGLGVGIPG-----GVVG 79
Db 339 LGLSLGPIGGIPGIGTASSTSGAGLGGVGAAGSAGLGGAGAGSAGAGLGGIG 398
QY 80 AGPAAAAAATAAKAAQFGLV-----GAAAGLGLGVGGLVPGVGGGL 122
Db 399 AGSGSSAASAGSAGAGEVIVIDRSSAASRAAASAGSAGLGGGLGGLGPGYGGIGL 458
QY 123 GGIPTAAAKAAYGAAGLGGVLCGAGQFPLGGVAARPGFGLSPIFGGACLG 175
Db 459 NGVSSASAL-----GAGLGGV-GTAGASGLGGIG---GAGVSAVGPAGAGLG 501

Search completed: November 19, 2004, 16:36:54
Job time : 38.9996 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2004, 16:37:11 ; Search time 2.12314 Seconds
(without alignments)
2168.321 Million cell updates/sec

Title: US-09-743-818a-13
Perfect score: 59
Sequence: I ALAAKAAKYGAA 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
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19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	100.0	617	US-10-104-047-2915	Sequence 2915, Ap
2	59	100.0	663	US-10-108-260A-2477	Sequence 2477, Ap
3	59	100.0	692	US-10-210-172-40	Sequence 40, Appl
4	59	100.0	730	US-09-961-403-8	Sequence 8, Appl
5	59	100.0	731	US-09-964-662-1	Sequence 1, Appl
6	56	94.9	711	US-10-210-172-38	Sequence 38, Appl
7	49	83.1	144	US-10-424-599-269890	Sequence 9, Appl
8	46	78.0	117	US-09-964-662-9	Sequence 10, Appl
9	46	78.0	118	US-09-964-662-11	Sequence 11, Appl
10	46	78.0	199	US-09-964-662-11	Sequence 2, Appl
11	46	78.0	200	US-09-964-662-2	Sequence 12700, Ap
12	41	69.5	277	US-10-437-963-122700	Sequence 9086, Ap
13	40	67.8	378	US-10-369-493-9086	

14	39	66.1	342	14	US-10-369-493-19927	Sequence 19927, A
15	39	66.1	485	14	US-10-369-493-16900	Sequence 16900, A
16	39	66.1	569	13	US-10-078-929-116	Sequence 116, App
17	38	64.4	129	15	US-10-424-599-209451	Sequence 209451, Ap
18	38	64.4	149	9	US-09-738-626-6936	Sequence 6936, Ap
19	38	64.4	159	17	US-10-425-115-340008	Sequence 340008, Ap
20	38	64.4	177	16	US-10-437-963-163840	Sequence 163840, Ap
21	38	64.4	233	13	US-10-068-134-4	Sequence 4, Appl
22	38	64.4	251	13	US-10-068-134-4	Sequence 4, Appl
23	38	64.4	463	14	US-10-369-493-8096	Sequence 9096, Ap
24	38	64.4	463	14	US-10-369-493-8049	Sequence 8049, Ap
25	37	62.7	86	17	US-10-425-115-221398	Sequence 221398, Ap
26	37	62.7	152	17	US-10-425-115-353761	Sequence 353761, Ap
27	37	62.7	152	17	US-10-425-115-353768	Sequence 353768, Ap
28	37	62.7	152	17	US-10-425-115-353768	Sequence 353768, Ap
29	37	62.7	158	17	US-10-739-930-8468	Sequence 8468, Ap
30	37	62.7	177	17	US-10-425-115-353760	Sequence 353760, Ap
31	37	62.7	184	17	US-10-425-115-353770	Sequence 353770, Ap
32	37	62.7	192	16	US-10-437-963-123914	Sequence 123914, Ap
33	37	62.7	213	17	US-10-739-930-8462	Sequence 8462, Ap
34	37	62.7	385	14	US-10-156-761-12560	Sequence 12560, A
35	37	62.7	388	14	US-10-369-493-650	Sequence 650, App
36	37	62.7	452	14	US-10-369-493-17360	Sequence 17360, A
37	37	62.7	531	14	US-10-156-761-14639	Sequence 14639, A
38	37	62.7	698	14	US-10-017-161-1970	Sequence 1970, Ap
39	37	62.7	698	14	US-10-292-798-1618	Sequence 1618, Ap
40	37	62.7	902	15	US-10-437-963-138437	Sequence 138437, A
41	37	62.7	1589	16	US-10-282-122A-63655	Sequence 63655, A
42	36	61.0	55	15	US-10-424-599-153020	Sequence 153020, A
43	36	61.0	71	17	US-10-425-115-211597	Sequence 211597, A
44	36	61.0	109	16	US-10-437-963-164333	Sequence 164333, A
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46	36	61.0	142	17	US-10-425-115-267771	Sequence 267771, A
47	36	61.0	194	14	US-10-012-542-397	Sequence 397, App
48	36	61.0	194	14	US-10-115-123-397	Sequence 397, App
49	36	61.0	196	15	US-10-282-122A-56899	Sequence 56899, A
50	36	61.0	204	16	US-10-437-963-160892	Sequence 160892, A
51	36	61.0	217	15	US-10-051-874-95	Sequence 95, Appl
52	36	61.0	222	13	US-10-027-806-58	Sequence 58, Appl
53	36	61.0	222	13	US-10-034-623-58	Sequence 58, Appl
54	36	61.0	222	14	US-10-027-801-58	Sequence 58, Appl
55	36	61.0	222	14	US-10-029-120-58	Sequence 58, Appl
56	36	61.0	224	14	US-10-099-322-303	Sequence 303, App
57	36	61.0	224	15	US-10-044-564-303	Sequence 303, App
58	36	61.0	235	14	US-10-369-493-16176	Sequence 16176, A
59	36	61.0	238	14	US-10-369-493-15794	Sequence 15794, A
60	36	61.0	244	14	US-10-369-493-15426	Sequence 15426, A
61	36	61.0	251	16	US-10-437-963-201970	Sequence 201970, A
62	36	61.0	274	9	US-09-738-626-6076	Sequence 6076, Ap
63	36	61.0	293	14	US-10-369-493-8030	Sequence 8030, Ap
64	36	61.0	295	9	US-09-816-028A-32	Sequence 32, Appl
65	36	61.0	295	14	US-10-303-161-32	Sequence 32, Appl
66	36	61.0	295	14	US-10-303-118-32	Sequence 32, Appl
67	36	61.0	295	14	US-10-303-128-32	Sequence 32, Appl
68	36	61.0	295	14	US-10-303-134-32	Sequence 32, Appl
69	36	61.0	295	14	US-10-303-162-32	Sequence 32, Appl
70	36	61.0	295	17	US-10-820-536-32	Sequence 32, Appl
71	36	61.0	295	17	US-10-845-408-32	Sequence 32, Appl
72	36	61.0	295	17	US-10-845-412-32	Sequence 32, Appl
73	36	61.0	309	17	US-10-846-219-32	Sequence 32, Appl
74	36	61.0	309	16	US-10-437-963-196196	Sequence 196196, Ap
75	36	61.0	330	16	US-10-437-963-196197	Sequence 196197, Ap
76	36	61.0	330	16	US-10-437-963-196197	Sequence 196197, Ap
77	36	61.0	436	17	US-10-425-115-356194	Sequence 356194, Ap
78	36	61.0	575	15	US-10-425-114-45940	Sequence 45940, A
79	36	61.0	623	16	US-10-437-963-109127	Sequence 109127, A
80	36	61.0	688	16	US-10-437-963-152448	Sequence 152448, A
81	36	61.0	698	16	US-10-437-963-168409	Sequence 168409, A
82	36	61.0	766	15	US-10-282-122A-66102	Sequence 66102, A
83	36	61.0	845	15	US-10-424-599-206032	Sequence 206032, A
84	36	61.0	880	16	US-10-437-963-126058	Sequence 126058, A
85	36	61.0	890	16	US-10-437-963-177048	Sequence 177048, A
86	36	61.0	1257	15	US-10-282-122A-74310	Sequence 74310, A

Sequence 196404, Sequence 177050, Sequence 1761, Ap Sequence 167410, Sequence 254505, Sequence 135427, Sequence 13247, A Sequence 13588, A Sequence 6, Appli Sequence 20, Appl Sequence 1441, Ap Sequence 1270, Ap Sequence 74026, A Sequence 680, App

ALIGNMENTS

RESULT 1
US-10-104-047-2915
; Sequence 2915, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2915
; LENGTH: 617
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2915

Query Match 100.0%; Score 59; DB 14; Length 617;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAYGAA 13
Db 497 ALAAAKAAYGAA 509

RESULT 2
US-10-108-260A-2477
; Sequence 2477, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2477
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-2477

Query Match 100.0%; Score 59; DB 15; Length 663;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAYGAA 13
Db 525 ALAAAKAAYGAA 537

RESULT 3
US-10-210-172-40
; Sequence 40, Application US/10210172
; Publication No. US20040043928A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Miller, Charles
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol
; APPLICANT: Rieger, Daniel
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Li, Li
; APPLICANT: Ji, Weizhen
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Casman, Stacie
; APPLICANT: Voss, Edward
; APPLICANT: Boldog, Ferenc
; APPLICANT: Gorman, Linda
; APPLICANT: Leite, Mario
; APPLICANT: Vernet, Corine
; APPLICANT: Anderson, David
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zhong, Mei
; APPLICANT: Gerlach, Valerie
; APPLICANT: Hjalt, Tord
; APPLICANT: Rastelli, Luca
; APPLICANT: Spytek, Kimberly
; APPLICANT: Edinger, Shlomit
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Alsobrook II, John
; APPLICANT: Lepley, Denise et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-416 A
; CURRENT APPLICATION NUMBER: US/10/210,172
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/309,501
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/323,994
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/373,814
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/310,291
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/310,951
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/310,544
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: 60/311,292
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/311,979
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/313,201
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/312,892
; PRIOR FILING DATE: 2001-08-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 327
; SOFTWARE: CuraSeqlist version 0.1
; SEQ ID NO 40
; LENGTH: 692
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-210-172-40

Query Match 100.0%; Score 59; DB 15; Length 692;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAYGAA 13
| | | | | | | | | |
Db 554 ALAAAKAAYGAA 566

RESULT 4

US-09-961-403-8
; Sequence 8, Application US/09961403
; Publication No. US20030077589A1
; GENERAL INFORMATION:
; APPLICANT: HE-STUMPP, HOLGER
; APPLICANT: HAENDLER, BERNARD
; APPLICANT: KRAETZSCHMAR, JOERN
; APPLICANT: KREFT, BERTHOLT
; APPLICANT: WINTERHAGER, ELKE
; APPLICANT: REGIDOR, PEDRO
; APPLICANT: SCOTTI, SIMONE
; TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS
; FILE REFERENCE: SCH-1789
; CURRENT APPLICATION NUMBER: US/09/961,403
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 730
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-961-403-8

Query Match 100.0%; Score 59; DB 10; Length 730;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAYGAA 13
| | | | | | | | | |
Db 592 ALAAAKAAYGAA 604

RESULT 5

US-09-964-662-1
; Sequence 1, Application US/09964662
; Publication No. US20030166846A1
; GENERAL INFORMATION:
; APPLICANT: PROTEIN SPECIALTIES LTD.
; APPLICANT: HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP
; TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN AND
; TITLE OF INVENTION: OTHER FIBROUS PROTEINS
; FILE REFERENCE: 041082/0112
; CURRENT APPLICATION NUMBER: US/09/964,662
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: 09/340,736
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 731
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-964-662-1

Query Match 100.0%; Score 59; DB 10; Length 731;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAYGAA 13
| | | | | | | | | |
Db 593 ALAAAKAAYGAA 605

RESULT 6

US-10-210-172-38
; Sequence 38, Application US/10210172

; Publication No. US20040043928A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Miller, Charles
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol
; APPLICANT: Rieger, Daniel
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Li, Li
; APPLICANT: Ji, Weizhen
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Casman, Stacie
; APPLICANT: Voss, Edward
; APPLICANT: Boldog, Ferenc
; APPLICANT: Gorman, Linda
; APPLICANT: Leite, Mario
; APPLICANT: Vermet, Corine
; APPLICANT: Anderson, David
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zhong, Mei
; APPLICANT: Gerlach, Valerie
; APPLICANT: Hjalt, Tord
; APPLICANT: Rastelli, Luca
; APPLICANT: Spytek, Kimberly
; APPLICANT: Edinger, Shlomit
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Alsobrook II, John
; APPLICANT: Lepley, Denise et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-416 A
; CURRENT APPLICATION NUMBER: US/10/210,172
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/309,501
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/323,994
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/373,814
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/310,291
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/310,951
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/310,544
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: 60/311,292
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/311,979
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/313,201
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/312,892
; PRIOR FILING DATE: 2001-08-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 327
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 38
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-210-172-38

Query Match 94.9%; Score 56; DB 15; Length 711;
Best Local Similarity 92.3%; Pred. No. 0.18;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAYGAA 13
| | | | | | | | | |
Db 591 ALAAAKAAYGAA 603

```

; APPLICANT: PROTEIN SPECIALTIES LTD.
; APPLICANT: HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP
; TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN AND
; TITLE OF INVENTION: OTHER FIBROUS PROTEINS
; FILE REFERENCE: 041082/0112
; CURRENT APPLICATION NUMBER: US/09/964,662
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: 09/340,736
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-964-662-10

Query Match      78.0%; Score 46; DB 10; Length 118;
Best Local Similarity 90.9%; Pred. No. 1.7;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAAAKAAKYG 11
   | | | | | | | | | |
Db 40 AAAAAKAAKYG 50

RESULT 10
US-09-964-662-11
; Sequence 11, Application US/09964662
; Publication No. US20030166846A1
; GENERAL INFORMATION:
; APPLICANT: PROTEIN SPECIALTIES LTD.
; APPLICANT: HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP
; TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN AND
; TITLE OF INVENTION: OTHER FIBROUS PROTEINS
; FILE REFERENCE: 041082/0112
; CURRENT APPLICATION NUMBER: US/09/964,662
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: 09/340,736
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 11
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-964-662-11

Query Match      78.0%; Score 46; DB 10; Length 199;
Best Local Similarity 90.9%; Pred. No. 2.9;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAAAKAAKYG 11
   | | | | | | | | | |
Db 39 AAAAAKAAKYG 49

RESULT 11
US-09-964-662-2
; Sequence 2, Application US/09964662
; Publication No. US20030166846A1
; GENERAL INFORMATION:
; APPLICANT: PROTEIN SPECIALTIES LTD.
; APPLICANT: HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP
; TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN AND
; TITLE OF INVENTION: OTHER FIBROUS PROTEINS
; FILE REFERENCE: 041082/0112
; CURRENT APPLICATION NUMBER: US/09/964,662
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: 09/340,736
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; US-10-424-599-269890
; Sequence 269890, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21153223B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 269890
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(144)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_85730C.1.pep
; US-10-424-599-269890

Query Match      83.1%; Score 49; DB 15; Length 144;
Best Local Similarity 91.7%; Pred. No. 0.59;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAAAKAAKYG 12
   | | | | | | | | | |
Db 79 AAAAAKAAKYG 90

RESULT 8
US-09-964-662-9
; Sequence 9, Application US/09964662
; Publication No. US20030166846A1
; GENERAL INFORMATION:
; APPLICANT: PROTEIN SPECIALTIES LTD.
; APPLICANT: HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP
; TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN AND
; TITLE OF INVENTION: OTHER FIBROUS PROTEINS
; FILE REFERENCE: 041082/0112
; CURRENT APPLICATION NUMBER: US/09/964,662
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: 09/340,736
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-964-662-9

Query Match      78.0%; Score 46; DB 10; Length 117;
Best Local Similarity 90.9%; Pred. No. 1.6;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAAAKAAKYG 11
   | | | | | | | | | |
Db 39 AAAAAKAAKYG 49

RESULT 9
US-09-964-662-10
; Sequence 10, Application US/09964662
; Publication No. US20030166846A1
; GENERAL INFORMATION:

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```
; SEQ ID NO 2
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: polypeptide
US-09-964-662-2

Query Match          78.0%; Score 46; DB 10; Length 200;
Best Local Similarity 90.9%; Pred. No. 2.9;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALAAAKAAYG 11
Db 40 AAAAAKAYG 50

RESULT 12
US-10-437-963-122700
; Sequence 122700, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 122700
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_25604C.1.pep
US-10-437-963-122700

Query Match          69.5%; Score 41; DB 16; Length 277;
Best Local Similarity 69.2%; Pred. No. 31;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALAAAKAAYGAA 13
Db 255 AVVAHKAASYGAA 267

RESULT 13
US-10-369-493-9086
; Sequence 9086, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 9086
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Caulobacter crescentus
US-10-369-493-9086

Query Match          66.1%; Score 39; DB 14; Length 485;
Best Local Similarity 72.7%; Pred. No. 1.3e+02;

; LENGTH: 378
; TYPE: PRT
; ORGANISM: Chloroflexus aurantiacus
US-10-369-493-9086

Query Match          67.8%; Score 40; DB 14; Length 378;
Best Local Similarity 75.0%; Pred. No. 65;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LAAAKAAYGAA 13
Db 292 LAAARALVYGAA 303

RESULT 14
US-10-369-493-19927
; Sequence 19927, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 19927
; LENGTH: 342
; TYPE: PRT
; ORGANISM: No. US20030233675Altoc punctiforme
US-10-369-493-19927

Query Match          66.1%; Score 39; DB 14; Length 342;
Best Local Similarity 75.0%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 LAAAKAAYGAA 13
Db 14 LAAAKGLYGAA 25

RESULT 15
US-10-369-493-16900
; Sequence 16900, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 16900
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Caulobacter crescentus
US-10-369-493-16900

Query Match          66.1%; Score 39; DB 14; Length 485;
Best Local Similarity 72.7%; Pred. No. 1.3e+02;
```

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALAAAKAAYG 11
| | | | | : | |
Db 391 ALAAANATRYG 401

RESULT 16
US-10-078-929-116
; Sequence 116, Application US/10078929
; Publication No. US20020152497A1
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Sakai, Hajime
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Odell, Joan T.
; APPLICANT: Meyers, Blake
; APPLICANT: Thorpe, Catherine
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
; TITLE OF INVENTION: Stress Response
; FILE REFERENCE: BB1357 US NA
; CURRENT APPLICATION NUMBER: US/10/078, 929
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/566, 394
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/133038
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133042
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133427
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133437
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133428
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133438
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133436
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/137667
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 116
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-078-929-116

Query Match 66.1%; Score 39; DB 13; Length 569;
Best Local Similarity 61.5%; Pred. No. 1.5e+02;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALAAAKAAYGAA 13
| | | | | : | |
Db 164 ALSAAKEKFGSA 176

RESULT 17
US-10-424-599-209451
; Sequence 209451, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 209451
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_31161C.1.pap
US-10-424-599-209451

Query Match 64.4%; Score 38; DB 15; Length 129;
Best Local Similarity 61.5%; Pred. No. 48;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALAAAKAAYGAA 13
| | | | | : | |
Db 61 AMAHLEAAKYGGA 73

RESULT 18
US-09-738-626-6936
; Sequence 6936, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738, 626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6936
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6936

Query Match 64.4%; Score 38; DB 9; Length 149;
Best Local Similarity 72.7%; Pred. No. 56;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALAAAKAAYG 11
| | | | | : | |
Db 38 ALATAEAAKHG 48

RESULT 19
US-10-425-115-340008
; Sequence 340008, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 340008
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(159)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_73254C.1.pap
US-10-425-115-340008

Query Match 64.4%; Score 38; DB 17; Length 159;
Best Local Similarity 76.9%; Pred. No. 60;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALAAAKAAYGAA 13
||| ||| |||
Db 100 ALAAAKAAYGAA 112

RESULT 20
US-10-437-963-163840
; Sequence 163840, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 163840
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_62799C.1.pap
US-10-437-963-163840

Query Match 64.4%; Score 38; DB 16; Length 177;
Best Local Similarity 61.5%; Pred. No. 67;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALAAAKAAYGAA 13
| | : | | | |
Db 48 ATAGKQASKYGA 60

RESULT 21
US-10-056-744B-4
; Sequence 4, Application US/10056744B
; Publication No. US20020193303A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 58860, A HUMAN CHOLESTERYL ESTER
; TITLE OF INVENTION: HYDROLASE AND USES THEREOF
; FILE REFERENCE: MP12001-026PIRM
; CURRENT APPLICATION NUMBER: US/10/056,744B
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/264,167

; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-056-744B-4

Query Match 64.4%; Score 38; DB 13; Length 233;
Best Local Similarity 90.0%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALAAAKAAY 10
||| ||| |||
Db 55 ALAAAYAAKY 64

RESULT 22
US-10-068-134-4
; Sequence 4, Application US/10068134
; Publication No. US20020156264A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: 22012, A No. US20020156264A1 Human Carboxypeptidase
; FILE REFERENCE: 5800-38
; CURRENT APPLICATION NUMBER: US/10/068,134
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US/09/345,469
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for the alpha/beta hydrolase
; OTHER INFORMATION: family from the Prosite database of protein
; OTHER INFORMATION: patterns
US-10-068-134-4

Query Match 64.4%; Score 38; DB 13; Length 251;
Best Local Similarity 90.0%; Pred. No. 97;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALAAAKAAY 10
||| ||| |||
Db 55 ALAAAYAAKY 64

RESULT 23
US-10-369-493-9096
; Sequence 9096, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 9096
; LENGTH: 463

; TYPE: PRT
; ORGANISM: Chloroflexus aurantiacus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(463)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-9096

Query Match 64.4%; Score 38; DB 14; Length 463;
Best Local Similarity 81.8%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ALAAAKAAYG 11
||| ||| |||
Db 290 ALAAAAALYG 300

RESULT 24
US-10-369-493-8449
; Sequence 8449, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 8449
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Ralstonia metallidurans
US-10-369-493-8449

Query Match 64.4%; Score 38; DB 14; Length 482;
Best Local Similarity 61.5%; Pred. No. 1.9e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ALAAAKAAYGAA 13
|: ||| | : |||
Db 403 AVAAANATEYGLA 415

RESULT 25
US-10-425-115-221398
; Sequence 221398, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 221398
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_133506C.1.pap
US-10-425-115-221398

Query Match 62.7%; Score 37; DB 17; Length 86;
Best Local Similarity 58.3%; Pred. No. 48;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 2 LAATAAKAYGAA 13
: ||| : ||| :
Db 12 IAASKTAQYGKA 23

RESULT 26

US-10-425-115-353761
; Sequence 353761, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 353761
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_85804C.1.pap
US-10-425-115-353761

Query Match 62.7%; Score 37; DB 17; Length 152;
Best Local Similarity 69.2%; Pred. No. 86;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ALAAAKAAYGAA 13
||| ||| |||
Db 17 ALKVAKAVKSGAA 29

RESULT 27

US-10-425-115-353768
; Sequence 353768, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 353768
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_85810C.1.pap
US-10-425-115-353768

Query Match 62.7%; Score 37; DB 17; Length 152;
Best Local Similarity 69.2%; Pred. No. 86;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ALAAAKAAYGAA 13
||| ||| |||
Db 17 ALKVAKAVKSGAA 29

RESULT 28
US-10-425-115-368385
; Sequence 368385, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 368385
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(152)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_99138C.1.pep
US-10-425-115-368385

Query Match 62.7%; Score 37; DB 17; Length 152;
Best Local Similarity 69.2%; Pred. No. 86;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 ALAAAKAAKYGAA 13
||| ||| ||| |||
Db 17 ALKVAKAVKSGAA 29

RESULT 29
US-10-739-930-8468
; Sequence 8468, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 8468
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(158)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: ZEAWA-23APR03-C7210_82.p
US-10-739-930-8468

Query Match 62.7%; Score 37; DB 17; Length 158;
Best Local Similarity 69.2%; Pred. No. 90;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 ALAAAKAAKYGAA 13
||| ||| ||| |||
Db 25 ALKVAKAVKSGAA 37

RESULT 30
US-10-425-115-353760
; Sequence 353760, Application US/10425115
; Publication No. US20040214272A1

; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 353760
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_85803C.1.pep
US-10-425-115-353760

Query Match 62.7%; Score 37; DB 17; Length 177;
Best Local Similarity 69.2%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 ALAAAKAAKYGAA 13
||| ||| ||| |||
Db 42 ALKVAKAVKSGAA 54

Search completed: November 19, 2004, 17:13:21
Job time : 4.12314 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2004, 15:19:20 ; Search time 2.65677 Seconds
(without alignments)
1755.321 Million cell updates/sec

Title: US-09-743-818A-13

Perfect score: 59

Sequence: 1 ALAAKAAKYGAA 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: A_Geneseq_23Sep04.*

2: Geneseqp1980s.*

3: Geneseqp1990s.*

4: Geneseqp2000s.*

5: Geneseqp2001s.*

6: Geneseqp2002s.*

7: Geneseqp2003as.*

8: Geneseqp2003bs.*

9: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	100.0	147	2	AAY01304 Human tro
2	59	100.0	171	3	AAY69137 Amino aci
3	59	100.0	183	2	AAY01311 Human tro
4	59	100.0	183	3	AAY69138 Amino aci
5	59	100.0	200	2	AAY01305 Human tro
6	59	100.0	216	2	AAY01310 Human tro
7	59	100.0	472	4	AAB88422 Human mem
8	59	100.0	617	7	ADB64761 Human pro
9	59	100.0	663	7	ADM03792 Human pro
10	59	100.0	692	7	ADB40134 Human tro
11	59	100.0	698	2	AAY01302 Human NOV
12	59	100.0	698	3	AAY69069 Amino aci
13	59	100.0	712	3	AAB08630 Amino aci
14	59	100.0	730	2	AAY01315 Human tro
15	59	100.0	730	3	AAB08631 Human tro
16	59	100.0	730	5	AAO17360 Human tro
17	59	100.0	730	8	ADQ19747 Human sof
18	59	100.0	731	3	AAY69068 Amino aci
19	59	100.0	731	4	AAB66657 Human tro
20	59	100.0	731	6	ABU08725 Human tro
21	59	100.0	731	7	ADL96420 Human tro
22	59	100.0	733	2	AAB66653 Human tro
23	59	100.0	733	2	AAY01301 Amino aci
24	59	100.0	757	7	ABG75223 Human tro
25	59	100.0	757	7	ADP65160 Human tro

26	56	94.9	711	7	ADL40132	AdL40132 Human NOV
27	55	93.2	12	3	AAY69144	Aay69144 Peptidomi
28	55	93.2	660	2	AAY01303	Aay01303 Human tro
29	54	91.5	515	3	AAY69135	Aay69135 Amino aci
30	54	91.5	571	3	AAY69071	Aay69071 Amino aci
31	54	91.5	870	7	ADE08527	AdE08527 Novel pro
32	53	89.8	864	7	ADE56670	AdE56670 Rat Prote
33	51	86.4	60	2	AAY01306	Aay01306 Human tro
34	49	83.1	294	1	AAP82484	Aap82484 Tropoeelas
35	46	78.0	117	4	AAB66659	Aab66659 MFU-3. 4/
36	46	78.0	117	6	ABU08733	Abu08733 Human ela
37	46	78.0	117	7	ADL96422	AdL96422 Human ela
38	46	78.0	118	4	AAB66660	AbB66660 MFU-4. 4/
39	46	78.0	118	6	ABU08734	Abu08734 Human ela
40	46	78.0	118	8	ADL96423	AdL96423 Human ela
41	46	78.0	199	4	AAB66661	Aab66661 MFU-5. 4/
42	46	78.0	199	6	ABU08735	Abu08735 Human ela
43	46	78.0	199	7	ADL96424	AdL96424 Human ela
44	46	78.0	200	4	AAB66658	Aab66658 MFU-2. 4/
45	46	78.0	200	6	ABU08726	Abu08726 Human ela
46	46	78.0	200	7	ADL96421	AdL96421 Human ela
47	46	78.0	201	2	AAW46316	Aaw46316 Non-natur
48	43	72.9	33	8	ADP29751	AdP29751 Human sec
49	39	66.1	11	2	AAR04180	Aar04180 Monomer o
50	39	66.1	569	6	ABU58205	Abu58205 Rice stre
51	38	64.4	89	4	AAB79885	Aab79885 Corynebac
52	38	64.4	89	4	AAB79209	Aab79209 Corynebac
53	38	64.4	149	4	AAG93182	Aag93182 C glutami
54	38	64.4	233	7	ADB80253	Adb80253 Human 588
55	38	64.4	251	4	AAB60302	Aab60302 Alpha/bet
56	37	62.7	18	8	ADP29725	AdP29725 Human sec
57	37	62.7	25	4	AAB66787	AbB66787 Amphipath
58	37	62.7	84	5	ABP08143	Abp08143 Human ORF
59	37	62.7	122	3	AAG54636	Aag54636 Zea may
60	37	62.7	130	3	AAG54638	Aag54638 Zea may
61	37	62.7	141	8	ADN46915	Adn46915 Thermococ
62	37	62.7	149	3	AAG54635	Aag54635 Zea may
63	37	62.7	151	3	AAG40734	Aag40734 Zea may
64	37	62.7	152	3	AAG54637	Aag54637 Zea may
65	37	62.7	159	3	AAG40733	Aag40733 Zea may
66	37	62.7	388	4	ABH52633	Abh52633 Escherich
67	37	62.7	388	7	ADC01505	Adc01505 Enteroha
68	37	62.7	410	5	ABH82174	Abh82174 C. acidov
69	37	62.7	698	7	ADC87165	Adc87165 Human GPC
70	37	62.7	902	6	ABU35731	Abu35731 Protein e
71	37	62.7	920	6	ABR55195	AbR55195 Nucleotid
72	37	62.7	920	6	ABR55195	AbR55195 Nucleotid
73	37	62.7	924	4	ABH67489	Abh67489 Drosophil
74	36	61.0	65	3	ABH01883	Abh01883 Streptoco
75	36	61.0	109	8	ADM47764	Adm47764 Thermococ
76	36	61.0	146	3	AAG35144	Aag35144 Arabidops
77	36	61.0	154	3	AAG29134	Aag29134 Arabidops
78	36	61.0	154	3	ADG09369	Adg09369 Arabidops
79	36	61.0	154	7	ADC87850	Adc87850 Ribosom
80	36	61.0	154	7	ADC87957	Adc87957 Ribosom
81	36	61.0	166	3	AAG35143	Aag35143 Arabidops
82	36	61.0	174	3	AAG09368	Aag09368 Arabidops
83	36	61.0	194	3	AAY86471	Aay86471 Human gen
84	36	61.0	194	6	ABO53623	AbO53623 Novel hum
85	36	61.0	196	6	ABU28975	Abu28975 Protein e
86	36	61.0	206	7	ADH86199	Adh86199 Enterococ
87	36	61.0	222	3	ABO67919	AbO67919 Pseudomon
88	36	61.0	251	7	ABO67919	AbO67919 Pseudomon
89	36	61.0	274	4	ABO67919	AbO67919 Pseudomon
90	36	61.0	295	6	ABU97200	Abu97200 Campyloba
91	36	61.0	295	6	ABJ18494	Abj18494 Campyloba
92	36	61.0	388	4	AAG91336	Aag91336 C glutami
93	36	61.0	389	8	ADN24517	Adn24517 Human mod
94	36	61.0	389	8	ADN06042	Adn06042 Antipsori
95	36	61.0	406	4	ABH95251	Abh95251 Human pro
96	36	61.0	406	7	ADH60425	Adh60425 Human pro
97	36	61.0	406	7	ADH45850	Adh45850 Human pro
98	36	61.0	406	7	ADH60421	Adh60421 Human pro

99 36 61.0 450 7 ADF05791 Agf05791 Bacterial
100 36 61.0 489 6 ADA33347 Ada33347 Acinetoba

ALIGNMENTS

RESULT 1
ID AAY01304 standard; protein; 147 AA.
XX AAY01304;
XX 07-JUN-1999 (first entry)
XX Human tropoelastin derivative SHELgamma.
XX Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;
KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
KW hand lotion; surgical implant; industrial product; human; SHEL; variant.
XX Homo sapiens.
OS Synthetic.
XX WO9903886-A1.
PN 28-JAN-1999.
XX 17-JUL-1998; 98WO-AU000564.
XX 18-JUL-1997; 97AU-00008117.
XX (UNSY) UNIV SYDNEY.
XX Weiss AS;
XX WPI; 1999-132162/11.
DR N-PSDB; AAX27706.
XX New derivatives of human tropoelastin - with elastin-like or
PT macromolecular binding properties, useful e.g. as surgical implants.
PT Claim 19; Fig 7; 82pp; English.
XX The invention relates to a derivative or variant of human tropoelastin
CC (hTE) having elastin-like and/or macromolecule (specifically
CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors
CC comprising the nucleic acids encoding the variants or derivatives are
CC used to produce the proteins recombinantly. The tropoelastin derivatives
CC or hybrid proteins containing the derivatives are useful in medical,
CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
CC wrinkle or hand lotions, also as surgical implants, foods and industrial
CC products. The hybrid protein have controllable GAG-binding properties,
CC depending on presence or absence of a specific fragment, designated
CC peptide 26A, from hTE. The present sequence represents a human
CC tropoelastin derivative SHELgamma excluding the product encoded by exon
XX 26A
SQ Sequence 147 AA;
Query Match 100.0%; Score 59; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALAAAKAAKYGAA 13
Db 9 ALAAAKAAKYGAA 21
RESULT 2
AAY69137
ID AAY69137 standard; protein; 171 AA.
XX

AC AAY69137;
XX 30-MAY-2000 (first entry)
DT Amino acid sequence of a human tropoelastin derivative.
XX Tropoelastin; derivative; proteolysis; protease; antiwrinkle;
XX hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;
KW peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.
XX Homo sapiens.
OS WO200004043-A1.
XX 27-JAN-2000.
XX 19-JUL-1999; 99WO-AU000580.
XX 17-JUL-1998; 98AU-00004723.
XX (UNSY) UNIV SYDNEY.
XX Weiss AS;
XX WPI; 2000-182399/16.
XX New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
PT cell growth.
XX Disclosure; Page 133-134; 136pp; English.
XX The present sequence represents a human tropoelastin derivative, which is
CC representative of tropoelastin derivatives of the invention. In the
CC tropoelastin derivatives of the invention a subsequence has been mutated
CC so that susceptibility to proteolysis is reduced or eliminated, or a
CC subsequence has been inserted so that susceptibility to proteolysis is
CC increased. The derivatives have with reduced susceptibility, and can be
CC used where the wild-type protein would be degraded too easily, e.g. in
CC contact with serum or wound exudate. The tropoelastin derivatives provide
CC competitive inhibition of protease activity. The tropoelastin
CC derivatives, and other polypeptides containing tropoelastin derivative-
CC derived protease-susceptibility sites, are useful in human or veterinary
CC medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents
CC and for inducing chemotaxis. They are also useful for proliferation or
CC growth inhibition, particularly of smooth muscle cells, epithelial or
CC endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets.
CC Peptidomimetics that mimic the protease cleavage site in tropoelastin
CC derivatives are competitive inhibitors of the protease, and are used for
CC protecting against lung damage caused by elastin, for inhibiting or
CC controlling localized growth of cancers or metastases, or to limit
CC protease activity that causes blood clotting
XX Sequence 171 AA;
SQ Query Match 100.0%; Score 59; DB 3; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALAAAKAAKYGAA 13
Db 33 ALAAAKAAKYGAA 45
RESULT 3
AAY01311
ID AAY01311 standard; protein; 183 AA.
XX AAY01311;
XX 07-JUN-1999 (first entry)
XX Human tropoelastin derivative SHEL26-36 (excluding exon 26A product).
XX

KW Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;
 KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
 XX hand lotion; surgical implant; industrial product; human; SHEL; variant.

OS Homo sapiens.
 XX Synthetic.

XX WO9903886-A1.

PD 28-JAN-1999.

XX 17-JUL-1998; 98WO-AU000564.

XX 18-JUL-1997; 97AU-00008117.

XX (UNSY) UNIV SYDNEY.

XX Weiss AS;

XX WPI; 1999-132162/11.

XX New derivatives of human tropoelastin - with elastin-like or
 PT macromolecular binding properties, useful e.g. as surgical implants.

XX Claim 39; Page 11; 82pp; English.

XX The invention relates to a derivative or variant of human tropoelastin
 CC (hTE) having elastin-like and/or macromolecule (specifically
 CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors
 CC comprising the nucleic acids encoding the variants or derivatives are
 CC used to produce the proteins recombinantly. The tropoelastin derivatives
 CC or hybrid proteins containing the derivatives are useful in medical,
 CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
 CC wrinkle or hand lotions, also as surgical implants, foods and industrial
 CC products. The hybrid protein have controllable GAG-binding properties,
 CC depending on presence or absence of a specific fragment, designated
 CC peptide 26A, from hTE. The present sequence represents a human
 CC tropoelastin derivative SHEL26-36 excluding exon 26A product

XX Sequence 183 AA;

Query Match 100.0%; Score 59; DB 2; Length 183;

Best Local Similarity 100.0%; Pred. No. 0.022;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGAA 13

Db 45 ALAAAKAAKYGAA 57

RESULT 4

AAAY69138

ID AAY69138 standard; protein; 183 AA.

XX AC

XX AAY69138;

DT 30-MAY-2000 (first entry)

XX Amino acid sequence of a human tropoelastin derivative.

DE OS

XX Tropoelastin; derivative; proteolysis; protease; antiwrinkle;

XX hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;

XX Peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.

XX OS

XX Homo sapiens.

XX WO200004043-A1.

XX 27-JAN-2000.

XX 19-JUL-1999; 99WO-AU000580.

XX 17-JUL-1998; 98AU-00004723.

XX

PA (UNSY) UNIV SYDNEY.

XX Weiss AS;

XX WPI; 2000-182399/16.

XX New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
 PT cell growth.

XX Disclosure; Page 134-135; 136pp; English.

XX The present sequence represents a human tropoelastin derivative, which is
 CC representative of tropoelastin derivatives of the invention. In the
 CC tropoelastin derivatives of the invention a subsequence has been mutated
 CC so that susceptibility to proteolysis is reduced or eliminated, or a
 CC subsequence has been inserted so that susceptibility to proteolysis is
 CC increased. The derivatives have with reduced susceptibility, and can be
 CC used where the wild-type protein would be degraded too easily, e.g. in
 CC contact with serum or wound exudate. The tropoelastin derivatives provide
 CC competitive inhibition of protease activity. The tropoelastin
 CC derivatives, and other polypeptides containing tropoelastin derivative-
 CC derived protease-susceptibility sites, are useful in human or veterinary
 CC medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents
 CC and for inducing chemotaxis. They are also useful for proliferation or
 CC growth inhibition, particularly of smooth muscle cells, epithelial or
 CC endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets.
 CC Peptidomimetics that mimic the protease cleavage site in tropoelastin
 CC derivatives are competitive inhibitors of the protease, and are used for
 CC protecting against lung damage caused by elastin, for inhibiting or
 CC controlling localized growth of cancers or metastases, or to limit
 CC protease activity that causes blood clotting

XX Sequence 183 AA;

Query Match 100.0%; Score 59; DB 3; Length 183;

Best Local Similarity 100.0%; Pred. No. 0.022;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGAA 13

Db 45 ALAAAKAAKYGAA 57

RESULT 5

AAAY01305

ID AAY01305 standard; protein; 200 AA.

XX AC

XX AAY01305;

DT 07-JUN-1999 (first entry)

XX Human tropoelastin derivative SHELgamma.

XX Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;
 KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
 XX hand lotion; surgical implant; industrial product; human; SHEL; variant.

OS Homo sapiens.

XX Synthetic.

XX WO9903886-A1.

XX 28-JAN-1999.

XX 17-JUL-1998; 98WO-AU000564.

XX 18-JUL-1997; 97AU-00008117.

XX (UNSY) UNIV SYDNEY.

XX Weiss AS;

XX

```
DR WPI; 1999-132162/11.
DR N-PSDB; AAX27707.
XX
PT New derivatives of human tropoelastin - with elastin-like or
PT macromolecular binding properties, useful e.g. as surgical implants.
XX
PS Claim 15; Fig 8; 82pp; English.
XX
CC The invention relates to a derivative or variant of human tropoelastin
CC (hTE) having elastin-like and/or macromolecule (specifically
CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors
CC comprising the nucleic acids encoding the variants or derivatives are
CC used to produce the proteins recombinantly. The tropoelastin derivatives
CC or hybrid proteins containing the derivatives are useful in medical,
CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
CC wrinkle or hand lotions, also as surgical implants, foods and industrial
CC products. The hybrid protein have controllable GAG-binding properties,
CC depending on presence or absence of a specific fragment, designated
CC peptide 26A, from hTE. The present sequence represents a human
CC tropoelastin derivative SHELgamma
XX
SQ Sequence 200 AA;
Query Match 100.0%; Score 59; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALAAAKAAYGAA 13
Db 62 ALAAAKAAYGAA 74
RESULT 6
AAY01310
ID AAY01310 standard; protein; 216 AA.
XX
AC AAY01310;
XX
DT 07-JUN-1999 (first entry)
XX
DE Human tropoelastin derivative SHEL26-36.
XX
KW Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;
KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
KW hand lotion; surgical implant; industrial product; human; SHEL; variant.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9503886-A1.
XX
PD 28-JAN-1999.
XX
PF 17-JUL-1998; 98WO-AU000564.
XX
PR 18-JUL-1997; 97AU-00008117.
XX
PA (UNSY) UNIV SYDNEY.
XX
PI Weiss AS;
XX
DR WPI; 1999-132162/11.
XX
PT New derivatives of human tropoelastin - with elastin-like or
PT macromolecular binding properties, useful e.g. as surgical implants.
XX
PS Claim 35; Page 11; 82pp; English.
XX
CC The invention relates to a derivative or variant of human tropoelastin
CC (hTE) having elastin-like and/or macromolecule (specifically
CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors
CC comprising the nucleic acids encoding the variants or derivatives are
CC used to produce the proteins recombinantly. The tropoelastin derivatives
or hybrid proteins containing the derivatives are useful in medical,
pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
wrinkle or hand lotions, also as surgical implants, foods and industrial
products. The hybrid protein have controllable GAG-binding properties,
depending on presence or absence of a specific fragment, designated
peptide 26A, from hTE. The present sequence represents a human
tropoelastin derivative SHELgamma
XX
SQ Sequence 216 AA;
Query Match 100.0%; Score 59; DB 2; Length 216;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALAAAKAAYGAA 13
Db 78 ALAAAKAAYGAA 90
RESULT 7
AAB88422
ID AAB88422 standard; protein; 472 AA.
XX
AC AAB88422;
XX
DT 23-MAY-2001 (first entry)
XX
DE Human membrane or secretory protein clone PSEC0191.
XX
KW Human; secretory protein; membrane protein; vaccine; gene therapy;
KW rheumatoid arthritis; diabetes.
XX
OS Homo sapiens.
XX
PN EPI067182-A2.
XX
PD 10-JAN-2001.
XX
PF 07-JUL-2000; 2000EP-00114090.
XX
PR 08-JUL-1999; 99JP-00194179.
PR 11-JAN-2000; 2000JP-00118775.
PR 02-MAY-2000; 2000JP-00183766.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
XX
DR WPI; 2001-093989/11.
DR N-PSDB; AAF93849.
XX
PT Nucleic acids encoding secretory proteins/membrane proteins, useful in
PT gene therapy or as candidate target molecules in drug development.
XX
PS Claim 1; SEQ ID NO 212; 609pp + Sequence Listing; English.
XX
CC This invention relates to nucleic acid sequences AAF93744 - AAF93916
CC which encode human secretory or membrane proteins represented by AAB88317
CC - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and
CC AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the
CC invention. The invention also includes methods for the production of
CC antibodies directed against the proteins, and cDNA sequences, which can
CC be used in vaccines. The polynucleotide sequences can be used in gene
CC therapy. The polynucleotide sequences and the proteins they encode may be
CC used in the prevention, treatment and diagnosis of diseases associated
CC with inappropriate secretory protein/membrane protein expression. The
CC nucleic acids and complementary sequences may also be used as DNA probes
CC in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect
CC and quantitate the presence of similar nucleic acid sequences in samples.
CC They may also be used to study the expression and function of secretory
CC proteins/membrane polypeptides and their role in metabolism. The
CC polypeptides may be used as antigens in the production of antibodies
CC against them and in assays to identify modulators (agonists and
```

CC antagonists) of expression and activity. The antibodies and antagonists
 CC may also be used as therapeutic agents to down regulate expression and
 CC activity. The antibodies may also be used as diagnostic agents for
 CC detecting the presence of the polypeptides in samples (e.g. by enzyme
 CC linked immunosorbent assay (ELISA) Examples of diseases which may be
 CC treated include rheumatoid arthritis and diabetes

SQ Sequence 472 AA;

Query Match 100.0%; Score 59; DB 4; Length 472;
 Best Local Similarity 100.0%; Pred. No. 0.06; Mismatches 0; Indels 0; Gaps 0;
 Matches 13; Conservative 0;

QY 1 ALAAAKAAYGAA 13
 |||||
 Db 360 ALAAAKAAYGAA 372

RESULT 8
 ADB64761
 ID ADB64761 standard; protein; 617 AA.
 XX
 AC ADB64761;
 XX
 DT 04-DEC-2003 (first entry)
 DE Human protein encoded by clone NT2RP70003110.
 XX
 KW Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;
 KW cell regeneration; membrane protein; signal transduction-related protein;
 KW transcription-related protein; osteoporosis; neurological disease;
 KW cancer; tumour.
 XX
 OS Homo sapiens.
 XX
 PN EP1308459-A2.
 XX
 PD 07-MAY-2003.
 XX
 PF 28-MAR-2002; 2002EP-00007401.
 XX
 PR 05-NOV-2001; 2001JP-00373298.
 PR 25-JAN-2002; 2002US-00350978.
 XX
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
 XX WPI; 2003-450961/43.
 DR N-PSDB; ADB62791.
 XX
 PT New polynucleotides and polypeptides, useful for developing a diagnostic
 PT marker or medicines for regulation of their expression and activity, or
 PT as targets of gene therapy.
 XX
 PS Claim 1; Page; 222pp; English.
 XX
 CC The invention discloses a polynucleotide comprising a sequence selected
 CC from 1970 fully defined nucleotide sequences which encode novel
 CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
 CC or its partial peptide, an antibody binding to the polypeptide or peptide
 CC of the polynucleotide, immunologically assaying the polypeptide or
 CC peptide of the polynucleotide by contacting the polypeptide or peptide
 CC with the antibody of the encoded protein, and observing the binding
 CC between the two, a transformant carrying the polynucleotide in an
 CC expressible manner and an antisense polynucleotide. The oligonucleotide
 CC is useful as a primer for synthesizing the polynucleotide, or as a probe
 CC for detecting the polynucleotide. The polynucleotides and encoded
 CC proteins are useful as pharmaceutical agents and many disease-related
 CC genes may be included in them, for developing a diagnostic marker or

CC medicines for regulation of their expression and activity, or as targets
 CC of gene therapy. The genes are involved in tissue and/or cell
 CC regeneration. Membrane proteins, signal transduction-related proteins,
 CC transcription-related proteins, disease-related proteins and genes
 CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
 CC neurological diseases, cancer, tumours. The cDNA may be used to regulate
 CC the activity or expression of the encoded protein to treat diseases. The
 CC sequence presented is a protein of the invention. Note: Some of the
 CC sequence data for this patent is not represented in the printed
 CC specification, but is based on sequence information supplied by the
 CC European Patent Office.

SQ Sequence 617 AA;

Query Match 100.0%; Score 59; DB 7; Length 617;
 Best Local Similarity 100.0%; Pred. No. 0.08; Mismatches 0; Indels 0; Gaps 0;
 Matches 13; Conservative 0;

QY 1 ALAAAKAAYGAA 13
 |||||
 Db 497 ALAAAKAAYGAA 509

RESULT 9
 ADM03792
 ID ADM03792 standard; protein; 663 AA.
 XX
 AC ADM03792;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human protein of the invention SEQ ID NO:2477.
 XX
 KW human; gene therapy; diagnostic marker; pharmaceutical.

OS Homo sapiens.

PN EP1347046-A1.

PD 24-SEP-2003.

PF 12-APR-2002; 2002EP-00008400.

PR 22-MAR-2002; 2002JP-00137785.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.

PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;

PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;

PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;

XX WPI; 2003-723558/69.

DR N-PSDB; ADM01349.

XX New polynucleotides and polypeptides are useful in gene therapy, for
 PT developing a diagnostic marker or medicines for regulating their
 PT expression and activity, or as a target of gene therapy.

PS Claim 1; SEQ ID NO 2477; 305pp; English.

XX The invention relates to a novel human polynucleotide and the encoded
 CC polypeptide. A polynucleotide of the invention may have a use in gene
 CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
 CC as a primer for synthesizing the polynucleotide or as a probe for
 CC detecting the polynucleotide. The polynucleotides ADM01316-ADM01758 are
 CC useful in gene therapy, for developing a diagnostic marker or medicines
 CC for regulating their expression and activity, or as a target of gene
 CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
 CC are useful as pharmaceutical agents. The present sequence represents a
 CC protein sequence of the invention.

SQ Sequence 663 AA;

Query Match 100.0%; Score 59; DB 7; Length 663;
 Best Local Similarity 100.0%; Pred. No. 0.086;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAYGAA 13
 DB 525 ALAAAKAAYGAA 537

RESULT 10
 ADE40134
 ID ADE40134 standard; protein; 692 AA.
 XX AC
 AC ADE40134;
 XX AC
 DT 29-JAN-2004 (first entry)
 DE Human NOV16b protein - SEQ ID 40.
 XX NOVX; cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic;
 KW antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic;
 KW antiparkinsonian; antiasthmatic; gynaecological; cardiomyopathy;
 KW atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;
 KW multiple sclerosis; graft-versus-host disease; Alzheimer's; Parkinson's;
 KW aschma; fertility disorder; vaccine; gene therapy; chromosome mapping;
 KW tissue typing; human; NOV.
 XX OS
 OS Homo sapiens.
 XX WO2003064589-A2.
 XX 07-AUG-2003.
 XX 02-AUG-2002; 2002WO-US024483.
 XX 02-AUG-2001; 2001US-0309501P.
 XX 03-AUG-2001; 2001US-0310291P.
 XX 07-AUG-2001; 2001US-0310544P.
 XX 08-AUG-2001; 2001US-0310951P.
 XX 09-AUG-2001; 2001US-0311292P.
 XX 13-AUG-2001; 2001US-0311979P.
 XX 16-AUG-2001; 2001US-0312892P.
 XX 17-AUG-2001; 2001US-0313201P.
 XX 17-AUG-2001; 2001US-0313415P.
 XX 20-AUG-2001; 2001US-0313643P.
 XX 20-AUG-2001; 2001US-0313702P.
 XX 21-AUG-2001; 2001US-0314031P.
 XX 23-AUG-2001; 2001US-0314466P.
 XX 28-AUG-2001; 2001US-0315403P.
 XX 29-AUG-2001; 2001US-0315853P.
 XX 17-SEP-2001; 2001US-0322716P.
 XX 21-SEP-2001; 2001US-0323994P.
 XX 14-DEC-2001; 2001US-0340233P.
 XX 05-FEB-2002; 2002US-0354591P.
 XX 19-MAR-2002; 2002US-0365478P.
 XX 19-APR-2002; 2002US-0373814P.
 XX 19-APR-2002; 2002US-0373825P.
 XX 19-APR-2002; 2002US-0373989P.
 XX 23-APR-2002; 2002US-0374632P.
 XX 07-JUN-2002; 2002US-0386971P.
 XX 01-AUG-2002; 2002US-00210172.
 XX (CURA-) CURAGEN CORP.
 XX Kekuda R, Miller CE, Patturajan M, Pena CEA, Rieger DK;
 PI Shinkets RA, Zerhusen BD, Li L, Padigaru M, Casman SJ;
 PI Voss EZ, Bolldog FL, Gorman L, Leite MW, Vernet CAM, Anderson DW;
 PI Gao X, Zhong M, Gerlach VL, Hjalt T, Rastelli L, Spytek KA;
 PI Edinger SR, Ellerman K, Malyankar UM, Macdougall JR, Stone DU;
 PI Alsobrook JP, Lepley DM, Burgess CE, Majumder K, Wolenc AR,
 PI Smithson G;
 XX WPI; 2003-663472/62..

DR N-PSDB; ADE40133.
 XX New NOVX polypeptides and nucleic acids, useful for preventing or
 PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
 PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.
 XX
 PS Claim 1; SEQ ID NO 40; 560pp; English.
 XX
 CC The invention relates to a novel NOVX polypeptide. The polypeptide of the
 CC invention demonstrates cardiant, antiarteriosclerotic, hypotensive,
 CC cytostatic, anorectic, antidiabetic, immunosuppressive, anti-HIV,
 CC neuroprotective, nootropic, antiparkinsonian, antiasthmatic and
 CC gynaecological activities and may be useful in diagnosing, treating or
 CC preventing NOVX-associated disorders including cardiomyopathy,
 CC atherosclerosis, hypertension, cancer, obesity, diabetes, Parkinson's
 CC sclerosis, graft-versus-host disease, Alzheimer's disease, multiple
 CC disease, asthma or fertility disorders. Furthermore, the polypeptides may
 CC be utilised as vaccines whilst the nucleic acids may be used as
 CC hybridisation probes, in gene therapy, chromosome mapping, tissue typing,
 CC preventive medicine and pharmacogenomics. The current sequence is that of
 CC the human NOV protein of the invention.
 XX
 SQ Sequence 692 AA;
 Query Match 100.0%; Score 59; DB 7; Length 692;
 Best Local Similarity 100.0%; Pred. No. 0.09;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAYGAA 13
 DB 554 ALAAAKAAYGAA 566

RESULT 11
 AAY01302
 ID AAY01302 standard; protein; 698 AA.
 XX AC
 AC AAY01302;
 XX 07-JUN-1999 (first entry)
 XX Human tropoelastin variant SHELdelta26A.
 XX
 KW Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;
 KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
 KW hand lotion; surgical implant; industrial product; human; SHEL; variant.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX WO9903886-A1.
 XX 28-JAN-1999.
 XX 17-JUL-1998; 98WO-AU000564.
 XX 18-JUL-1997; 97AU-00008117.
 XX (UNSY) UNIV SYDNEY.
 XX Weiss AS;
 XX WPI; 1999-132162/11.
 XX New derivatives of human tropoelastin - with elastin-like or
 PT macromolecular binding properties, useful e.g. as surgical implants.
 XX
 PS Claim 13; Fig 2; 82pp; English.
 XX The invention relates to a derivative or variant of human tropoelastin
 CC (hTE) having elastin-like and/or macromolecule (specifically
 CC glycosaminoglycan (GAG)) -binding properties. Cells containing vectors

CC comprising the nucleic acids encoding the variants or derivatives are
 CC used to produce the proteins recombinantly. The tropoelastin derivatives
 CC or hybrid proteins containing the derivatives are useful in medical,
 CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
 CC wrinkle or hand lotions, also as surgical implants, foods and industrial
 CC products. The hybrid protein have controllable GAG-binding properties,
 CC depending on presence or absence of a specific fragment, designated
 CC peptide 26A, from hTE. The present sequence represents the synthetic
 CC human tropoelastin variant SHELDelta26A
 XX
 SQ Sequence 698 AA;

Query Match 100.0%; Score 59; DB 2; Length 698;
 Best Local Similarity 100.0%; Pred. No. 0.091;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALAAAKAAKYGAA 13
 |||||
 DB 560 ALAAAKAAKYGAA 572

RESULT 12
 AAY69069
 ID AAY69069 standard; protein; 698 AA.
 AC AAY69069;
 XX
 DT 30-MAY-2000 (first entry)
 XX
 DE Amino acid sequence of a human reduced tropoelastin derivative.
 XX
 KW Tropoelastin; derivative; SHELDelta-26a; SHEL; proteolysis; protease;
 KW antiwrinkle; hand lotion; bulking agent; chemotaxis; proliferation;
 KW growth inhibition; peptidomimetic; lung damage; elastin; cancer;
 KW metastasis; blood clotting.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO200004043-A1.
 XX
 PD 27-JAN-2000.
 XX
 PF 19-JUL-1999; 99WO-AU000580.
 XX
 PR 17-JUL-1998; 98AU-00004723.
 XX
 PA (UNSY) UNIV SYDNEY.
 XX
 PI Weiss AS;
 XX
 DR WPI; 2000-182399/16.
 DR N-PSDB; AAZ61144.
 XX
 PT New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
 PT cell growth.
 XX
 PS Disclosure; Page 110-112; 136pp; English.
 XX

The present sequence represents a human reduced tropoelastin derivative,
 CC designated SHELDelta-26a. The sequence is produced by removing exon 26a
 CC of SHEL (SHEL not defined). The protein is representative of tropoelastin
 CC derivatives of the invention, in which a subsequence has been mutated so
 CC that susceptibility to proteolysis is reduced or eliminated, or a
 CC subsequence has been inserted so that susceptibility to proteolysis is
 CC increased. The derivatives have with reduced susceptibility, and can be
 CC used where the wild-type protein would be degraded too easily, e.g. in
 CC contact with serum or wound exudate. The tropoelastin derivatives provide
 CC competitive inhibition of protease activity. The tropoelastin
 CC derivatives, and other polypeptides containing tropoelastin derivative-
 CC derived protease-susceptibility sites, are useful in human or veterinary
 CC medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents
 CC and for inducing chemotaxis. They are also useful for proliferation or

CC growth inhibition, particularly of smooth muscle cells, epithelial or
 CC endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets.
 CC Peptidomimetics that mimic the protease cleavage site in tropoelastin
 CC derivatives are competitive inhibitors of the protease, and are used for
 CC protecting against lung damage caused by elastin, for inhibiting or
 CC controlling localized growth of cancers or metastases, or to limit
 CC protease activity that causes blood clotting
 XX
 SQ Sequence 698 AA;

Query Match 100.0%; Score 59; DB 3; Length 698;
 Best Local Similarity 100.0%; Pred. No. 0.091;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALAAAKAAKYGAA 13
 |||||
 DB 560 ALAAAKAAKYGAA 572

RESULT 13
 AAB08630
 ID AAB08630 standard; peptide; 712 AA.
 XX
 AC AAB08630;
 XX
 DT 20-DEC-2000 (first entry)
 XX
 DE Amino acid sequence of a human elastin polypeptide.
 XX
 KW Tropoelastin; elastin; elastic fibre; smooth muscle cell proliferation;
 KW smooth muscle cell differentiation; smooth muscle cell migration;
 KW smooth muscle cell function; atherosclerosis; restenosis; aneurysm;
 KW vascular bypass graft stenosis; transplant arteriopathy; dissection;
 KW SVAS; hypertension; transplant arteriopathy.
 XX
 OS Homo sapiens.
 XX
 PN WO2000050068-A2.
 XX
 PD 31-AUG-2000.
 XX
 PF 28-FEB-2000; 2000WO-US002526.
 XX
 PR 26-FEB-1999; 99US-00258217.
 XX
 PA (UTAH) UNIV UTAH RES FOUND.
 XX
 PI Keating MT, Li DY;
 XX
 DR WPI; 2000-533134/48.
 XX
 PT Elastin based compositions useful for treating atherosclerosis,
 PT restenosis, vascular bypass graft stenosis, transplant arteriopathy,
 PT aneurysm, dissection SVAS and/or hypertension.
 XX
 PS Example 3; Page 46; 79pp; English.
 XX

The present sequence represents a human elastin. Peptides derived from
 CC elastin are used in compositions of the invention. The specification
 CC describes elastin based compositions that are potent regulators of smooth
 CC muscle cell proliferation, differentiation and migration in vivo. The
 CC elastin-based compositions comprise at least one elastic fibre, elastins,
 CC tropoelastins (or fragments of them) which have biological activities
 CC comprising: inhibiting the proliferation of smooth muscle cells in vivo;
 CC stimulating the differentiation of smooth muscle cells in vivo;
 CC regulating the migration of smooth muscle cells in vivo; and
 CC may be used for the prophylaxis or treatment of a disorder characterized
 CC by diminished capacity to regulate smooth muscle cell function such as
 CC atherosclerosis, restenosis, vascular bypass graft stenosis, transplant
 CC arteriopathy, aneurysm and/or dissection. Disorders which may be treated
 CC also include SVAS (undefined), hypertension, and transplant arteriopathy
 XX
 SQ Sequence 712 AA;

Query Match 100.0%; Score 59; DB 3; Length 712;
 Best Local Similarity 100.0%; Pred. No. 0.093;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAYGAA 13
 |||||
 DB 592 ALAAAKAAYGAA 604

RESULT 14
 AAW46315
 ID AAW46315 standard; protein; 730 AA.
 XX
 AC AAW46315;
 XX
 DT 23-JUL-1998 (first entry)
 XX
 DE Human elastin containing non-natural polypeptide MFU-1 sequence.
 XX
 KW MFU-1; minimal functional unit; elastin; human; fibrous protein;
 KW beta-sheet; coating; wound dressing.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Protein 374..499
 FT /note= "MFU-1 polypeptide"
 XX
 PN WO9805685-A2.
 XX
 PD 12-FEB-1998.
 XX
 PE 07-AUG-1997; 97WO-CA000560.
 XX
 PR 07-AUG-1996; 96US-0023552P.
 PR 07-AUG-1997; 97US-00911364.
 XX
 PA (PROT-) PROTEIN SPECIALTIES LTD.
 PA (HOSP-) HOSPITAL FOR SICK CHILDREN.
 XX
 PI Rothstein A, Keeley FW, Rothstein SJ;
 XX
 PF MPI; 1998-145551/13.
 XX
 PT New non-natural polypeptide with multiple beta-sheet, beta-turn
 PT structures - particularly based on human elastin, useful for coating
 PT prostheses, as wound dressings, etc., allows ingrowth of cells.
 XX
 PS Claim 5; Fig 1B; 39pp; English.
 XX

This represents the human elastin sequence containing the minimal
 functional unit (MFU)-1 polypeptide of the invention. This MFU-1 is a
 polypeptide that has at least 3 beta-sheet/ beta-turn structures, but is
 not a naturally occurring fibrous protein. Each beta-sheet structure has
 3-7 (preferably 5-7) amino acids and the MFU polypeptide may include at
 least 1 amino acid that can take part in crosslinking. The polypeptide
 can also be derived from the sequences of animal elastin, lamprin and
 spider silk protein. The MFU polypeptides are self-aligning peptides
 having the same primary structure as part of a natural fibrous protein.
 They are used to coat prostheses made of animal or synthetic material or
 metal, particularly for use as blood vessel or heart valve replacements,
 wound or burn dressings, or stents. They can be used in cosmetic, elastic
 or high-tensile strength materials, e.g. ropes or parachute cord,
 prostheses based on the MFU allow penetration of endothelial cells, so
 become permanent, living, tissue replacements. The MFU polypeptides have
 better biocompatibility than known elastin-based materials. They are well
 defined, homogeneous material and are easier to manipulate and produce
 than full-length elastins. They are non-thrombogenic and non-immunogenic.
 Materials can be made from 2 or more different MFU polypeptides to allow
 properties to be tailored for particular applications, e.g. combining the
 high extensibility of elastin and the high tensile strength of spider
 silk protein

Query Match 100.0%; Score 59; DB 3; Length 730;
 Best Local Similarity 100.0%; Pred. No. 0.095;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAYGAA 13
 |||||
 DB 593 ALAAAKAAYGAA 605

RESULT 15
 AAB08631
 ID AAB08631 standard; peptide; 730 AA.
 XX
 AC AAB08631;
 XX
 DT 20-DEC-2000 (first entry)
 XX
 DE Fusion protein comprising human elastin and c-myc.
 XX
 KW Tropoelastin; elastin; elastic fibre; smooth muscle cell proliferation;
 KW smooth muscle cell differentiation; smooth muscle cell migration;
 KW smooth muscle cell function; atherosclerosis; restenosis; aneurysm;
 KW vascular bypass graft stenosis; transplant arteriopathy; dissection;
 KW SVAS; hypertension; transplant arteriopathy.
 XX
 OS Synthetic.
 OS Homo sapiens.
 OS Unidentified.
 XX
 PN WO200050068-A2.
 XX
 PD 31-AUG-2000.
 XX
 PR 28-FEB-2000; 2000WO-US002526.
 XX
 PR 26-FEB-1999; 99US-00258217.
 XX
 PA (UTAH) UNIV UTAH RES FOUND.
 XX
 PI Keating MT, Li DY;
 XX
 PF MPI; 2000-533134/48.
 XX
 PT Elastin based compositions useful for treating atherosclerosis,
 PT restenosis, vascular bypass graft stenosis, transplant arteriopathy,
 PT aneurysm, dissection SVAS and/or hypertension.
 XX
 PS Example 3; Page 48; 79pp; English.
 XX

The present sequence represents a fusion protein, comprising human
 elastin and c-myc, preceded by a His tag. The protein is used in
 compositions of the invention. The specification describes elastin based
 compositions that are potent regulators of smooth muscle cell
 proliferation, differentiation and migration in vivo. The elastin-based
 compositions comprise at least one elastic fibre, elastins, tropoelastins
 (or fragments of them) which have biological activities comprising:
 inhibiting the proliferation of smooth muscle cells in vivo; stimulating
 the differentiation of smooth muscle cell in vivo; and regulating the
 migration of smooth muscle cells in vivo. The compositions may be used
 for the prophylaxis or treatment of a disorder characterized by
 diminished capacity to regulate smooth muscle cell function such as
 atherosclerosis, restenosis, vascular bypass graft stenosis, transplant
 arteriopathy, aneurysm and/or dissection. Disorders which may be treated
 also include SVAS (undefined), hypertension, and transplant arteriopathy

QY 1 ALAAAKAAKYGAA 13
 Db 601 ALAAAKAAKYGAA 613

RESULT 16
 AAO17360
 ID AAO17360 standard; protein; 730 AA.
 AC AAO17360;
 XX
 DT 19-JUL-2002 (first entry)
 XX
 DE Human elastin.
 XX
 KW Human; endometriosis; DNA chip; fibronectin; p27; reticulocalbin;
 KW aldehyde dehydrogenase 6; gravin; phospholipase C epsilon; elastin;
 KW insulin-like growth factor binding protein-2; alpha-2 type IV collagen;
 KW transmembrane receptor PK7; collagen type XVIII alpha 1;
 KW platelet derived growth factor receptor alpha; laminin M chain;
 KW subtilisin like protein PACE4; nidogen.
 XX
 OS Homo sapiens.
 XX
 PN EP1191107-A2.
 XX
 PD 27-MAR-2002.
 XX
 PF 21-AUG-2001; 2001EP-00250300.
 XX
 PR 25-SEP-2000; 2000DE-01048633.
 XX
 PA (SCHD) SCHERING AG.
 XX
 PI Hess-Stumpp H, Haendler B, Kraetzschmar J, Kreft B, Winterhager E;
 PI Regidor P, Scotti S;
 XX
 DR WPI; 2002-317413/36.
 XX
 PT In vitro diagnosis and monitoring of endometriosis, comprises detecting
 PT reduced expression of specific gene products, e.g. from the fibronectin
 PT gene.
 XX
 PS Claim 1; Page 15-16; 21pp; German.
 XX
 CC The present invention relates to a method for the in vitro diagnosis of
 CC endometriosis by determining the amount of gene product from at least one
 CC specific gene in a patient sample and comparing this with the amount of
 CC gene product in a control sample. A reduced level is indicative of
 CC endometriosis. The gene products may be fibronectin, p27, reticulocalbin,
 CC aldehyde dehydrogenase 6, gravin, phospholipase C epsilon, elastin,
 CC insulin-like growth factor binding protein-2, alpha-2 type IV collagen,
 CC transmembrane receptor PK7, collagen type XVIII alpha 1, platelet
 CC derived growth factor receptor alpha, laminin M chain, subtilisin like
 CC protein PACE4 or nidogen. The method is useful for initial diagnosis of
 CC endometriosis, and also for monitoring progress and treatment of the
 CC disease. The present sequence is human elastin
 XX
 SQ Sequence 730 AA;
 Query Match 100.0%; Score 59; DB 5; Length 730;
 Best Local Similarity 100.0%; Pred. No. 0.095;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGAA 13
 Db 592 ALAAAKAAKYGAA 604

RESULT 17
 ADQ19747
 ID ADQ19747 standard; protein; 730 AA.

XX ADQ19747;
 AC
 XX
 DT 26-AUG-2004 (first entry)
 XX
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2566.
 XX
 KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2004048938-A2.
 XX
 PD 10-JUN-2004.
 XX
 PF 26-NOV-2003; 2003WO-US038193.
 XX
 PR 26-NOV-2002; 2002US-0429739P.
 XX
 PA (PROT-) PROTEIN DESIGN LABS INC.
 XX
 PI Aziz N, Ginsburg WM, Zlotnik A;
 XX
 DR WPI; 2004-441208/41.
 XX
 PT Early detection of soft tissue sarcoma comprises determining expression
 PT of a gene in a first soft tissue sample and a normal soft tissue sample
 PT and comparing the gene expression, also useful in treating soft tissue
 PT sarcoma.
 XX
 PS Example 2; SEQ ID NO 2566; 210pp; English.
 XX
 CC The invention relates to a novel method for detecting soft tissue sarcoma
 CC which comprises obtaining a first soft tissue sample from an individual
 CC and a normal soft tissue sample from the same or different individual,
 CC determining the expression of a gene in both samples and comparing the
 CC expression of the gene in both soft tissue samples, where a higher level
 CC of protein expression in the first soft tissue sample indicates the
 CC presence of soft tissue sarcoma. The method of the invention has
 CC cytostatic applications and may be useful for detecting soft tissue
 CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
 CC acid sequences may be useful in diagnostic and screening applications.
 CC The current sequence is that of a human soft tissue sarcoma-upregulated
 CC protein of the invention. The current sequence is not shown within the
 CC specification per se but was submitted in CD format by the inventor.
 XX
 SQ Sequence 730 AA;
 Query Match 100.0%; Score 59; DB 8; Length 730;
 Best Local Similarity 100.0%; Pred. No. 0.095;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGAA 13
 Db 592 ALAAAKAAKYGAA 604

RESULT 18
 AAY69068
 ID AAY69068 standard; protein; 731 AA.
 XX
 AC AAY69068;
 XX
 DT 30-MAY-2000 (first entry)
 XX
 DE Amino acid sequence of a human tropoelastin splice form.
 XX
 KW Tropoelastin; derivative; proteolysis; protease; antiwrinkle;
 KW hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;
 KW peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.
 XX
 OS Homo sapiens.
 XX

PT characterized by three beta-sheet/beta-turn structures, and is not a
 XX naturally occurring fibrous protein.

XX Claim 1; Fig 1B; 21pp; English.

XX The invention describes a polypeptide (I) comprising a minimal
 CC functioning unit (MFU) which is present in the sequence of human elastin
 CC and comprised of at least three beta-sheet/beta-turn structures, and at
 CC least one amino acid residue that participates in cross-linking, and not
 CC a naturally occurring fibrous protein. The MFU material can be used to
 CC construct human elastin-like prostheses such as tubes for blood vessel
 CC replacement, heart replacement valves and sheets for other uses such as
 CC burns or wounds to promote healing. MFUs can be co-aggregated with other
 CC proteins, for e.g. collagen, to provide prostheses material that
 CC resembles the natural structural materials of the body. MFUs modeled on
 CC lamprin and other fibrous proteins e.g. spider silk, can be used to make
 CC a variety of materials, for a number of different applications, for e.g.
 CC in cords and ropes for use in parachutes and in cosmetics. Coating
 CC synthetic prostheses with MFUs modeled on human elastin significantly
 CC inhibits platelet binding and activation. The human-like MFU material is
 CC more biocompatible than other elastin-containing materials. In contrast
 CC to solubilised fragments of elastin used before, an MFU is a single
 CC peptide of defined composition. The MFU is considerably smaller than the
 CC parent protein, simpler in structure, easier to produce or express in
 CC quantity, to handle in solution and to manipulate for experimental and
 CC practical purposes. Like other elastin preparations, the MFU is non-
 CC thrombogenic and provides a friendly environment for cell infiltration.
 CC Being composed entirely of a human elastin sequence, MFU is non-
 CC immunogenic, thus providing a truly biocompatible material. MFUs modeled
 CC on lamprin and other fibrous proteins can be used to make a variety of
 CC materials having high tensile strength, elasticity and plasticity of
 CC their parent proteins. This is the amino acid sequence of mature human
 CC elastin on which the MFU peptides of the invention are based
 XX

SQ Sequence 731 AA;

Query Match 100.0%; Score 59; DB 6; Length 731;
 Best Local Similarity 100.0%; Pred. No. 0.096;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAAKAAKYGAA 13
 |||||
 Db 593 ALAAAKAAKYGAA 605

RESULT 21
 ADL96420

ID ADL96420 standard; protein; 731 AA.

XX AC ADL96420;

XX 20-MAY-2004 (first entry)

XX Human elastin protein fragment.

XX fibrous protein; prosthesis; elastin; lamprin; spider silk protein;
 XX blood vessel; wound; burn healing; collagen.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Region 19..160

FT /note= "region specifically claimed in claim 6"

FT Region 188..367

FT /note= "region specifically claimed in claim 6"

FT Region 374..499

FT /note= "region specifically claimed in claim 6"

FT Region 607..717

FT /note= "region specifically claimed in claim 6"

XX US2003166846-A1.

XX 04-SEP-2003.

XX 28-SEP-2001; 2001US-00964662.

XX 07-AUG-1996; 96US-0023522P.

XX 29-JUN-1999; 99US-00340736.

XX (ROTH/) ROTHSTEIN A.

XX (KEEL/) KEELEY F.

XX (ROTH/) ROTHSTEIN S.

XX ROTHSTEIN A, Keeley F, Rothstein S;

XX WPI; 2003-898105/82.

XX Polypeptide for constructing human elastin-like prostheses such as tubes

XX for blood vessel replacement and sheets for other uses such as wound or

XX burn healing, comprises three beta sheets and three beta turns.

XX Claim 5; Fig 1B; 17pp; English.

XX This invention describes a polypeptide that comprises three beta

XX sheet/beta turn structures and that is not a naturally occurring fibrous

XX protein. The invention also describes a prosthesis comprising an animal,

XX metal or synthetic material, where the surface is coated with the

XX polypeptide, a cosmetic material comprising the polypeptide, an elastic

XX material comprising the polypeptide, a high tensile strength material

XX comprising the polypeptide, a material comprising two or more

XX polypeptides selected from (a) a polypeptide consisting essentially of a

XX portion of the polypeptide comprising at least three beta sheet/beta turn

XX structures, (b) a polypeptide consisting essentially of a portion of the

XX amino acid sequence of an animal elastin comprising at least three beta

XX sheets/beta turns, (c) a polypeptide consisting essentially of a portion

XX of lamprin comprising at least three beta sheets/beta turns, and (d) a

XX polypeptide consisting essentially of a spider silk protein comprising at

XX least three beta sheets/beta turns, a polypeptide having the primary

XX structure of a portion of a naturally occurring fibrous protein and a

XX secondary structure comprising at least three beta sheets/beta turns,

XX where each of the beta sheet/beta turn structures comprises from 3 to

XX about 7 amino acids and the polypeptide is not a naturally occurring

XX fibrous protein. The minimal functional unit (MFU) of the invention is

XX useful to construct human elastin-like prostheses such as tubes for blood

XX vessel replacement and sheets for other uses such as wound or burn

XX healing. Alternatively the MFU can be co-aggregated with other proteins,

XX for example collagen, to provide prostheses material that resembles the

XX natural structural materials of the body. The MFU based material is

XX subject to infiltration of cells growing in the patient, including

XX endothelial cells, and the prosthesis can become a permanent living

XX tissue replacement. The material is more biocompatible than other elastin

XX -containing materials proposed for prostheses.

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PT New derivatives of human tropoelastin - with elastin-like or
PT macromolecular binding properties, useful e.g. as surgical implants.
PS
PS Disclosure; Fig 1; 82pp; English.
XX
XX The invention relates to a derivative or variant of human tropoelastin
CC (hTE) having elastin-like and/or macromolecule (specifically
CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors
CC comprising the nucleic acids encoding the variants or derivatives are
CC used to produce the proteins recombinantly. The tropoelastin derivatives
CC or hybrid proteins containing the derivatives are useful in medical,
CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
CC wrinkle or hand lotions, also as surgical implants, foods and industrial
CC products. The hybrid protein have controllable GAG-binding properties,
CC depending on presence or absence of a specific fragment, designated
CC peptide 26A, from hTE. The present sequence represents the amino acid
CC sequence of the synthetic human tropoelastin SHEL
XX
XX Sequence 733 AA;
SQ
Query Match 100.0%; Score 59; DB 2; Length 733;
Best Local Similarity 100.0%; Pred. No. 0.096;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ALAAAKAAKYGAA 13
Db 595 ALAAAKAAKYGAA 607
|||||
RESULT 24
ABG75223
ID ABG75223 standard; protein; 757 AA.
XX
XX AC ABG75223;
XX
XX DT 12-FEB-2004 (first entry)
XX
XX DE Human tropoelastin protein.
XX
XX Human; tropoelastin; elastin; body vessel occlusion; stenosis;
KW vascular smooth muscle cell; elastin signaling; vasotrophic.
XX
XX OS Homo sapiens.
XX
XX PN WO2003082203-A2.
XX
XX PD 09-OCT-2003.
XX
XX PF 27-MAR-2003; 2003WO-US009391.
XX
XX PR 27-MAR-2002; 2002US-0368084P.
XX
XX PA (UTAH) UNIV UTAH RES FOUND.
XX
XX PI Li DY, Karnik S;
XX
XX FI WPI; 2003-833516/77.
XX
XX Use of an agent that promotes elastin signaling in smooth muscle cells
PT for e.g. decreasing or preventing occlusion of a body vessel by smooth
PT muscle cells, treating or preventing obstructive vascular disease, or
PT preventing stenosis.
XX
XX Claim 24; Page 138-141; Opp; English.
XX
XX The present invention relates to the use of an agent that promotes
CC elastin signaling in smooth muscle cells for decreasing or preventing
CC occlusion of a body vessel by smooth muscle cells, decreasing vascular
CC obstruction, promoting actin stress fiber formation or actin
CC polymerisation, increasing F-actin ratio in a smooth muscle cell,
CC treating or preventing obstructive vascular disease (e.g. restenosis), or
CC preventing stenosis. The agent that promotes elastin signaling in smooth
CC muscle cells is useful for decreasing or preventing occlusion of a body

CC vessel by smooth muscle cells, decreasing vascular obstruction, promoting
 CC actin stress fiber formation or actin polymerization, increasing F- α
 CC actin ratio in a smooth muscle cell, treating or preventing obstructive
 CC vascular disease (e.g. restenosis following angioplasty), or preventing
 CC stenosis. It is also useful in manufacturing a medicament for the
 CC treatment or prevention of occlusion of a vessel. The present sequence is
 CC the human tropoelastin protein as shown in the exemplification of the
 CC invention

XX Sequence 757 AA;

Query Match 100.0%; Score 59; DB 7; Length 757;
 Best Local Similarity 100.0%; Pred. No. 0.099;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAAAKAAKYGAA 13
 |||||
 Db 619 ALAAAKAAKYGAA 631

RESULT 25
 ADP65160
 ID ADP65160 standard; protein; 757 AA.

XX ADP65160;

XX 12-AUG-2004 (first entry)

XX Human elastin.

XX autoimmune disease; arthritis; gene expression analysis;
 KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
 KW antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;
 KW immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;
 KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
 KW immune; human.

XX Homo sapiens.

XX WO2003072827-A1.

PD 04-SEP-2003.

PF 31-OCT-2002; 2002WO-US035433.

XX 31-OCT-2001; 2001US-0336220P.

XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

XX Hirsch R, Thorton SL;

XX WPI; 2003-712740/67.

XX GENBANK; NP_000492.

XX Diagnosing and analyzing autoimmune disease using gene expression
 PT profiles and microarray technology, useful for diagnosing and treating
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
 PT gout.

XX Disclosure; Page; 56pp; English.

XX The invention relates to a novel method for diagnosing and analysing a
 CC autoimmune disease or arthritis. The method comprises obtaining a
 CC patient sample containing mRNA, analysing gene expression using the mRNA
 CC that results in a gene expression signature of the mRNA, and using that
 CC gene expression signature to diagnose or analyse the autoimmune disease
 CC or arthritis in the patient, where gene expression of at least 60% of
 CC the genes correlates with that of the gene signature. The invention
 CC further comprises: a treatment of rheumatoid arthritis; identification of
 CC genes for targeting in the treatment of rheumatoid arthritis in a mammal
 CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
 CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
 CC analyses of autoimmune disease or rheumatoid arthritis; screening the

CC efficacy of a candidate drug in vitro for the treatment of collagen-
 CC induced arthritis; and reducing the symptoms associated with collagen-
 CC induced arthritis. The compositions of the invention have the following
 CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
 CC antigout, antiinflammatory, dermatological, and immunomodulatory. The
 CC methods and compositions of the present invention are useful for
 CC diagnosing and treating autoimmune disease or arthritis, such as
 CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
 CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
 CC immune disease caused by an infectious agent. This sequence represents a
 CC protein sequence relating to the genes used in the analysis and treatment
 CC of autoimmune diseases or arthritis. Note: This sequence is not shown
 CC in the specification. It has been supplied in an electronic format from
 CC WIFO.

XX Sequence 757 AA;

Query Match 100.0%; Score 59; DB 7; Length 757;
 Best Local Similarity 100.0%; Pred. No. 0.099;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALAAAKAAKYGAA 13
 |||||
 Db 619 ALAAAKAAKYGAA 631

RESULT 26

ADE40132
 ID ADE40132 standard; protein; 711 AA.

XX ADE40132;

XX 29-JAN-2004 (first entry)

XX Human NOV16a protein - SEQ ID 38.

XX NOVX; cardiac; antiarteriosclerotic; hypotensive; cytostatic; anorectic;
 KW antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic;
 KW antiparkinsonian; antiasthmatic; gynaecological; cardiomyopathy;
 KW atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;
 KW multiple sclerosis; graft-versus-host disease; Alzheimer's; Parkinson's;
 KW asthma; fertility disorder; vaccine; gene therapy; chromosome mapping;
 KW tissue typing; human; NOV.

XX Homo sapiens.

XX WO2003064589-A2.

XX 07-AUG-2003.

XX 02-AUG-2002; 2002WO-US024483.

XX 02-AUG-2001; 2001US-0309501P.

XX 03-AUG-2001; 2001US-0310291P.

XX 07-AUG-2001; 2001US-0310544P.

XX 08-AUG-2001; 2001US-0310951P.

XX 09-AUG-2001; 2001US-0311292P.

XX 13-AUG-2001; 2001US-0311979P.

XX 16-AUG-2001; 2001US-0312892P.

XX 17-AUG-2001; 2001US-0313201P.

XX 17-AUG-2001; 2001US-0313415P.

XX 20-AUG-2001; 2001US-0313643P.

XX 20-AUG-2001; 2001US-0313702P.

XX 21-AUG-2001; 2001US-0314031P.

XX 23-AUG-2001; 2001US-0314466P.

XX 28-AUG-2001; 2001US-0315403P.

XX 29-AUG-2001; 2001US-0315853P.

XX 17-SEP-2001; 2001US-0322716P.

XX 21-SEP-2001; 2001US-0323994P.

XX 14-DEC-2001; 2001US-0340233P.

XX 05-FEB-2002; 2002US-0354591P.

XX 19-MAR-2002; 2002US-0365478P.

XX 19-APR-2002; 2002US-0373814P.

PR 19-APR-2002; 2002US-0373825P.
 PR 19-APR-2002; 2002US-0373989P.
 PR 23-APR-2002; 2002US-0374632P.
 PR 07-JUN-2002; 2002US-0386971P.
 PR 01-AUG-2002; 2002US-00210172.
 PR (CURA-) CURAGEN CORP.
 XX Kekuda R, Miller CB, Patturajan M, Pena CEA, Rieger DK;
 PI Shimkets RA, Zerhusen BD, Li L, Ji W, Padigar M, Casman SJ;
 PI Voss EZ, Boldog FL, Gorman L, Leite MW, Vernet CM, Anderson DW;
 PI Guo X, Zhong M, Gerlach VL, Hjal T, Rastelli L, Spytek KA;
 PI Edinger SR, Ellerman K, Malyankar UM, Macdougall JB, Stone DJ;
 PI Alsebrook JP, Lepley DW, Burgess CE, Majumder K, Wolenc AR;
 PI Smithson G;
 XX WPI; 2003-663472/62.
 DR N-PSDB; ADE40131.
 DR New NOVX polypeptides and nucleic acids, useful for preventing or
 PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
 PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.
 XX Claim 1; SEQ ID NO 38; 560pp; English.
 XX The invention relates to a novel NOVX polypeptide. The polypeptide of the
 CC invention demonstrates cardiac, antiarteriosclerotic, hypotensive,
 CC cytotatic, anorectic, antidiabetic, immunosuppressive, anti-HIV,
 CC neuroprotective, nootropic, antiparkinsonian, antiasthmatic and
 CC gynaecological activities and may be useful in diagnosing, treating or
 CC preventing NOVX-associated disorders including cardiomyopathy,
 CC atherosclerosis, hypertension, cancer, obesity, diabetes, AIDS, multiple
 CC sclerosis, graft-versus-host disease, Alzheimer's disease, Parkinson's
 CC disease, asthma or fertility disorders. Furthermore, the polypeptides may
 CC be utilised as vaccines whilst the nucleic acids may be used as
 CC hybridisation probes, in gene therapy, chromosome mapping, tissue typing,
 CC preventive medicine and pharmacogenomics. The current sequence is that of
 CC the human NOV protein of the invention.
 XX
 SQ Sequence 711 AA;
 Query Match 94.9%; Score 56; DB 7; Length 711;
 Best Local Similarity 92.3%; Pred. No. 0.31;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAAAKAAKYGAA 13
 DB 591 ALAAAKAAKYGAA 603
 RESULT 27
 ID AAY69144
 AC AAY69144 standard; peptide; 12 AA.
 XX AAY69144;
 XX 30-MAY-2000 (first entry)
 DE Peptidomimetic of a cleavage site of a human tropoelastin.
 DE
 DE Tropoelastin; derivative; proteolysis; protease; antiwrinkle;
 KW hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;
 KW peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.
 XX
 OS Homo sapiens.
 XX WO200004043-A1.
 XX 27-JAN-2000.
 XX 19-JUL-1999; 99WO-AU000580.
 XX Weiss AS;
 PI

PR 17-JUL-1998; 98AU-00004723.
 XX (UNSY) UNIV SYDNEY.
 PA Weiss AS;
 PI WPI; 2000-182399/16.
 DR
 XX New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
 PT cell growth.
 PT Claim 76; Page 73; 136pp; English.
 XX The present sequence represents a peptidomimetic of a cleavage site of a
 CC human tropoelastin. The specification describes human tropoelastin
 CC derivatives, in which a subsequence has been mutated so that
 CC susceptibility to proteolysis is reduced or eliminated, or a subsequence
 CC has been inserted so that susceptibility to proteolysis is increased. The
 CC derivatives have with reduced susceptibility, and can be used where the
 CC wild-type protein would be degraded too easily, e.g. in contact with
 CC serum or wound exudate. The tropoelastin derivatives provide competitive
 CC inhibition of protease activity. The tropoelastin derivatives, and other
 CC polypeptides containing tropoelastin derivative-derived protease-
 CC susceptibility sites, are useful in human or veterinary medicine,
 CC cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents and for
 CC inducing chemotaxis. They are also useful for proliferation or growth
 CC inhibition, particularly of smooth muscle cells, epithelial or
 CC endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets.
 CC Peptidomimetics that mimic the protease cleavage site in tropoelastin
 CC derivatives are competitive inhibitors of the protease, and are used for
 CC protecting against lung damage caused by elastin, for inhibiting or
 CC controlling localized growth of cancers or metastases, or to limit
 CC protease activity that causes blood clotting
 XX
 SQ Sequence 12 AA;
 Query Match 93.2%; Score 55; DB 3; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0065;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LAARAKAAKYGAA 13
 DB 1 LAARAKAAKYGAA 12
 RESULT 28
 ID AAY01303 standard; protein; 660 AA.
 XX AAY01303;
 AC AAY01303;
 XX 07-JUN-1999 (first entry)
 DE Human tropoelastin derivative SHELDeltamodified.
 DE
 DE Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;
 KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
 KW hand lotion; surgical implant; industrial product; human; SHEL.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX WO9903885-A1.
 XX 28-JAN-1999.
 XX 17-JUL-1998; 98WO-AU000564.
 XX 18-JUL-1997; 97AU-00008117.
 XX (UNSY) UNIV SYDNEY.
 XX Weiss AS;
 PI

XX WPI; 1999-132162/11.
 DR N-PSDB; AAX27705.
 XX
 PT New derivatives of human tropoelastin - with elastin-like or
 PT macromolecular binding properties, useful e.g. as surgical implants.
 PS Claim 7; Fig 3; 82pp; English.
 XX
 CC The invention relates to a derivative or variant of human tropoelastin
 CC (hTE) having elastin-like and/or macromolecule (specifically
 CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors
 CC comprising the nucleic acids encoding the variants or derivatives are
 CC used to produce the proteins recombinantly. The tropoelastin derivatives
 CC or hybrid proteins containing the derivatives are useful in medical,
 CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
 CC wrinkle or hand lotions, also as surgical implants, foods and industrial
 CC products. The hybrid protein have controllable GAG-binding properties,
 CC depending on presence or absence of a specific fragment, designated
 CC peptide 26A, from hTE. The present sequence represents a human
 CC tropoelastin derivative SHELDeltamodified
 XX
 SQ Sequence 660 AA;
 Query Match 93.2%; Score 55; DB 2; Length 660;
 Best Local Similarity 100.0%; Pred. No. 0.43;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALAAAKAAKYGA 12
 Db 523 ALAAAKAAKYGA 534
 RESULT 29
 AAY69135
 ID AAY69135 standard; protein; 515 AA.
 AC AAY69135;
 XX
 DT 30-MAY-2000 (first entry)
 XX
 DE Amino acid sequence of a human tropoelastin derivative.
 XX
 KW Tropoelastin; derivative; proteolysis; protease; antiwrinkle;
 KW hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;
 KW peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.
 XX
 OS Homo sapiens.
 XX
 XN WO200004043-A1.
 XX
 PD 27-JAN-2000.
 XX
 PF 19-JUL-1999; 99WO-AU0000580.
 XX
 PR 17-JUL-1998; 98AU-00004723.
 XX
 PA (UNSY) UNIV SYDNEY.
 XX
 PI Weiss AS;
 XX
 DR WPI; 2000-182399/16.
 XX
 PT New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
 PT cell growth.
 PS Disclosure; Page 131-133; 136pp; English.
 XX
 CC The present sequence represents a human tropoelastin derivative, which is
 CC representative of tropoelastin derivatives of the invention. In the
 CC tropoelastin derivatives of the invention a subsequence has been mutated
 CC so that susceptibility to proteolysis is reduced or eliminated, or a
 CC subsequence has been inserted so that susceptibility to proteolysis is
 CC increased. The derivatives have with reduced susceptibility, and can be
 CC used where the wild-type protein would be degraded too easily, e.g. in
 CC contact with serum or wound exudate. The tropoelastin derivatives provide
 CC competitive inhibition of protease activity. The tropoelastin
 CC derivatives, and other polypeptides containing tropoelastin derivative-
 CC derived protease-susceptibility sites, are useful in human or veterinary

CC increased. The derivatives have with reduced susceptibility, and can be
 CC used where the wild-type protein would be degraded too easily, e.g. in
 CC contact with serum or wound exudate. The tropoelastin derivatives provide
 CC competitive inhibition of protease activity. The tropoelastin
 CC derivatives, and other polypeptides containing tropoelastin derivative-
 CC derived protease-susceptibility sites, are useful in human or veterinary
 CC medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents
 CC and for inducing chemotaxis. They are also useful for proliferation or
 CC growth inhibition, particularly of smooth muscle cells, epithelial or
 CC endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets.
 CC Peptidomimetics that mimic the protease cleavage site in tropoelastin
 CC derivatives are competitive inhibitors of the protease, and are used for
 CC protecting against lung damage caused by elastin, for inhibiting or
 CC controlling localized growth of cancers or metastases, or to limit
 CC protease activity that causes blood clotting
 XX
 SQ Sequence 515 AA;
 Query Match 91.5%; Score 54; DB 3; Length 515;
 Best Local Similarity 92.3%; Pred. No. 0.49;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ALAAAKAAKYGA 13
 Db 281 ALAAAKAAKYGA 293
 RESULT 30
 AAY69071
 ID AAY69071 standard; protein; 571 AA.
 XX
 AC AAY69071;
 XX
 DT 30-MAY-2000 (first entry)
 XX
 DE Amino acid sequence of a human tropoelastin derivative.
 XX
 KW Tropoelastin; derivative; proteolysis; protease; antiwrinkle;
 KW hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;
 KW peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.
 XX
 OS Homo sapiens.
 XX
 XN WO200004043-A1.
 XX
 PD 27-JAN-2000.
 XX
 PF 19-JUL-1999; 99WO-AU0000580.
 XX
 PR 17-JUL-1998; 98AU-00004723.
 XX
 PA (UNSY) UNIV SYDNEY.
 XX
 PI Weiss AS;
 XX
 DR WPI; 2000-182399/16.
 XX
 PT New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
 PT cell growth.
 PS Disclosure; Page 115-117; 136pp; English.
 XX
 CC The present sequence represents a human tropoelastin derivative, which is
 CC representative of tropoelastin derivatives of the invention. In the
 CC tropoelastin derivatives of the invention a subsequence has been mutated
 CC so that susceptibility to proteolysis is reduced or eliminated, or a
 CC subsequence has been inserted so that susceptibility to proteolysis is
 CC increased. The derivatives have with reduced susceptibility, and can be
 CC used where the wild-type protein would be degraded too easily, e.g. in
 CC contact with serum or wound exudate. The tropoelastin derivatives provide
 CC competitive inhibition of protease activity. The tropoelastin
 CC derivatives, and other polypeptides containing tropoelastin derivative-
 CC derived protease-susceptibility sites, are useful in human or veterinary

CC medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents
CC and for inducing chemotaxis. They are also useful for proliferation or
CC growth inhibition, particularly of smooth muscle cells, epithelial or
CC endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets.
CC Peptidomimetics that mimic the protease cleavage site in tropoelastin
CC derivatives are competitive inhibitors of the protease, and are used for
CC protecting against lung damage caused by elastin, for inhibiting or
CC controlling localized growth of cancers or metastases, or to limit
CC protease activity that causes blood clotting

XX Sequence 571 AA;

SQ Query Match 91.5%; Score 54; DB 3; Length 571;
Best Local Similarity 92.3%; Pred. No. 0.55;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 ALAAKAAKYGAA 13
| | | | | | | | | |
Db 281 ALAAKAAKYGAA 293

Search completed: November 19, 2004, 16:28:39
Job time : 6.65677 secs

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OM protein - protein search, using sw model

Run on: November 19, 2004, 15:19:20 ; Search time 142.648 Seconds
(without alignments)
1755.321 Million cell updates/sec

Title: US-09-743-818A-5

Perfect score: 3615

Sequence: 1 GGVEGAIPGGVPGVFPFGA.....LSPIFGGACLGKACGRKRK 698

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: A_Geneseq_23Sep04.*

2: Geneseqpl1990s.*

3: Geneseqpl1990s.*

4: Geneseqpl2000s.*

5: Geneseqpl2000s.*

6: Geneseqpl2000s.*

7: Geneseqpl2000s.*

8: Geneseqpl2000s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Match	Length	ID	Description
1	3615	100.0	698	2	AA01302	Human tro
2	3615	100.0	698	3	AA01302	Human tro
3	3602	99.6	730	5	AA017360	Amino aci
4	3602	99.6	730	8	AD019747	Human ela
5	3588.5	99.3	731	3	AA019747	Human sof
6	3588.5	99.3	731	4	AA019747	Human sof
7	3588.5	99.3	733	2	AA019747	Human ela
8	3588.5	99.3	733	2	AA019747	Human ela
9	3588.5	99.3	757	7	ABG75223	Human tro
10	3588.5	99.3	757	7	ABG75223	Human tro
11	3580.5	99.0	731	7	AD196420	Human ela
12	3578.5	99.0	731	6	ABU08725	Human ela
13	3572	98.8	730	2	AA019747	Human ela
14	3486.5	96.4	711	7	AA019747	Human ela
15	3485	96.4	712	3	AA019747	Human ela
16	3485	96.4	730	3	AA019747	Human ela
17	3366	93.1	692	7	AA019747	Human ela
18	3248.5	89.9	660	2	AA019747	Human ela
19	3233.5	89.4	663	7	AD0303792	Human tro
20	3038	84.0	870	7	AD0303792	Human tro
21	2951.5	81.6	617	7	AD0303792	Human tro
22	2869	79.4	571	3	AA019747	Human ela
23	2680	74.1	515	3	AA019747	Human ela
24	2315.5	64.1	864	7	AA019747	Human ela
25	1679	46.4	472	4	AA019747	Human mem

26	1155	32.0	988	2	AA019747	Human ela
27	1155	32.0	988	5	AA019747	Human ela
28	1150.5	31.8	832	2	AA019747	Human ela
29	1150.5	31.8	832	5	AA019747	Human ela
30	1139.5	31.5	936	2	AA019747	Human ela
31	1139.5	31.5	936	5	AA019747	Human ela
32	1133	31.3	745	2	AA019747	Human ela
33	1131.5	31.3	1002	2	AA019747	Human ela
34	1131.5	31.3	1002	5	AA019747	Human ela
35	1131.5	31.3	1002	3	AA019747	Human ela
36	1131.5	31.3	1002	5	AA019747	Human ela
37	1131.5	31.3	1002	7	AA019747	Human ela
38	1129.5	31.2	1412	2	AA019747	Human ela
39	1129.5	31.2	1413	1	AA019747	Human ela
40	1129.5	31.2	1413	2	AA019747	Human ela
41	1129.5	31.2	1413	2	AA019747	Human ela
42	1129.5	31.2	1464	3	AA019747	Human ela
43	1129.5	31.2	1465	5	AA019747	Human ela
44	1129.5	31.2	1465	7	AA019747	Human ela
45	1127	31.2	768	2	AA019747	Human ela
46	1127	31.2	877	2	AA019747	Human ela
47	1127	31.2	877	2	AA019747	Human ela
48	1125.5	31.1	884	2	AA019747	Human ela
49	1125.5	31.1	884	2	AA019747	Human ela
50	1125.5	31.1	884	2	AA019747	Human ela
51	1125.5	31.1	884	2	AA019747	Human ela
52	1125.5	31.1	884	3	AA019747	Human ela
53	1125.5	31.1	884	3	AA019747	Human ela
54	1125.5	31.1	884	7	AA019747	Human ela
55	1122.5	31.1	1056	2	AA019747	Human ela
56	1122.5	31.1	1056	5	AA019747	Human ela
57	1115.5	30.9	768	5	AA019747	Human ela
58	1109.5	30.7	972	2	AA019747	Human ela
59	1109.5	30.7	972	2	AA019747	Human ela
60	1108.5	30.7	968	5	AA019747	Human ela
61	1108.5	30.7	2257	1	AA019747	Human ela
62	1108.5	30.7	2257	2	AA019747	Human ela
63	1108.5	30.7	2257	2	AA019747	Human ela
64	1108.5	30.7	2257	2	AA019747	Human ela
65	1108.5	30.7	2257	2	AA019747	Human ela
66	1108.5	30.7	2257	5	AA019747	Human ela
67	1108.5	30.7	2257	7	AA019747	Human ela
68	1093.5	30.2	936	2	AA019747	Human ela
69	1093.5	30.2	936	3	AA019747	Human ela
70	1093.5	30.2	936	3	AA019747	Human ela
71	1093.5	30.2	936	7	AA019747	Human ela
72	1093.5	30.2	937	2	AA019747	Human ela
73	1092	30.2	1040	5	AA019747	Human ela
74	1091.5	30.2	696	5	AA019747	Human ela
75	1091.5	30.2	696	5	AA019747	Human ela
76	1091.5	30.2	696	8	AA019747	Human ela
77	1082	29.9	768	5	AA019747	Human ela
78	1080	29.9	696	8	AA019747	Human ela
79	1080	29.9	1024	2	AA019747	Human ela
80	1080	29.9	1024	5	AA019747	Human ela
81	1074	29.7	2055	1	AA019747	Human ela
82	1074	29.7	2055	1	AA019747	Human ela
83	1074	29.7	2055	2	AA019747	Human ela
84	1074	29.7	2055	2	AA019747	Human ela
85	1074	29.7	2055	3	AA019747	Human ela
86	1074	29.7	2055	5	AA019747	Human ela
87	1074	29.7	2055	7	AA019747	Human ela
88	1048.5	29.0	966	2	AA019747	Human ela
89	1048.5	29.0	966	3	AA019747	Human ela
90	1048.5	29.0	966	5	AA019747	Human ela
91	1048.5	29.0	966	7	AA019747	Human ela
92	1021	28.2	780	8	AA019747	Human ela
93	1009.5	27.9	782	2	AA019747	Human ela
94	1009.5	27.9	782	2	AA019747	Human ela
95	1006.5	27.8	1085	5	AA019747	Human ela
96	1004.5	27.8	975	5	AA019747	Human ela
97	990	27.4	859	1	AA019747	Human ela
98	990	27.4	859	2	AA019747	Human ela

99 990 27.4 859 2 AAW26344 ELPI synt
100 990 27.4 859 2 AAW53520 Amino aci

ALIGNMENTS

RESULT 1
AA01302
ID AAY01302 standard; protein; 698 AA.
AC AAY01302;
XX 07-JUN-1999 (first entry)
XX Human tropoelastin variant SHELDelta26A.
XX Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;
KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
KW hand lotion; surgical implant; industrial product; human; SHEL; variant.
XX Homo sapiens.
OS Synthetic.
XX WO9903886-A1.
XX 28-JAN-1999.
XX 17-JUL-1998; 98WO-AU000564.
XX PR 18-JUL-1997; 97AU-00008117.
XX (UNSY) UNIV SYDNEY.
XX Weiss AS;
XX WPI; 1999-132162/11.
XX New derivatives of human tropoelastin - with elastin-like or
PT macromolecular binding properties, useful e.g. as surgical implants.
XX Claim 13; Fig 2; 82pp; English.
XX The invention relates to a derivative or variant of human tropoelastin
CC (hTE) having elastin-like and/or macromolecule (specifically
CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors
CC comprising the nucleic acids encoding the variants or derivatives are
CC used to produce the proteins recombinantly. The tropoelastin derivatives
CC or hybrid proteins containing the derivatives are useful in medical,
CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
CC wrinkle or hand lotions, also as surgical implants, foods and industrial
CC products. The hybrid protein have controllable GAG-binding properties,
CC depending on presence or absence of a specific fragment, designated
CC peptide 26A, from hTE. The present sequence represents the synthetic
CC human tropoelastin variant SHELDelta26A
XX
XX Sequence 698 AA;
Query Match 100.0%; Score 3615; DB 2; Length 698;
Best Local Similarity 100.0%; Pred. No. 6.8e-202;
Matches 698; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGVPGAIPGGVPGGVYPGAGLGGALGGKPLKVPVGGLAGAGLGAAGPAAVT 60
DB 1 GGVPGAIPGGVPGGVYPGAGLGGALGGKPLKVPVGGLAGAGLGAAGPAAVT 60
QY 61 FPGALVPGGVADAAAYKAAKAGAGLGGVPGVGGAGVAVVPPQPGAGVKGKVPVGVGL 120
DB 61 FPGALVPGGVADAAAYKAAKAGAGLGGVPGVGGAGVAVVPPQPGAGVKGKVPVGVGL 120
QY 121 PGVYPGGVLPGARFPFGVGLPGVPTGAGVKPKAPGVGGAFAGIPGVGPPGPGQVPLGY 180
DB 121 PGVYPGGVLPGARFPFGVGLPGVPTGAGVKPKAPGVGGAFAGIPGVGPPGPGQVPLGY 180

QY 181 PIKAPKLPGGVGLPYTTGKLPYGVGPGGVAGAAKAGYPTGTGTGVPQAAAAAKAAAKF 240
DB 181 PIKAPKLPGGVGLPYTTGKLPYGVGPGGVAGAAKAGYPTGTGTGVPQAAAAAKAAAKF 240
QY 241 GAGAAGVLPVGGAGVPGVPGAIPGIGIAGVGTTPAAAAAATAAATAAAGLPGG 300
DB 241 GAGAAGVLPVGGAGVPGVPGAIPGIGIAGVGTTPAAAAAATAAATAAAGLPGG 300
QY 301 PGFPGVGVPGAGVPGVPGAGIPVVPAGIPGAAPVGVVSPAAAAKAAKAYGAR 360
DB 301 PGFPGVGVPGAGVPGVPGAGIPVVPAGIPGAAPVGVVSPAAAAKAAKAYGAR 360
QY 361 PGVGGIPVTVGVGAGGPGFPGVGGIPGVAGVPSVGGVPGVPGVGTSPSAQAAAA 420
DB 361 PGVGGIPVTVGVGAGGPGFPGVGGIPGVAGVPSVGGVPGVPGVGTSPSAQAAAA 420
QY 421 AKAAKYGVGTTPAAAAAATAAATAAAGLPGVGGVAGVPGVPGVGTSPSAQAAAA 480
DB 421 AKAAKYGVGTTPAAAAAATAAATAAAGLPGVGGVAGVPGVPGVGTSPSAQAAAA 480
QY 481 VGVAPGVVAPGIPGPGVAAAAKAAKAAQVAAQVAAQVAAQVAAQVAAQVAAQVAA 540
DB 481 VGVAPGVVAPGIPGPGVAAAAKAAKAAQVAAQVAAQVAAQVAAQVAAQVAAQVAA 540
QY 541 GVPGLGVGAGVPGFAGVPGALAAAAKAAKAAQVAAQVAAQVAAQVAAQVAAQVAAQVAA 600
DB 541 GVPGLGVGAGVPGFAGVPGALAAAAKAAKAAQVAAQVAAQVAAQVAAQVAAQVAAQVAA 600
QY 601 AAAKAAKAAQVGLVGAAGLGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGV 660
DB 601 AAAKAAKAAQVGLVGAAGLGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGV 660
QY 661 GGAGQFPLGGVAAAPGGLSPFPGGACLGKACGRKRK 698
DB 661 GGAGQFPLGGVAAAPGGLSPFPGGACLGKACGRKRK 698

RESULT 2
AAY69069
ID AAY69069 standard; protein; 698 AA.
XX
XX AAY69069;
XX 30-MAY-2000 (first entry)
XX Amino acid sequence of a human reduced tropoelastin derivative.
XX Tropoelastin; derivative; SHEL-delta-26a; SHEL; proteolysis; protease;
KW antiwrinkle; hand lotion; bulking agent; chemotaxis; proliferation;
KW growth inhibition; peptidomimetic; lung damage; elastin; cancer;
KW metastasis; blood clotting.
XX Synthetic.
OS Homo sapiens.
XX WO200004043-A1.
XX 27-JAN-2000.
XX 19-JUL-1999; 99WO-AU000580.
XX 17-JUL-1998; 98AU-00004723.
XX (UNSY) UNIV SYDNEY.
XX Weiss AS;
XX WPI; 2000-182399/16.
XX N-PSDB; AAZ61144.
XX New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
PT cell growth.

D	b	601	AAAAAATAAAQAQFLVGAAGLGLGVGGLGVPGVGGLGGIPAPAAAATKAKYGAAGLGVL	600
Q	y	661	GGAGQFPLGGVAARPGELSPFFPGGACLGKACGRKK	698
D	b	661	GGAGQFPLGGVAARPGELSPFFPGGACLGKACGRKK	698
RESULT 3				
A	A	O17360		
I	D	AAO17360 standard; protein; 730 AA.		
X	X	AAO17360;		
X	X			
D	T	19-JUL-2002 (first entry)		
X	X	Human elastin.		
D	E			
X	X			
K	M	Human; endometriosis; DNA chip; fibronectin; p27; reticulocalbin;		
K	W	aldehyde dehydrogenase 6; gravin; phospholipase C epsilon; elastin;		
K	W	insulin-like growth factor binding protein-2; alpha-2 type IV collagen;		
K	W	transmembrane receptor PTK7; collagen type XVIII alpha 1;		
K	W	platelet derived growth factor receptor alpha; laminin M chain;		
K	W	subtilisin like protein PACE4; nidogen.		
X	X			
S	H	Homo sapiens.		
X	X			
P	N	EP1191107-A2.		
X	X			
P	D	27-MAR-2002.		
X	X			
F	F	21-AUG-2001; 2001EP-C0250300.		
X	X			
P	R	25-SEP-2000; 2000DE-01048633.		
X	X			
P	A	(SCHD) SCHERING AG.		
X	X			
P	I	Hess-Stumpp H, Haendler B, Kraetzschmar J, Kreft B, Winterhager E;		
P	I	Regidor P, Scotti S;		
D	R	WPI; 2002-317413/36.		
X	X			
P	T	In vitro diagnosis and monitoring of endometriosis, comprises detecting		
P	T	reduced expression of specific gene products, e.g. from the fibronectin		
P	T	gene.		
X	S	Claim 1; Page 15-16; 21pp; German.		
X	X			
C	C	The present invention relates to a method for the in vitro diagnosis of		
C	C	endometriosis by determining the amount of gene product from at least one		
C	C	specific gene in a patient sample and comparing this with the amount of		
C	C	gene product in a control sample. A reduced level is indicative of		
C	C	endometriosis. The gene products may be fibronectin, p27, reticulocalbin,		
C	C	aldehyde dehydrogenase 6, gravin, phospholipase C epsilon, elastin,		
C	C	insulin-like growth factor binding protein-2, alpha-2 type IV collagen,		
C	C	transmembrane receptor PTK7, collagen type XVIII alpha 1, platelet		
C	C	derived growth factor receptor alpha, laminin M chain, subtilisin like		
C	C	protein PACE4 or nidogen. The method is useful for initial diagnosis of		
C	C	endometriosis, and also for monitoring progress and treatment of the		
C	C	disease. The present sequence is human elastin		
X	X			
S	Q	Sequence 730 AA;		
Query Match 99.6%; Score 3602; DB 5; Length 730;				
Best Local Similarity 99.1%; Pred. No. 4e-201;				
Matches 698; Conservative 0; Mismatches 0; Indels 6; Gaps 1;				
Q	Y	1	GGVFPAIPGGVPGGVFPYCGAGLGGALGGGKPLKVPDGLAGAGLGGALGAFRAVT	60
D	b	27	GGVFPAIPGGVPGGVFPYCGAGLGGALGGGKPLKVPDGLAGAGLGGALGAFRAVT	86
Q	Y	61	PPGALVPGGVADAAAAYKAAGAAGILGGVPGVGGLGSAGAVVDPFGAGVKPKVPGVGL	120
b	b	87	PPGALVPGGVADAAAAYKAAGAAGILGGVPGVGGLGSAGAVVDPFGAGVKPKVPGVGL	145

121 PGVPGVLPQARPPGVGVLPVGTGACVVKPAPCVGAGAFAGIPGVPGPQGVPLGY 180
147 PGVPGVLPQARPPGVGVLPVGTGACVVKPAPCVGAGAFAGIPGVPGPQGVPLGY 206
181 PIKAPKLPGGVGLPYTTGKLPYGVGGVAGAGAGYPTGTGVPQAAAAAATAAKAF 240
207 PIKAPKLPGGVGLPYTTGKLPYGVGGVAGAGAGYPTGTGVPQAAAAAATAAKAF 266
241 GAGAAGVLPVGGAGVPGVPGAIPIGIGIAGVGTAAAAAATAAKAAGLVPGG 300
267 GAGAAGVLPVGGAGVPGVPGAIPIGIGIAGVGTAAAAAATAAKAAGLVPGG 326
301 PGFPGVGVPGVAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 360
327 PGFPGVGVPGVAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 386
361 PGVGVGGIPTYGVGAGGFPFGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGV 420
387 PGVGVGGIPTYGVGAGGFPFGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGV 446
421 AKAAYGVGTAAAAAATAAKAQAQF-----GLVPGVGVAPGVGVAPGVGVGLAPG 474
447 AKAAYGVGTAAAAAATAAKAQAQFALLNLNLAGLVPGVGVAPGVGVGVGLAPG 506
475 VGVAPGVGVAPGVGVAPGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGV 534
507 VGVAPGVGVAPGVGVAPGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGV 566
535 GLGVGAGVPGV 594
567 GLGVGAGVPGV 626
595 AGPAAAAAATAAKAQAQFGLVGAAGLVGGVGGVGGVGGVGGVGGVGGVGGVGG 654
627 AGPAAAAAATAAKAQAQFGLVGAAGLVGGVGGVGGVGGVGGVGGVGGVGGVGG 686
655 GLGVGAGGAGFPFLGGVAAAPFGVGLSPIPPGGACLGKACGRKK 698
687 GLGVGAGGAGFPFLGGVAAAPFGVGLSPIPPGGACLGKACGRKK 730

RESULT 4

ADQ19747
ID ADQ19747 standard; protein; 730 AA.
XX AC ADQ19747;
XX DT 26-AUG-2004 (first entry)
XX DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2566.
XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
XX KW Homo sapiens.
XX OS WO2004048938-A2.
XX PN 10-JUN-2004.
XX PD 26-NOV-2003; 2003WO-US038193.
XX PF 26-NOV-2002; 2002US-0429739P.
XX PR (PROT-) PROTEIN DESIGN LABS INC.
XX PA Aziz N, Ginsburg WM, Zlotnik A;
XX PI WPI; 2004-441208/41.
XX DR

Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue

PT sarcoma.
XX Example 2; SEQ ID NO 2566; 210pp; English.
PS The invention relates to a novel method for detecting soft tissue sarcoma
XX which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytosolic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC protein of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX Sequence 730 AA;
SQ

Query Match 99.6%; Score 3602; DB 8; Length 730;
Best Local Similarity 99.1%; Pred. No. 4e-201;
Matches 698; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

Qy 1 GGVPGALIPGGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 60
Db 27 GGVPGALIPGGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 86
Qy 61 PPGALVPGVADAAAAAATAKAGAGLVGGVGGVGGVGGVGGVGGVGGVGGVGGV 120
Db 87 PPGALVPGVADAAAAAATAKAGAGLVGGVGGVGGVGGVGGVGGVGGVGGVGGV 146
Qy 121 PGVTPGGVLPQARPPGVGVLPVGTGACVVKPAPCVGAGAFAGIPGVPGPQGVPLGY 180
Db 147 PGVTPGGVLPQARPPGVGVLPVGTGACVVKPAPCVGAGAFAGIPGVPGPQGVPLGY 206
Qy 181 PIKAPKLPGGVGLPYTTGKLPYGVGGVAGAGAGYPTGTGVPQAAAAAATAAKAF 240
Db 207 PIKAPKLPGGVGLPYTTGKLPYGVGGVAGAGAGYPTGTGVPQAAAAAATAAKAF 266
Qy 241 GAGAAGVLPVGGAGVPGVPGAIPIGIGIAGVGTAAAAAATAAKAAGLVPGG 300
Db 267 GAGAAGVLPVGGAGVPGVPGAIPIGIGIAGVGTAAAAAATAAKAAGLVPGG 326
Qy 301 PGFPGVGVPGVAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 360
Db 327 PGFPGVGVPGVAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 386
Qy 361 PGVGVGGIPTYGVGAGGFPFGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGV 420
Db 387 PGVGVGGIPTYGVGAGGFPFGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGV 446
Qy 421 AKAAYGVGTAAAAAATAAKAQAQF-----GLVPGVGVAPGVGVAPGVGVGLAPG 474
Db 447 AKAAYGVGTAAAAAATAAKAQAQFALLNLNLAGLVPGVGVAPGVGVGVGLAPG 506
Qy 475 VGVAPGVGVAPGVGVAPGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGV 534
Db 507 VGVAPGVGVAPGVGVAPGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGV 566
Qy 535 GLGVGAGVPGV 594
Db 567 GLGVGAGVPGV 626
Qy 595 AGPAAAAAATAAKAQAQFGLVGAAGLVGGVGGVGGVGGVGGVGGVGGVGGVGG 654
Db 627 AGPAAAAAATAAKAQAQFGLVGAAGLVGGVGGVGGVGGVGGVGGVGGVGGVGG 686
Qy 655 GLGVGAGGAGFPFLGGVAAAPFGVGLSPIPPGGACLGKACGRKK 698
Db 687 GLGVGAGGAGFPFLGGVAAAPFGVGLSPIPPGGACLGKACGRKK 730

RESULT 5
 AAY69068
 ID AAY69068 standard; protein; 731 AA.
 XX AC AAY69068;
 XX DT 30-MAY-2000 (first entry)
 XX
 DE Amino acid sequence of a human tropoelastin splice form.
 XX
 KW Tropoelastin; derivative; proteolysis; protease; antiwrinkle;
 KW hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;
 KW peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Cleavage-site 441..442
 FT Cleavage-site 503..504
 FT Cleavage-site 515..516
 FT Cleavage-site 564..565
 XX WO200004043-A1.
 XX
 XX 27-JAN-2000.
 PD
 XX 19-JUL-1999; 99WO-AU000580.
 XX
 XX 17-JUL-1998; 98AU-00004723.
 XX
 XX (UNSY) UNIV SYDNEY.
 PA
 XX Weiss AS;
 PI
 XX WPI; 2000-182399/16.
 DR N-PSDB; AA261146.
 XX
 FT New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
 PT cell growth.
 XX
 PS Disclosure; Page 107-109; 136pp; English.
 XX
 CC The present sequence represents a human tropoelastin splice form. The
 CC specification describes tropoelastin derivatives, in which a subsequence
 CC has been mutated so that susceptibility to proteolysis is reduced or
 CC eliminated, or a subsequence has been inserted so that susceptibility to
 CC proteolysis is increased. The derivatives have with reduced
 CC susceptibility, and can be used where the wild-type protein would be
 CC degraded too easily, e.g. in contact with serum or wound exudate. The
 CC tropoelastin derivatives provide competitive inhibition of protease
 CC activity. The tropoelastin derivatives, and other polypeptides containing
 CC tropoelastin derivative-derived protease-susceptibility sites, are useful
 CC in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand
 CC lotions), as bulking agents and for inducing chemotaxis. They are also
 CC useful for proliferation or growth inhibition, particularly of smooth
 CC muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes,
 CC chondrocytes and platelets. Peptidomimetics that mimic the protease
 CC cleavage site in tropoelastin derivatives are competitive inhibitors of
 CC the protease, and are used for protecting against lung damage caused by
 CC elastin, for inhibiting or controlling localized growth of cancers or
 CC metastases, or to limit protease activity that causes blood clotting
 XX
 SQ Sequence 731 AA;
 Query Match 99.3%; Score 3588.5; DB 3; Length 731;
 Best Local Similarity 95.5%; Pred. No. 2.4e-200;
 Matches 698; Conservative 0; Mismatches 0; Indels 33; Gaps 1;
 QY 1 GGVPGAIPGGVPGVPGAGLGGGALGPGKPLKVPVPGLAGAGLGAFFAVT 60
 DB 1 GGVPGAIPGGVPGVPGVPGAGLGGGALGPGKPLKVPVPGLAGAGLGAFFAVT 60
 QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVSAGAVVPGAGVKPGVGVGL 120

Db 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVSAGAVVPGAGVKPGVGVGL 120
 QY 121 PGVYPGGVLPGARPPGGVLPVPGVPTGAGVKPKAPGVGGAFAFAGIPGVGPFPGVPLGY 180
 Db 121 PGVYPGGVLPGARPPGGVLPVPGVPTGAGVKPKAPGVGGAFAFAGIPGVGPFPGVPLGY 180
 QY 181 PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPOAAAAAATAAKF 240
 Db 181 PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPOAAAAAATAAKF 240
 QY 241 GAGAAGVLPVGGAGVPGVPGCAIPGIGIAGVGTAAAAAATAAKAAGAGLVPGG 300
 Db 241 GAGAAGVLPVGGAGVPGVPGCAIPGIGIAGVGTAAAAAATAAKAAGAGLVPGG 300
 QY 301 PGFPGVWVPGAGVPGVPGVPGAGIPVPGAGIPGAAVPGVWVSPAAAAAATAAKYCAR 360
 Db 301 PGFPGVWVPGAGVPGVPGVPGAGIPVPGAGIPGAAVPGVWVSPAAAAAATAAKYCAR 360
 QY 361 PGVGVGGIPYGYGAGGFPFGVGGIPGVAGVPSVGGVPGVGGVPGVGI SPSAQAATA 420
 Db 361 PGVGVGGIPYGYGAGGFPFGVGGIPGVAGVPSVGGVPGVGGVPGVGI SPSAQAATA 420
 QY 421 AKAAKYGVGTAAAAAATAAKAQAQFGLVPGVGVAPGVGVAPGVGVAPGLA PGVGVAPG 480
 Db 421 AKAAKYGVGTAAAAAATAAKAQAQFGLVPGVGVAPGVGVAPGVGVAPGLA PGVGVAPG 480
 QY 481 VGVAPGVGVAPGIGPGGVAAAAAATAAKAQAQFGLVPGVGVAPGVGVAPGLVGVGA 540
 Db 481 VGVAPGVGVAPGIGPGGVAAAAAATAAKAQAQFGLVPGVGVAPGVGVAPGLVGVGA 540
 QY 541 GVPGLGVGAGVPGFGA-----VPGALAAKAA 567
 Db 541 GVPGLGVGAGVPGFGAGADEGVRRSLSPELREGDPSQSQHLPTSPSPRVPGALAAKAA 600
 QY 568 KYGAAVPGVGLGALGGVIGIPGVGVGAGPAAAAAATAAKAQAQFGLVGAAGLGLGVG 627
 Db 601 KYGAAVPGVGLGALGGVIGIPGVGVGAGPAAAAAATAAKAQAQFGLVGAAGLGLGVG 660
 QY 628 GLGVPGVGGVGLGIPAAAAAATAAKAQAQFGLVGGAGQFPLGGVAAARPGLSPFPGA 687
 Db 661 GLGVPGVGGVGLGIPAAAAAATAAKAQAQFGLVGGAGQFPLGGVAAARPGLSPFPGA 720
 QY 688 CLGKACGRK 698
 Db 721 CLGKACGRK 731
 RESULT 6
 AAB66657
 ID AAB66657 standard; protein; 731 AA.
 XX AC AAB66657;
 XX DT 05-APR-2001 (first entry)
 DE Human elastin protein without signal peptide.
 DE
 DE Minimal function unit; MFU; human; elastin prosthetic.
 KW
 XX Homo sapiens.
 OS
 XX WO200100666-A2.
 PN
 XX 04-JAN-2001.
 PD
 XX 29-JUN-2000; 2000WO-US017829.
 PF
 XX 29-JUN-1999; 99US-00340736.
 PR
 XX (PROT-) PROTEIN SPECIALTIES LTD.
 PA (HSCR-) HSC RES & DEV LP.
 XX

PI Rothstein A, Keeley F, Rothstein S, Stahl R;
XX WPI; 2001-102886/11.
XX Novel polypeptides that comprise three beta-sheet/beta-turn structures
PT and are not naturally occurring fibrous protein, used to produce
PT prosthesis suitable for implantation into humans, and cosmetic materials.
XX
XX
XX Claim 1; Fig 1; 39pp; English.
XX
XX The present invention relates to a minimal functional unit (MFU) of human
CC elastin polypeptide. This protein is useful in a cosmetic material or a
CC prosthetic material such as prosthesis for blood vessel replacements, for
CC heart valve replacement, tissue replacement, for covering burns, for
CC covering wounds and stents
XX
XX
SQ Sequence 731 AA;

Query Match 99.3%; Score 3588.5; DB 4; Length 731;
Best Local Similarity 95.5%; Pred. No. 2.4e-200;
Matches 698; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

Qy 1 GGVPGAIPGGVPGGVYFPGAGLGGALGPGGKPLKPVPGGLAGAGLGAFFPAVT 60
Db 1 GGVPGAIPGGVPGGVYFPGAGLGGALGPGGKPLKPVPGGLAGAGLGAFFPAVT 60

Qy 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVGSAGAVVPPQAGVPGKVPVGL 120
Db 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVGSAGAVVPPQAGVPGKVPVGL 120

Qy 121 PGVTPGGVLPGARFPGVGVLPQVPTGAGVKAPKAGVGGAFAGIPGVPGPGVPLGY 180
Db 121 PGVTPGGVLPGARFPGVGVLPQVPTGAGVKAPKAGVGGAFAGIPGVPGPGVPLGY 180

Qy 181 PIKAPKLPGGVGLPYTTGKLPYGYGPGVAGAGKAGYPTGTGVPQAAAAKAAKAF 240
Db 181 PIKAPKLPGGVGLPYTTGKLPYGYGPGVAGAGKAGYPTGTGVPQAAAAKAAKAF 240

Qy 241 GAGAAGVLPVGGAGVPGVPGAIPGIGGIAGVGTTPAAAAAATAKAAKAGLIVPGG 300
Db 241 GAGAAGVLPVGGAGVPGVPGAIPGIGGIAGVGTTPAAAAAATAKAAKAGLIVPGG 300

Qy 301 PGFPGVGVPGAGVPGVPGVPGAGIPVVPFGAGIPGAAGVPGVSPAAAAKAAKYGAR 360
Db 301 PGFPGVGVPGAGVPGVPGVPGAGIPVVPFGAGIPGAAGVPGVSPAAAAKAAKYGAR 360

Qy 361 PGVGGVGIPTYGVAGGPGFPGVGGVPGVAGVSPVGGVPGVGGVPGVGGVPGVGGV 420
Db 361 PGVGGVGIPTYGVAGGPGFPGVGGVPGVAGVSPVGGVPGVGGVPGVGGVPGVGGV 420

Qy 421 AKAAKYGVGTTPAAAAAATAKAAKAGLGGVPGVGGVPGVGGVPGVGGVPGVGGV 480
Db 421 AKAAKYGVGTTPAAAAAATAKAAKAGLGGVPGVGGVPGVGGVPGVGGVPGVGGV 480

Qy 481 VGVAPGVAPGIPGPGVAAAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 540
Db 481 VGVAPGVAPGIPGPGVAAAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 540

Qy 541 GVPGLGVAGVPGFGA-----VPGALAAKAA 567
Db 541 GVPGLGVAGVPGFGADEGVRRSLSPELREGDPSSQHLPTSPSPRVPVPGALAAKAA 600

Qy 568 KYGAAPVGLGLGALGVGIPGVVVGAGPAAAAAATAKAAKAAKAAKAAKAAKAAKAAK 627
Db 601 KYGAAPVGLGLGALGVGIPGVVVGAGPAAAAAATAKAAKAAKAAKAAKAAKAAK 660

Qy 628 GLGVPGVGLGGLIPAAAAAATAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAK 687
Db 661 GLGVPGVGLGGLIPAAAAAATAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAK 720

Qy 688 CLGKACGRKK 698
Db 721 CLGKACGRKK 731

RESULT 7
AAR56653
ID AAR56653 standard; protein; 733 AA.
XX AAR56653;
AC AAR56653;
XX
DT 25-MAR-2003 (revised)
DT 22-MAR-1995 (first entry)
XX
DE Synthetic human tropoelastin (SHEL).
XX
KW Tropoelastin; pharmaceutical; surgical dressing.
XX
OS Synthetic.
XX
XX WO9414958-A1.
XX
XX 07-JUL-1994.
XX
XX 16-DEC-1993; 93WO-AU000655.
XX
XX 22-DEC-1992; 92AU-00006520.
PR 28-JUN-1993; 93AU-00009661.
XX
XX (UNSY) UNIV SYDNEY.
XX
XX Weiss AS, Martin SL;
XX
XX WPI; 1994-263633/32.
DR N-PSDB; AAQ70941.
XX
XX Synthetic polynucleotide(s) - encode recombinant tropoelastins and
PT variants.
XX
XX Disclosure; Page 30; 77pp; English.
XX
XX Human synthetic tropoelastin is susceptible to hydrolytic breakdown of
CC the crosslinks. Such material may be useful in e.g. surgical
CC applications, where the gradual loss of material over time is intended.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 733 AA;

Query Match 99.3%; Score 3588.5; DB 2; Length 733;
Best Local Similarity 95.5%; Pred. No. 2.4e-200;
Matches 698; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

Qy 1 GGVPGAIPGGVPGGVYFPGAGLGGALGPGGKPLKPVPGGLAGAGLGAFFPAVT 60
Db 3 GGVPGAIPGGVPGGVYFPGAGLGGALGPGGKPLKPVPGGLAGAGLGAFFPAVT 62

Qy 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVGSAGAVVPPQAGVPGKVPVGL 120
Db 63 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVGSAGAVVPPQAGVPGKVPVGL 122

Qy 121 PGVTPGGVLPGARFPGVGVLPQVPTGAGVKAPKAGVGGAFAGIPGVPGPGVPLGY 180
Db 123 PGVTPGGVLPGARFPGVGVLPQVPTGAGVKAPKAGVGGAFAGIPGVPGPGVPLGY 182

Qy 181 PIKAPKLPGGVGLPYTTGKLPYGYGPGVAGAGKAGYPTGTGVPQAAAAAATAKAAKAF 240
Db 183 PIKAPKLPGGVGLPYTTGKLPYGYGPGVAGAGKAGYPTGTGVPQAAAAAATAKAAKAF 242

Qy 241 GAGAAGVLPVGGAGVPGVPGAIPGIGGIAGVGTTPAAAAAATAKAAKAGLIVPGG 300
Db 243 GAGAAGVLPVGGAGVPGVPGAIPGIGGIAGVGTTPAAAAAATAKAAKAGLIVPGG 302

Qy 301 PGFPGVGVPGAGVPGVPGVPGAGIPVVPFGAGIPGAAGVPGVSPAAAAKAAKYGAR 360
Db 303 PGFPGVGVPGAGVPGVPGVPGAGIPVVPFGAGIPGAAGVPGVSPAAAAKAAKYGAR 362

QY 361 PGVGVGIGPIYGVAGGFPFGVGVGGIPGVAGVPSVGGVGVGGVGSPEAQAAAA 420
 |||||
 Db 363 PGVGVGIGPIYGVAGGFPFGVGVGGIPGVAGVPSVGGVGVGGVGSPEAQAAAA 422
 |||||
 QY 421 AKAAKYGVCTPAAAAKAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGVAPGV 480
 |||||
 Db 423 AKAAKYGVCTPAAAAKAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGVAPGV 482
 |||||
 QY 481 VGVAPGVGVAPGIPGVGVAAAAKAAKAAQLRRAAAGLGGAGIPGLGVGVGVGVGV 540
 |||||
 Db 483 VGVAPGVGVAPGIPGVGVAAAAKAAKAAQLRRAAAGLGGAGIPGLGVGVGVGV 542
 |||||
 QY 541 GVPGLGV 567
 |||||
 Db 543 GVPGLGV 602
 |||||
 QY 568 KYGAAPVGVVLGGI-GALGGVGIPIGVGVGVGVGVGVGVGVGVGVGVGVGVGV 627
 |||||
 Db 603 KYGAAPVGVVLGGI-GALGGVGIPIGVGVGVGVGVGVGVGVGVGVGVGVGVGV 662
 |||||
 QY 628 GLGVPGVGGIGGIPPPAAAAKAAKAAAGLGGVVLGGAGQPLGGVAAAPGFGLSPI 687
 |||||
 Db 663 GLGVPGVGGIGGIPPPAAAAKAAKAAAGLGGVVLGGAGQPLGGVAAAPGFGLS 722
 |||||
 QY 688 CLGKACGRKRK 698
 |||||
 Db 723 CLGKACGRKRK 733
 |||||

RESULT 8

AA01301

ID AAY01301 standard; protein; 733 AA.

AC AAY01301;

XX AAY01301;

XX 07-JUN-1999 (first entry)

XX Amino acid sequence of synthetic human tropoelastin SHEL.

DE Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;

KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;

KW hand lotion; surgical implant; industrial product; human; SHEL.

XX Synthetic.

OS Homo sapiens.

XX WO9903886-A1.

PN 28-JAN-1999.

XX 17-JUL-1998; 98WO-AU000564.

PF 18-JUL-1997; 97AU-00008117.

XX (UNSY) UNIV SYDNEY.

PA Weiss AS;

XX WPI; 1999-132162/11.

DR N-PSDB; AAX27704.

XX New derivatives of human tropoelastin - with elastin-like or

PT macromolecular binding properties, useful e.g. as surgical implants.

XX Disclosure; Fig 1; 82pp; English.

PS The invention relates to a derivative or variant of human tropoelastin

XX (hTE) having elastin-like and/or macromolecule (specifically

CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors

CC comprising the nucleic acids encoding the variants or derivatives are

CC used to produce the proteins recombinantly. The tropoelastin derivatives

CC or hybrid proteins containing the derivatives are useful in medical,

XX pharmaceutical, veterinary and cosmetic applications, e.g. as anti-

CC wrinkle or hand lotions, also as surgical implants, foods and industrial
 CC products. The hybrid protein have controllable GAG-binding properties,
 CC depending on presence or absence of a specific fragment, designated
 CC peptide 26A, from hTE. The present sequence represents the amino acid
 CC sequence of the synthetic human tropoelastin SHEL
 XX Sequence 733 AA;

Query Match

Best Local Similarity 99.3%; Score 3588.5; DB 2; Length 733;

Matches 698; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

QY 1 GGVPGLPGV 60
 |||||
 Db 3 GGVPGLPGV 62
 |||||
 QY 61 FPGALVPGGVADAAAAKAAKAGAGLGGVGVGVGVGVGVGVGVGVGVGVGVGVGV 120
 |||||
 Db 63 FPGALVPGGVADAAAAKAAKAGAGLGGVGVGVGVGVGVGVGVGVGVGVGVGVGV 122
 |||||
 QY 121 PGVPGGVLPGARFPFGVGVLPVGVTPGAGVVKPAKAPGVGGAPAGIPGVPGFP 180
 |||||
 Db 123 PGVPGGVLPGARFPFGVGVLPVGVTPGAGVVKPAKAPGVGGAPAGIPGVPGFP 182
 |||||
 QY 181 PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAGKAGYPTGTGVGPQAAAAKAA 240
 |||||
 Db 183 PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAGKAGYPTGTGVGPQAAAAKAA 242
 |||||
 QY 241 GAGAAGLVPGGV 300
 |||||
 Db 243 GAGAAGLVPGGV 302
 |||||
 QY 301 PGFPGV 360
 |||||
 Db 303 PGFPGV 362
 |||||
 QY 361 PGVGVGGIPTYGVGAGGFPFGVGVGGIPGVAGVPSVGGVGVGVGVGVGVGVGV 420
 |||||
 Db 363 PGVGVGGIPTYGVGAGGFPFGVGVGGIPGVAGVPSVGGVGVGVGVGVGVGVGV 422
 |||||
 QY 421 AKAAKYGVGTTPAAAAKAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGVAPGV 480
 |||||
 Db 423 AKAAKYGVGTTPAAAAKAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGVAPGV 482
 |||||
 QY 481 VGVAPGVGVAPGIPGVGVAAAAKAAKAAQLRRAAAGLGGAGIPGLGVGVGVGVGV 540
 |||||
 Db 483 VGVAPGVGVAPGIPGVGVAAAAKAAKAAQLRRAAAGLGGAGIPGLGVGVGVGVGV 542
 |||||
 QY 541 GVPGLGV 567
 |||||
 Db 543 GVPGLGV 602
 |||||
 QY 568 KYGAAPVGVVLGGI-GALGGVGIPIGVGVGVGVGVGVGVGVGVGVGVGVGVGV 627
 |||||
 Db 603 KYGAAPVGVVLGGI-GALGGVGIPIGVGVGVGVGVGVGVGVGVGVGVGVGVGV 662
 |||||
 QY 628 GLGVPGVGGIGGIPPPAAAAKAAKAAAGLGGVVLGGAGQPLGGVAAAPGFGLSPI 687
 |||||
 Db 663 GLGVPGVGGIGGIPPPAAAAKAAKAAAGLGGVVLGGAGQPLGGVAAAPGFGLSPI 722
 |||||
 QY 688 CLGKACGRKRK 698
 |||||
 Db 723 CLGKACGRKRK 733
 |||||

RESULT 9

ABG75223

ID ABG75223 standard; protein; 757 AA.

XX AC ABG75223;

XX DT 12-FEB-2004 (first entry)

XX

DE Human tropoelastin protein.
XX Human; tropoelastin; elastin; body vessel occlusion; stenosis;
KW vascular smooth muscle cell; elastin signaling; vasotropic.
XX
OS Homo sapiens.
XX WO2003082203-A2.
XX 09-OCT-2003.
XX 27-MAR-2003; 2003WO-US009391.
XX 27-MAR-2002; 2002US-0368084P.
XX (UTAH) UNIV UTAH RES FOUND.
XX Li DY, Karnik S;
XX WPI; 2003-833516/77.
XX Use of an agent that promotes elastin signaling in smooth muscle cells
XX for e.g. decreasing or preventing occlusion of a body vessel by smooth
XX muscle cells, treating or preventing obstructive vascular disease, or
XX preventing stenosis.
XX Claim 24; Page 138-141; Opp; English.
XX The present invention relates to the use of an agent that promotes
XX elastin signaling in smooth muscle cells for decreasing or preventing
XX occlusion of a body vessel by smooth muscle cells, decreasing vascular
XX obstruction, promoting actin stress fiber formation or actin
XX polymerisation, increasing F:G actin ratio in a smooth muscle cell,
XX treating or preventing obstructive vascular disease (e.g. restenosis), or
XX preventing stenosis. The agent that promotes elastin signaling in smooth
XX muscle cells is useful for decreasing or preventing occlusion of a body
XX vessel by smooth muscle cells, decreasing vascular obstruction, promoting
XX actin stress fiber formation or actin polymerization, increasing F:G
XX actin ratio in a smooth muscle cell, treating or preventing obstructive
XX vascular disease (e.g. restenosis following angioplasty), or preventing
XX stenosis. It is also useful in manufacturing a medicament for the
XX treatment or prevention of occlusion of a vessel. The present sequence is
XX the human tropoelastin protein as shown in the exemplification of the
XX invention
XX Sequence 757 AA;
SQ
Query Match 99.3%; Score 3588.5; DB 7; Length 757;
Best Local Similarity 95.5%; Pred. No. 2.5e-200;
Matches 698; Conservative 0; Mismatches 0; Indels 33; Gaps 1;
QY 1 GGVPGAIPGGVPGGVYFPGAGLGGALGGGALGGGKPLKVPVPGLAGAGLGAAGLGAFFAVT 50
DB 27 GGVPGAIPGGVPGGVYFPGAGLGGALGGGALGGGKPLKVPVPGLAGAGLGAAGLGAFFAVT 86
QY 61 FPGALVPGGVADAAAYAAKAGAGLGGVPGVGGVGSAGAVVPOPGAGVKGKVPVGL 120
DB 87 FPGALVPGGVADAAAYAAKAGAGLGGVPGVGGVGSAGAVVPOPGAGVKGKVPVGL 146
QY 121 PGVYFPGVLPGARFFPGVLPVPTGAGVKGKAPGVGGAFAGIPGVPGFPQPGVPLGY 180
DB 147 PGVYFPGVLPGARFFPGVLPVPTGAGVKGKAPGVGGAFAGIPGVPGFPQPGVPLGY 206
QY 181 PIKAPKLPGGYGLPYTTTKLPYGYPGGVAGAGKAGYPTCTGVGPQAAAAAAXAAKF 240
DB 207 PIKAPKLPGGYGLPYTTTKLPYGYPGGVAGAGKAGYPTCTGVGPQAAAAAAXAAKF 266
QY 241 GAGAGVLPGVGGAGVPGVPGAIPGIGGIAGVGTPTAAAAAAXAAKAYGAAAGLVPGG 300
DB 267 GAGAGVLPGVGGAGVPGVPGAIPGIGGIAGVGTPTAAAAAAXAAKAYGAAAGLVPGG 326
QY 301 PGFPGVGVPGGAGVPGVPGAGIPVVPAGIPGAAPVGVVSPPEAAAKAAKAYGAR 360

Db 327 PGFPGVGVPGGAGVPGVPGAGIPVVPAGIPGAAPVGVVSPPEAAAKAAKAYGAR 386
QY 361 PGVGVGGIPTYGVGAGGFPFGVGVGSIPIGVAGVPSVGGVPGVGVGSIPEAQAAAA 420
DB 387 PGVGVGGIPTYGVGAGGFPFGVGVGSIPIGVAGVPSVGGVPGVGVGSIPEAQAAAA 446
QY 421 AKAAKYGVGTPTAAAAAAXAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGVAPG 480
DB 447 AKAAKYGVGTPTAAAAAAXAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGVAPG 506
QY 481 VGVAPGVGVAPGIPGPGVAAAAAAXAAKAAQFGLVPGVGVAPGVGVAPGVGVAPG 540
DB 507 VGVAPGVGVAPGIPGPGVAAAAAAXAAKAAQFGLVPGVGVAPGVGVAPGVGVAPG 566
QY 541 GVPGLGVGAGVPGFGA-----VPGALAAAKAA 567
DB 567 GVPGLGVGAGVPGFGAGADEGVRSLSPLEIREGDPSSQHLPTPTSPRPGALAAAKAA 626
QY 568 KYGAAVPGVGLGALGGVGPVPGVAGPAAAAAAXAAKAAQFGLVGAAGLGLGVG 627
DB 627 KYGAAVPGVGLGALGGVGPVPGVAGPAAAAAAXAAKAAQFGLVGAAGLGLGVG 686
QY 628 GLGVPGVGLGIPPPAAAAAAXAAKAAQFGLVGAAGLGLGVGAAAPGGLSPFPGA 687
DB 687 GLGVPGVGLGIPPPAAAAAAXAAKAAQFGLVGAAGLGLGVGAAAPGGLSPFPGA 746
QY 688 CLGKACGRKK 698
DB 747 CLGKACGRKK 757
RESULT 10
ADP65160
ID ADP65160 standard; protein; 757 AA.
XX
AC ADP65160;
XX
DT 12-AUG-2004 (first entry)
DE Human elastin.
XX
KW autoimmune disease; arthritis; gene expression analysis;
KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
KW antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;
KW immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;
KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
KW immune; human.
XX
OS Homo sapiens.
XX
PN WO2003072827-A1.
XX
PD 04-SEP-2003.
XX
PF 31-OCT-2002; 2002WO-US035433.
XX
PR 31-OCT-2001; 2001US-0336220P.
XX
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
XX
PI Hirsch R, Thorton SL;
XX
DR WPI; 2003-712740/67.
DR GENBANK; NP_000492.
XX
XX Diagnosing and analyzing autoimmune disease using gene expression
XX profiles and microarray technology, useful for diagnosing and treating
XX rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
XX gout.
XX Disclosure; Page; 56pp; English.
XX The invention relates to a novel method for diagnosing and analysing

autoimmune disease or arthritides. The method comprises obtaining a patient sample containing mRNA, analysing gene expression using the mRNA that results in a gene expression signature of the mRNA, and using that gene expression signature to diagnose or analyse the autoimmune disease or arthritides in the patient, where gene expression of at least 60% of the genes correlates with that of the gene signature. The invention further comprises: a treatment of rheumatoid arthritis; identification of genes for targeting in the treatment of rheumatoid arthritis in a mammal other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an array or gene chip, specific for rheumatoid arthritis; diagnosis or analyses of autoimmune disease or rheumatoid arthritis; screening the efficacy of a candidate drug in vitro for the treatment of collagen-induced arthritis; and reducing the symptoms associated with collagen-induced arthritis. The compositions of the invention have the following activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic, antitumor, antiinflammatory, dermatological, and immunomodulatory. The methods and compositions of the present invention are useful for diagnosing and treating autoimmune disease or arthritides, such as rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis, fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an immune disease caused by an infectious agent. This sequence represents a protein sequence relating to the genes used in the analysis and treatment of autoimmune diseases or arthritides. Note: This sequence is not shown in the specification. It has been supplied in an electronic format from WIPO.

XX Sequence 757 AA;

Query Match 99.3%; Score 3588.5; DB 7; Length 757;
Best Local Similarity 95.5%; Pred. No. 2.5e-200;
Matches 698; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

QY 1 GGVGPAIPGGVGGVFFPGAGLGGALGGALPGGKPLKVPVGGLAGAGLGGAGPAPVT 60
DB 27 GGVGPAIPGGVGGVFFPGAGLGGALGGALPGGKPLKVPVGGLAGAGLGGAGPAPVT 86
QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVGGVGGVGGVGGVGGVGGVGGVGGV 120
DB 87 FPGALVPGGVADAAAAYKAAKAGAGLGGVGGVGGVGGVGGVGGVGGVGGVGGV 146
QY 121 PGVYPGSVLPGARFGVGVLPVGTAGVKKPAGVGGAPAGIPGVGGPGGPGVPLGY 180
DB 147 PGVYPGSVLPGARFGVGVLPVGTAGVKKPAGVGGAPAGIPGVGGPGGPGVPLGY 206
QY 181 PIKAPKLPGGYGLPYTTGKLPYGGVGGVAGAGKAGYPTGTGVPQAAAAAAYKAAKAAKF 240
DB 207 PIKAPKLPGGYGLPYTTGKLPYGGVGGVAGAGKAGYPTGTGVPQAAAAAAYKAAKAAKF 266
QY 241 GAGAGVLPVGGAGVPGVPGAIPTGTGAGVGGVGGVGGVGGVGGVGGVGGVGGV 300
DB 267 GAGAGVLPVGGAGVPGVPGAIPTGTGAGVGGVGGVGGVGGVGGVGGVGGVGGV 326
QY 301 PGFGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGV 360
DB 327 PGFGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGV 386
QY 361 PGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGV 420
DB 387 PGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGV 446
QY 421 AKAAKYGVGTAAAAAAYKAAKAAQGLVGGVGGVGGVGGVGGVGGVGGVGGVGGV 480
DB 447 AKAAKYGVGTAAAAAAYKAAKAAQGLVGGVGGVGGVGGVGGVGGVGGVGGVGGV 506
QY 481 VGVAVGVGVPAGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGV 540
DB 507 VGVAVGVGVPAGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGV 566
QY 541 VGPGLGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGV 567
DB 567 VGPGLGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGV 626
QY 568 KYGAAPVGLGGLGAGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGV 627

DB 627 KYGAAPVGLGGLGAGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGV 686
QY 628 GLGVPGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGV 687
DB 687 GLGVPGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGV 746
QY 588 CLGKACGKRRK 698
DB 747 CLGKACGKRRK 757

RESULT 11
ADL96420
ID ADL96420 standard; protein; 731 AA.
XX ADL96420;
XX AC
XX DT 20-MAY-2004 (first entry)
XX DE Human elastin protein fragment.
XX XX fibrous protein; prosthesis; elastin; lamprlin; spider silk protein;
XX KW blood vessel; wound; burn healing; collagen.
XX OS Homo sapiens.
XX PH
XX FT Key
XX FT Region 19..160 Location/Qualifiers
XX FT Region 188..367 /note= "region specifically claimed in claim 6"
XX FT Region /note= "region specifically claimed in claim 6"
XX FT Region 374..499 /note= "region specifically claimed in claim 6"
XX FT Region 607..717 /note= "region specifically claimed in claim 6"
XX FT
XX FT US2003166846-A1.
XX PN
XX PD 04-SEP-2003.
XX PF 28-SEP-2001; 2001US-00964662.
XX PR 07-AUG-1996; 96US-0023522P.
XX PR 07-AUG-1997; 97US-00911364.
XX PR 29-JUN-1999; 99US-00340736.
XX XX (ROTH/) ROTHSTEIN A.
XX PA (KEEL/) KEELEY F.
XX PA (ROTH/) ROTHSTEIN S.
XX XX Rothstein A, Keeley F, Rothstein S;
XX PI WPI; 2003-898105/82.
XX DR
XX DT
XX PT Polypeptide for constructing human elastin-like prostheses such as tubes
XX PT for blood vessel replacement and sheets for other uses such as wound or
XX PT burn healing, comprises three beta sheets and three beta turns.
XX PS Claim 5; Fig 1B; 17pp; English.
XX XX This invention describes a polypeptide that comprises three beta
XX CC sheet/beta turn structures and that is not a naturally occurring fibrous
XX CC protein. The invention also describes a prosthesis comprising an animal,
XX CC metal or synthetic material, where the surface is coated with the
XX CC polypeptide, a cosmetic material comprising the polypeptide, an elastic
XX CC material comprising the polypeptide, a high tensile strength material
XX CC comprising the polypeptide, a material comprising two or more
XX CC polypeptides selected from (a) a polypeptide consisting essentially of a
XX CC portion of the polypeptide comprising at least three beta sheet/beta turn
XX CC structures, (b) a polypeptide consisting essentially of a portion of the
XX CC amino acid sequence of an animal elastin comprising at least three beta
XX CC sheets/beta turns, (c) a polypeptide consisting essentially of a portion

Qy	1	GGVPGATPGGVGGVFPYGGAGLGGALGGGKPLKPVPGGLAGAGLGGALGACFAFPAVT	60
Db	1	GGVPGATPGGVGGVFPYGGAGLGGALGGGKPLKPVPGGLAGAGLGGALGACFAFPAVT	60
Qy	61	FPGALVPGGVADAAAAAAXKAAKAGAGLGGVPGVGGGLGVSAGAVPQPGAGVKPGKVPVGVL	120
Db	61	FPGALVPGGVADAAAAAAXKAAKAGAGLGGVPGVGGGLGVSAGAVPQPGAGVKPGKVPVGVL	120
Qy	121	PGVYPGGVILPGARPPGVGVLPGVETGAGVKPKAPGVGGAPAGIPGVGFPGQPQGPVLGY	180
Db	121	PGVYPGGVILPGARPPGVGVLPGVETGAGVKPKAPGVGGAPAGIPGVGFPGQPQGPVLGY	180
Qy	181	PIKAPKLPGGYGLPYTTTKLPGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAXKAAKF	240
Db	181	PIKAPKLPGGYGLPYTTTKLPGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAXKAAKF	240
Qy	241	GAGAAGVILPGVGGAGVPCVPGCAIPGIGIAGVGTAAAAAAXKAAKYGAAAGLVPGG	300
Db	241	GAGAAGVILPGVGGAGVPCVPGCAIPGIGIAGVGTAAAAAAXKAAKYGAAAGLVPGG	300
Qy	301	PGFGPVVGVPCAGVPGVGVPGAGIPVVPAGAGIPGAAVPGVVSPEAAAAKAAKAYGAR	360
Db	301	PGFGPVVGVPCAGVPGVGVPGAGIPVVPAGAGIPGAAVPGVVSPEAAAAKAAKAYGAR	360
Qy	361	PGVGVGGIPTVYGAGGPPGPGVGGIIPGVAGVPSGVGPGVGVGIGISPEAAAAA	420
Db	361	PGVGVGGIPTVYGAGGPPGPGVGGIIPGVAGVPSGVGPGVGVGIGISPEAAAAA	420
Qy	421	AKAAKYGVGTAAAAAAXKAAKAAQGLVPGVGAPGVGVPAGVGVAGLAPGVGVAPG	480
Db	421	AKAAKYGVGTAAAAAAXKAAKAAQGLVPGVGAPGVGVPAGVGVAGLAPGVGVAPG	480
Qy	481	VGVAPGVGVAPGIGIPGGVAAAAKAAKAAQAQLRAAGLGAAGIPGLGVGVGVPGLGVCA	540
Db	481	VGVAPGVGVAPGIGIPGGVAAAAKAAKAAQAQLRAAGLGAAGIPGLGVGVGVPGLGVCA	540
Qy	541	GVPGGLGVGAGVPGGCA-----VPGALAAAAA	567
Db	541	GVPGGLGVGAGVPGGCADEGVRSLSPELREGDPSSQHLPTPSSPRVPGALAAAAA	600
Qy	568	KYCAAVPGVILGSLGALGGVGIIPGVVVGAGPAAAAAAXKAAKAAQGLVGAAGLGGLVG	627
Db	601	KYCAAVPGVILGSLGALGGVGIIPGVVVGAGPAAAAAAXKAAKAAQGLVGAAGLGGLVG	660
Qy	628	GLGVGPGVGLGGIPPAAXKAAKAYGAAGLGGVLGGAGQFPLGGVAARPFGLSPIPPGGA	687
Db	661	GLGVGPGVGLGGIPPAAXKAAKAYGAAGLGGVLGGAGQFPLGGVAARPFGLSPIPPGGA	720
Qy	688	CLGKACGRREK	698

CC elastin on which the MFU peptides of the invention are based
XX
SQ Sequence 731 AA;

	QY	241	CAGACGVLPGVGGAGVPFGAIPGTIGTAGVCTPAAAAAAXAAKAKYGAAAGLVPFG	300
	Dd	241	GAGAAGLPGVGGAGVPFGAIPGTIGTAGVCTPAAAAAAXAAKAKYGAAAGLVPFG	300
	QY	301	PFGPGVVGVPGAGVPVGPGGAGIPVVPFCAGIPGAAPGVSPSEAAAAXAAKAKYCAR	360
	Dd	301	PFGPGVVGVPGAGVPVGVPFGGAGIPVVPFCAGIPGAAPGVSPSEAAAAXAAKAKYCAR	360
	QY	361	PGVGVGGIPTTVGVGAGGFPPGFGVGGIPGVAGVPSVGGVPGVGIISPEAQAAAA	420
	Dd	361	PGVGVGGIPTTVGVGAGGFPPGFGVGGIPGVAGVPSVGGVPGVGIISPEAQAAAA	420
	QY	421	AKAAYGYCTTAAARAAAXAAKAAAFGLVPGVGAVPGVGVAPGVGLAPGVGVAPG	480
	Dd	421	AKAAYGYCTTAAARAAAXAAKAAAFGLVPGVGAVPGVGVAPGVGLAPGVGVAPG	480
	QY	481	VGVAPGVGVAFIGIPGGVAAAXAAKAAQAALRAAAGLGAGIPGLGVGVGPGLGVGA	540
	Dd	481	VGVAPGVGVAFIGIPGGVAAAXAAKAAQAALRAAAGLGAGIPGLGVGVGPGLGVGA	540
	QY	541	GVPLGLGVGAGVPFGA-----VPGALAAAKAA	567
	Dd	541	GVPLGLGVGAGVPFGAGADEGVRRSLSELPRESPPSSQHLPSTPSSPRVPGHAAAKAA	600
	QY	568	KYCAAVPGVLGLGALGGVGIPIGGVWAGPAAAAAXAAKAAQFGLVGAAGLGLGVG	627
	Dd	601	KYCAAVPGVLGLGALGGVGIPIGGVWAGPAAAAAXAAKAAQFGLVGAAGLGLGVG	660
	QY	628	GLGVGPVGLGGIIPPAAXAAKAAKYGAAGLGVGGAGQFPLGGVVAARPFGLSPIPFPGA	687
	Dd	661	GLGVGPVGLGGIIPPAAXAAKAAKYGAAGLGVGGAG-QFPLGGVVAARPFGLSPIPFPGA	719
	QY	688	CLGKACGRKK	698
	Dd	720	CLGKACGRKK	730
		RESULT 14		
		ADE40132		
	ID	ADE40132 standard; protein; 711 AA.		
	XX	ADE40132;		
	AC			
	XX			
	DT	29-JAN-2004 (first entry)		
	XX			
	DE	Human NOV16a protein - SEQ ID 38.		
	XX			
	KW	NOVX; cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic;		
	KW	antiadrenergic; immunosuppressive; anti-HIV; neuroprotective; nootropic;		
	KW	antiparkinsonian; antiasthmatic; gynaecological; cardiomyopathy;		
	KW	atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;		
	KW	multiple sclerosis; graft-versus-host disease; Alzheimer's; Parkinson's;		
	KW	asthma; fertility disorder; vaccine; gene therapy; chromosome mapping;		
	KW	tissue typing; human; NOV.		
	OS	Homo sapiens.		
	FN	WO2003064589-A2.		
	XX			
	PD	07-AUG-2003.		
	XX			
	PF	02-AUG-2002; 2002WO-US024483.		
	XX			
	PR	02-AUG-2001; 2001US-0309501P.		
	PR	03-AUG-2001; 2001US-0310291P.		
	PR	07-AUG-2001; 2001US-0310544P.		
	PR	08-AUG-2001; 2001US-0310951P.		
	PR	09-AUG-2001; 2001US-0311292P.		
	PR	13-AUG-2001; 2001US-0311979P.		
	PR	16-AUG-2001; 2001US-0312892P.		
	PR	17-AUG-2001; 2001US-0313201P.		
	PR	17-AUG-2001; 2001US-0313415P.		

	20-AUG-2001; 2001US-0313643P.	
PR	20-AUG-2001; 2001US-0313702P.	
PR	21-AUG-2001; 2001US-0314031P.	
PR	23-AUG-2001; 2001US-0314466P.	
PR	28-AUG-2001; 2001US-0315403P.	
PR	29-AUG-2001; 2001US-0315853P.	
PR	17-SEP-2001; 2001US-0322716P.	
PR	21-SEP-2001; 2001US-0323994P.	
PR	14-DEC-2001; 2001US-0340233P.	
PR	05-FEB-2002; 2002US-0354591P.	
PR	19-MAR-2002; 2002US-0365478P.	
PR	19-APR-2002; 2002US-0373814P.	
PR	19-APR-2002; 2002US-0373825P.	
PR	19-APR-2002; 2002US-0373989P.	
PR	23-APR-2002; 2002US-0374632P.	
PR	07-JUN-2002; 2002US-0386971P.	
PR	01-AUG-2002; 2002US-0021017Z.	
XX	(CURA-) CURAGEN CORP.	
XX	Kekuda R, Miller CE, Patturajan M, Pena CEA, Rieger DK;	
XX	PI Shimkets RA, Zerkusen BD, Li L, Ji W, Padigara M, Casman SJ;	
PI	Voss EZ, Boldog F, Gorman L, Leite MW, Vernet CAM, Anderson DW;	
PI	Pi Guo X, Zhong M, Gerlach VL, Hjalit I, Rastelli L, Spytek KA;	
PI	Eldinger SR, Ellerman K, Malyankar UM, Macdougall JR, Stone DJ;	
PI	Alsobrook JP, Lepley DM, Burgess CE, Majumder K, Wolenc AR;	
PI	Smithson G;	
XX	WPI; 2003-663472/62.	
DR	N-PSDB; ADE40131.	
XX	New NOVX polypeptides and nucleic acids, useful for preventing or	
PT	treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,	
PT	atherosclerosis or diabetes, and in chromosome mapping, tissue typing or	
PT	pharmacogenomics.	
XX	Claim 1; SEQ ID NO 38; 560pp; English.	
XX	The invention relates to a novel NOVX polypeptide. The polypeptide of the	
CC	invention demonstrates cardiant, antiarteriosclerotic, hypotensive,	
CC	cystostatic, anorectic, antidiabetic, immunosuppressive, anti-HIV,	
CC	neuroprotective, nootropic, antiparkinsonian, antiasthmatic and	
CC	gynaecological activities and may be useful in diagnosing, treating or	
CC	preventing NOVX-associated disorders including cardiomyopathy	
CC	atherosclerosis, hypertension, cancer, obesity, diabetes, AIDS, multiple	
CC	sclerosis, graft-versus-host disease, Alzheimer's disease, Parkinson's	
CC	disease, asthma or fertility disorders. Furthermore, the polypeptides may	
CC	be utilised as vaccines whilst the nucleic acids may be used as	
CC	hybridisation probes, in gene therapy, chromosome mapping, tissue typing,	
CC	preventive medicine and pharmacogenomics. The current sequence is that of	
XX	the human NOV protein of the invention.	
SQ	Sequence 711 AA;	
	Query Match 96.4%; Score 3486.5; DB 7; Length 711;	
	Best Local Similarity 96.6%; Pred.No. 1.9e-194;	
	Matches 679; Conservative 1; Mismatches 0; Indels 23; Gaps 2;	
QY	1 GGVPGALPGGVGGVFPAGLGGALGGALPGCKPLKPVFGGLAGLAGLGAFFAVT 60	
Db	27 GGVPGALPGGVGGVFPAGLGGALGGALPGCKPLKPVFGGLAGLAGLGAFFAVT 86	
QY	61 PFGALVPGGVADAAAAYKAAGAGLGGVPGVGGLGUSA----GAVVPQGAGVKPKV 115	
Db	87 PFGALVPGGVADAAAAYKAAGAGLGGVPGVGGLGUSAARSVPGANVPPGAGVKPKV 146	
QY	116 PGVLGPVYPGCVLPGARFPFGVGLPVGVTGAGVKPKAPGVCGGAFAGIPGVGPPGQP 175	
Db	147 PCVGLPGVYPGCVLPGARFPFGVGLPVGVTGAGVKPKAPGVCGGAFAGIPGVGPPGQP 206	
QY	176 VPLGVPIIKAPLPGGYGLPYTTGKLPGYGPGGVAGAAGKAGYPTGTGVGPAAAAAAAK 235	
Db	207 VPLGVPIIKAPLPGGYGLPYTTGKLPGYGPGGVAGAAGKAGYPTGTGVGPAAAAAAAK 266	

Query Match	93.1%;	Score 3366;	DB 7;	Length 692;
Best Local Similarity	93.8%;	Pred. No. 1.8e-187;		
Matches 660;	Conservative 0;	Mismatches 0;	Indels 44;	Gaps 2;
1	GGVPGALPGGVGPGVFFPGAGLGGALGPGGKPLKVPVPGGLGAGLGGAGFAFPVTT	60		
27	GGVPGALPGGVGPGVFFPGAGLGGALGPGGKPLKVPVPGGLGAGLGGAGFAFPVTT	86		
61	FPGALVPGGVADAAAAKAAKACAGAGGGVPGVGGGLGVSSAGAVVPPGAGVPGKVPVGGVGL	120		
87	FPGALVPGGVADAAAAKAAKACAGAGGGVPGVGGGLGVSSAGAVVPPGAGVPGKV----	141		
121	PGVYPGGVLPGARFPGVGVLPGVPTGAGVKRPAAGVGGAFAGICPGVPGFFGGPQCPVLGY	180		
142	-----PGVGGAFAGICPGVPGFFGGPQCPVLGY	168		
181	PIKAPKLPGCVGLPYTTGKLPGYGPGGVAGAGKAGYPTGTGVPQAAAAAKAAAKF	240		
169	PIKAPKLPGCVGLPYTTGKLPGYGPGGVAGAGKAGYPTGTGVPQAAAAAKAAAKF	228		
241	GAGAAAGVLPGVGAGVPGVPGALPGTGGTAGVCTPAAAAAANAANAANAAGLVPGGG	300		
229	GAGAAAGVLPGVGAGVPGVPGALPGTGGTAGVCTPAAAAAANAANAANAAGLVPGGG	288		

used to produce the

CC
comprCC
compr

CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
CC wrinkle or hand lotions, also as surgical implants, foods and industrial
CC products. The hybrid protein have controllable GAG-binding properties,
CC depending on presence or absence of a specific fragment, designated
CC peptide 26A, from hIE. The present sequence represents a human
CC tropoelastin derivative SHELDeltamodified
XX
SQ Sequence 660 AA;

Query Match 89.9%; Score 3248.5; DB 2; Length 660;
Best Local Similarity 91.7%; Pred. No. 1.1e-180;
Matches 644; Conservative 3; Mismatches 8; Indels 47; Gaps 6;

QY 1 GGVFCALPGGVPGGVFFYFAGLGGALGGALPGGKPLKVPVGGLAGAGLGAFAVPT 60
Db 2 GGVFCALPGGVPGGVFFYFAGLGGALGGALPGGKPLKVPVGGLAGAGLGAFAVPT 25

QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVSGAGAVPQPGAGVPGKVPVGL 120
Db 26 -----VPGGVADAAAAYKAAKAGAGLGGVPGVGGVSGAGAVPQPGAGVPGKVPVGL 80

QY 121 PGVYVPG-GVLPFGARFPGVGLPGVPTGAGVKPKAPGVGGAFAGIPGVGPGQPGVPLG 179
Db 81 PGVYVPGFAGVPGARFPGVGLPGVPTGAGVKPKAPGVGGAFAGIPGVGPGQPGVPLG 140

QY 180 YPIKAPKLPGGVGLPYTTTGLPKPYGPGGVAGAGKAGVPTGTGVPQAAAAAATAAK 239
Db 141 YPIKAPKLPGGVGLPYTTTGLPKPYGPGGVAGAGKAGVPTGTGVPQAAAAAATAAK 199

QY 240 FGAAGAA--GVLPVGGAGVPGVPAIPGTTGGTAGVTPAAAAAATAAKAAGAGLV 297
Db 200 FGAAGAAFGVGGVGGVPGVPAIPGTTGGTAGVTPAAAAAATAAKAAGAGLV 259

QY 298 PGGPFGPGVGVPGAG--VPGVGVPGAGIPVPGAGIPGAAGVPGVVSPEAAAAATAAK 356
Db 260 PGGPFGPGVGVPGVPGAGIPVPGAGIPGAAGVPGVVSPEAAAAATAAK 319

QY 357 YGARPGVGGVGGIPTTYGVGAGGPGFPGVGGVGGIPGVAGVPSVGGVPGVGGISPEAQ 416
Db 320 YGARPGVGGVGGIPTTYGVGAGGPGFPGVGGVGGIPGVAGVPSVGGVPGVGGISPEAQ 379

QY 417 AAAAAKAAKYGVTAAAAAATAAKAQAQGLVPGVGVAGVPGVAGVPGVGLAPGVG 476
Db 380 AAAAAKAAKYGVTAAAAAATAAKAQAQGLVPGVGVAGVPGVAGVPGVGLAPGVG 439

QY 477 VAPGVGVAGVGVAGVPGVGGVAAKAAQAQGLVPGVGVAGVPGVAGVPGVGL 536
Db 440 VAPGVGVAGVGVAGVPGVGGVAAKAAQAQGLVPGVGVAGVPGVAGVPGVGL 499

QY 537 GVGAGVPLGVGAGVPGFAGVPGALAAKAAKAAQAQGLVPGVGGVGGIPGVGGVAG 596
Db 500 GVGAGVPLGVGAGVPGFAGVPGALAAKAAKAAQAQGLVPGVGGVGGIPGVGGVAG 558

QY 597 PAAAAAATAAKAAQAQGLVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGG 656
Db 559 PAAAAAATAAKAAQAQGLVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGG 618

QY 657 GGVLGAGGQPLGVGAARPGFGLSPIPPGACLGKACGRKRK 698
Db 619 GGVLGAGGQPLGVGAARPGFGLSPIPPGACLGKACGRKRK 660

RESULT 19
ADM03792
ID ADM03792 standard; protein; 663 AA.
XX AC
XX ADM03792;
XX DT 20-MAY-2004 (first entry)
XX DE Human protein of the invention SEQ ID NO:2477.
XX KW human; gene therapy; diagnostic marker; pharmaceutical.

XX Homo sapiens.
OS
XX EF1347046-A1.
XX
XX 24-SEP-2003.
XX
XX 12-APR-2002; 2002EP-00008400.
XX
XX 22-MAR-2002; 2002JP-00137785.
XX
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
XX Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irle R, Tamechika I;
XX Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
XX WPI; 2003-723558/69.
XX N-PSDB; ADM01349.
XX
XX New polynucleotides and polypeptides are useful in gene therapy, for
XX developing a diagnostic marker or medicines for regulating their
XX expression and activity, or as a target of gene therapy.
XX
XX Claim 1; SEQ ID NO 2477; 305pp; English.
XX
XX The invention relates to a novel human polynucleotide and the encoded
XX polypeptide. A polynucleotide of the invention may have a use in gene
XX therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
XX as a primer for synthesizing the polynucleotide or as a probe for
XX detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
XX useful in gene therapy, for developing a diagnostic marker or medicines
XX for regulating their expression and activity, or as a target of gene
XX therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
XX are useful as pharmaceutical agents. The present sequence represents a
XX protein sequence of the invention.
XX
XX Sequence 663 AA;

Query Match 89.4%; Score 3233.5; DB 7; Length 663;
Best Local Similarity 90.8%; Pred. No. 8.5e-180;
Matches 634; Conservative 0; Mismatches 3; Indels 61; Gaps 2;

QY 1 GGVPGCAIPGGVPGGVPGVPGAGLGGGALGGGKPLKVPVGGLAGAGLGAFAVPT 60
Db 27 GGVPGCAIPGGVPGGVPGVPGAGLGGGALGGGKPLKVPVGGLAGAGLGG 76

QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVSGAGAVPQPGAGVPGKVPVGL 120
Db 77 -----AGAGLGGVPGVGGVSGAGAVPQPGAGVPGKVPVGL 115

QY 121 PGVYVPGGVLPGARFPGVGLPGVPTGAGVKPKAPGVGGAFAGIPGVGPGQPGVPLGY 180
Db 116 PGVYVPGGVLPGARFPGVGLPGVPTGAGVKPKAPGVGGAFAGIPGVGPGQPGVPLGY 175

QY 181 PIKAPKLPGGVGLPYTTTGLPKPYGPGGVAGAGKAGVPTGTGVPQAAAAAATAAK 240
Db 176 PIKAPKLPGGVGLPYTTTGLPKPYGPGGVAGAGKAGVPTGTGVPQAAAAAATAAK 235

QY 241 GAGAGVLPVGGVGGVPGVPGALPGTGGIAGVGTAAAAAATAAKAAGLVPGG 300
Db 236 GAGAGVLPVGGVGGVPGVPGALPGTGGIAGVGTAAAAAATAAKAAGLVPGG 295

QY 301 PGFPGVGVGGVPGVPGVPGAGIPVVPAGIPGAAPVGVSPAAAAAATAAKAAGLV 360
Db 296 PGFPGVGVGGVPGVPGVPGAGIPVVPAGIPGAAPVGVSPAAAAAATAAKAAGLV 355

QY 361 PGVGVGGIPVYGVGAGGPGFPGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGG 420
Db 356 PGVGVGGIPTVGVGAGGPGFPGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGG 415

QY 421 AKAAYKVGTEPAAAAAATAAKAQAQGLVPGVGVAGVPGVAGVPGVGLAPGVG 480
Db 421 AKAAYKVGTEPAAAAAATAAKAQAQGLVPGVGVAGVPGVAGVPGVGLAPGVG 480

so that susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is increased. The derivatives have with reduced susceptibility, and can be used where the wild-type protein would be degraded too easily, e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivatives, and other polypeptides containing tropoelastin derivative-derived protease-susceptibility sites, are useful in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents and for inducing chemotaxis. They are also useful for proliferation or growth inhibition, particularly of smooth muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets. Peptidomimetics that mimic the protease cleavage site in tropoelastin derivatives are competitive inhibitors of the protease, and are used for protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit protease activity that causes blood clotting

SQ Sequence 571 AA;

Query Match 79.4%; Score 2869; DB 3; Length 571;
 Best Local Similarity 99.6%; Pred. No. 1e-158;
 Matches 552; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGVPGALPGGVGGVFPVGGAGLGGALGGALGGKPLKVPVGGLAGLGGAGLGAFFAVT 60
 Db 1 GGVPGALPGGVGGVFPVGGAGLGGALGGALGGKPLKVPVGGLAGLGGAGLGAFFAVT 60

QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVSAGAVVPGAGVKKPKVPGVGL 120
 Db 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVSAGAVVPGAGVKKPKVPGVGL 120

QY 121 PGVYGGVLPGARFPFGVGLPGVPTGAGVKPKAPGVGGAFAGIPGVPGFGPGVPLGY 180
 Db 121 PGVYGGVLPGARFPFGVGLPGVPTGAGVKPKAPGVGGAFAGIPGVPGFGPGVPLGY 180

QY 181 PIKAPKLPGGYGLPYTTGKLPYGYGGVAGAAKAGAGYPTGTGVPQAAAAAATAAKAF 240
 Db 181 PIKAPKLPGGYGLPYTTGKLPYGYGGVAGAAKAGAGYPTGTGVPQAAAAAATAAKAF 240

QY 241 GAGAAGVLPVGGAGVPGVPGAGIPVPGAGIPVPGAGIPVPGAGIPVPGAGIPVPGAG 300
 Db 241 GAGAAGVLPVGGAGVPGVPGAGIPVPGAGIPVPGAGIPVPGAGIPVPGAGIPVPGAG 300

QY 301 PGFPGVGVPGAGVPGVPGAGIPVPGAGIPVPGAGIPVPGAGIPVPGAGIPVPGAG 360
 Db 301 PGFPGVGVPGAGVPGVPGAGIPVPGAGIPVPGAGIPVPGAGIPVPGAGIPVPGAG 360

QY 361 PGVGGVGGIPTYGVGGFFPGFPGVGGIPGVAGVPSVGGVPGVGGVPGVGGVPGVGG 420
 Db 361 PGVGGVGGIPTYGVGGFFPGFPGVGGIPGVAGVPSVGGVPGVGGVPGVGGVPGVGG 420

QY 421 AKAAKYGVGTTPAAAATAAKAAKAAQGLVPGVGVAPGVGVAPGVGVAPGVGVAPGV 480
 Db 421 AKAAKYGVGTTPAAAATAAKAAKAAQGLVPGVGVAPGVGVAPGVGVAPGVGVAPGV 480

QY 481 VGAVPGVGVAPGIGPGVAAAAAKAAKAAQGLVPGVGVAPGVGVAPGVGVAPGVGV 540
 Db 481 VGAVPGVGVAPGIGPGVAAAAAKAAKAAQGLVPGVGVAPGVGVAPGVGVAPGVGV 540

QY 541 GVPGLGVAGVPGF 554
 Db 541 GVPGLGVAGVPGF 554

RESULT 23

AA569135

ID AA569135 standard; protein; 515 AA.

XX

AC

AA569135;

XX

DT

30-MAY-2000 (first entry)

XX

DE Amino acid sequence of a human tropoelastin derivative.
 XX
 KW Tropoelastin; derivative; proteolysis; protease; antiwrinkle;
 KW hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;
 KW peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.
 XX
 OS Homo sapiens.
 XX
 PN WO200004043-A1.
 XX
 PD 27-JAN-2000.
 XX
 PF 19-JUL-1999; 99WO-AU000580.
 XX
 PR 17-JUL-1998; 98AU-00004723.
 XX
 PA (UNSY) UNIV SYDNEY.

XX Weiss AS;

XX WPI; 2000-182399/16.

XX New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and cell growth.

XX Disclosure; Page 131-133; 136pp; English.

XX The present sequence represents a human tropoelastin derivative, which is representative of tropoelastin derivatives of the invention. In the tropoelastin derivatives of the invention a subsequence has been mutated so that susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is increased. The derivatives have with reduced susceptibility, and can be used where the wild-type protein would be degraded too easily, e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivatives, and other polypeptides containing tropoelastin derivative-derived protease-susceptibility sites, are useful in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents and for inducing chemotaxis. They are also useful for proliferation or growth inhibition, particularly of smooth muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets. Peptidomimetics that mimic the protease cleavage site in tropoelastin derivatives are competitive inhibitors of the protease, and are used for protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit protease activity that causes blood clotting

XX Sequence 515 AA;

Query Match 74.1%; Score 2680; DB 3; Length 515;
 Best Local Similarity 100.0%; Pred. No. 8.6e-148;
 Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGVPGALPGGVGGVFPVGGAGLGGALGGALGGKPLKVPVGGLAGLGGAGLGAFFAVT 60
 Db 1 GGVPGALPGGVGGVFPVGGAGLGGALGGALGGKPLKVPVGGLAGLGGAGLGAFFAVT 60

QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVSAGAVVPGAGVKKPKVPGVGL 120
 Db 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVSAGAVVPGAGVKKPKVPGVGL 120

QY 121 PGVYGGVLPGARFPFGVGLPGVPTGAGVKPKAPGVGGAFAGIPGVPGFGPGVPLGY 180
 Db 121 PGVYGGVLPGARFPFGVGLPGVPTGAGVKPKAPGVGGAFAGIPGVPGFGPGVPLGY 180

QY 181 PIKAPKLPGGYGLPYTTGKLPYGYGGVAGAAKAGAGYPTGTGVPQAAAAAATAAKAF 240
 Db 181 PIKAPKLPGGYGLPYTTGKLPYGYGGVAGAAKAGAGYPTGTGVPQAAAAAATAAKAF 240

QY 241 GAGAAGVLPVGGAGVPGVPGAGIPVPGAGIPVPGAGIPVPGAGIPVPGAGIPVPGAG 300
 Db 241 GAGAAGVLPVGGAGVPGVPGAGIPVPGAGIPVPGAGIPVPGAGIPVPGAGIPVPGAG 300

CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
xx
SQ Sequence 864 AA;

Query Match 64.1%; Score 2315.5; DB 7; Length 864;
Best Local Similarity 60.4%; Pred. No. 1.8e-126;
Matches 529; Conservative 26; Mismatches 102; Indels 219; Gaps 34;

Qy 1 GGVPGLPGGVPGGVFPYAGL-GALGGALPGGKPLKP-----VPGGLAGAGL 49
Db 30 GGVPGLPGGVPGGVFPYAGLGGGLGGALPGGKPKPGAGLLGAFAGPGGLGGAGP 89

Qy 50 GAGLGAPPAVTFPGALVPGGVADAAAYK-AAKAGAGLGGVPGV----- 92
Db 90 GAGLSY--ASRPGGLVPGGGAGAAAYKAAKAGAGLGGIGGVPGGVGVPGVAVG 147

Qy 93 -----GGLGVSAAGVVPQAGV---KPGKVPGVGLPGVYPGVLP--GARF 134
Db 148 GVPAGVGGIGGIGLGVSTGAVVPLGAGVGAGKPGKVPGVGLPGVYPGVLPQTGARF 207

Qy 135 PGVGLPGVFTAGVVKPAP--GVGGAFAPIPGVPGFGPQPGVPLGPIKAPLPGVGL 193
Db 208 PGVGLPGVFTGTGKAKVPGGGGAFSGIPGVPGFGQPGVPLGPIKAPLPGVGL 267

Qy 194 PYTTKPLPGVPGGVAGAAKAGVPTGTGVPOAAAAAATAAKAFGAGAGVLPVGG 253
Db 268 PYTNKLPY-----GVAGAGKAGTPTGTGVGSO-AAVAAKAAKYGAGGGVLPVGG 321

Qy 254 AGVPGVPAIPGIGIAGVTPAAAAAATAAKAAKYGAGAGVPGGVVPGVPCA 313
Db 322 GGI PGAGAIPIGGITGAGTPAAAAAATAAKAAKYGAGAGVPGGV-----VRVPGA 376

Qy 314 GVPVGVPGV-----AGIPVPGAGIPGAIV---PGVVSPEAAAAKAAKAY 357
Db 377 GIPVGI PGVGGIPGVGGIPGVGGIPGVGGIPGVGGIPGVGGIPGVGGIPGVGG 436

Qy 358 GARPVGVGGIPTVGVGAGGPGFGVGV----- 385
Db 437 GARGGV---GIPTYGVGAGGPGFGVGVGAGAGLGGASQAAAAAATAKAAKYGAGGAGTGG 493

Qy 386 -----GGIPGV--AGVP-----SVGVPVGVGGVPGVGISPEAAAAKAAKAYG 427
Db 494 LVPGAVPGALPGAVFGALPGAVFGALPGAVPGVPGTGGVPGAG-----TPAAAA- 542

Qy 428 VGTAAAAAATAKAAQFGLVPGVAPGVGVPAGVAPGVGVLGAGVAPGVVAPGV 487
Db 543 -----AAAAAATAKAAQGLVPGVGVPG--GV--GVGGLPG--GVGPG--GVT--GIGTGPST 592

Qy 488 GVAPG-IGPGVAAAAAATAKAAQFGLVPGVAPGVGVLGAGVPGVPGVPGV 546
Db 593 GLVPGDLGAGTAAAAAATAKAAQFGLVPGVAPGVGVLGAGVPGVPGVPGVAGAG--GFG 650

Qy 547 VGAGVPGF--GAVPGALAAAAKAAKYGAA-----VPGVGLGGLGALGGV-----GIFG 590
Db 651 AGAGVPGFAGAVPGSLAATAKAAKYGAAAGLGGPGGLGGPGGPGGPGGPGGPGV 710

Qy 591 GVVGAPAAAAAATAKAAQFGLVPGVAPGVGVLGAGVPGVPGVPGVPGV 630
Db 711 GVAGGAP-AAAAAATAKAAQFGLGAGGAGLGGAGLGGAGLGGAGLGGAGLGGAGG 769

Qy 631 --VPGVGGIGIPAAAAAATAKAAKYGAGLGGVGGAGQFPLGGVAAAPFGGLSPFP----- 684
Db 770 VIPGAVGLGVSPAAAAAATAKAAKYGAGLGGV--GARFPFGGVAAAPFGGLSPFPVPGGAG 828

QY 695 -----GGACLGKACGRKK 698
 DB 829 GLGVGGKFPKPYGGALGALGYQGGCFKSGCRKK 864

RESULT 25

ID AAB88422 standard; protein; 472 AA.

AC AAB88422;

DT 23-MAY-2001 (first entry)

DE Human membrane or secretory protein clone PSEC0191.

KW Human; secretory protein; membrane protein; vaccine; gene therapy;
 KW rheumatoid arthritis; diabetes.

OS Homo sapiens.

PN EPI067182-A2.

XX 10-JAN-2001.

PF 07-JUL-2000; 2000EP-00114090.

PR 08-JUL-1999; 99JP-00194179.

PR 11-JAN-2000; 2000JP-00118775.

PR 02-MAY-2000; 2000JP-00183766.

XX (HELI-) HELIX RES INST.

PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;

XX WPI; 2001-093989/11.

DR N-PSDB; AAF93849.

PT Nucleic acids encoding secretory proteins/membrane proteins, useful in
 PT gene therapy or as candidate target molecules in drug development.

XX Claim 1; SEQ ID NO 212; 609pp + Sequence Listing; English.

CC This invention relates to nucleic acid sequences AAF93744 - AAF93916
 CC which encode human secretory or membrane proteins represented by AAB88317
 CC - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and
 CC AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the
 CC invention. The invention also includes methods for the production of
 CC antibodies directed against the proteins, and cDNA sequences, which can
 CC be used in vaccines. The polynucleotide sequences can be used in gene
 CC therapy. The polynucleotide sequences and the proteins they encode may be
 CC used in the prevention, treatment and diagnosis of diseases associated
 CC with inappropriate secretory protein/membrane protein expression. The
 CC nucleic acids and complementary sequences may also be used as DNA probes
 CC in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect
 CC and quantitate the presence of similar nucleic acid sequences in samples.
 CC They may also be used to study the expression and function of secretory
 CC proteins/membrane polypeptides and their role in metabolism. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC against them and in assays to identify modulators (agonists and
 CC antagonists) of expression and activity. The antibodies and antagonists
 CC may also be used as therapeutic agents to down regulate expression and
 CC activity. The antibodies may also be used as diagnostic agents for
 CC detecting the presence of the polypeptides in samples (e.g. by enzyme
 CC linked immunosorbent assay (ELISA)). Examples of diseases which may be
 CC treated include rheumatoid arthritis and diabetes

XX Sequence 472 AA;

Query Match

Best Local Similarity 46.4%; Score 1679; DB 4; Length 472;

Matches 356; Conservative 60.5%; Pred. No. 8, 8e-90;

Mismatches 3; Indels 226; Gaps 5;

QY 1 GGVPGAIPGGVGGVFPFGALGGALGGKPLKPVFGLAGAGLAGAFAVPT 60

DB 27 GGVPGAIPGGVGGVFPFGALGGALGGKPLKPVFGLAGAGLAGA----- 81
 QY 61 FFGALVPGGVADAAAAAAYKAAKAGAGLGGVPGVGLGVSGAGAVVQPGAGVFKGVPGVL 120
 DB 82 -----LGGVGI----- 87
 QY 121 PGVTPGGVLPGARFPGGVLPVPGVTPGAGVKPAPGVGGAFAGIPGVPGFGPGQVPLGY 180
 DB 88 ----- 87
 QY 181 PIKAPKLPGGYGLPYTTTKLPYGYGPGGVAGAAGKAGYPTGTGTGVPQAAAAAATAAKF 240
 DB 88 -----PGWVGA-----GP----- 96
 QY 241 GAGAAAGVLPVGGAGVPGVPGAIPGIGGIAGVGTAAAAAATAAKAAYGAAAGLVPGG 300
 DB 97 -----AAAAAATAAKAAYGAAAGLVPGG 119
 QY 301 PGFGPGVVGVPAGVPGVPGAGIPVVPAGAGIPGAAPVGVSPAAAAAATAAKAAYGAAAGLVPGG 360
 DB 120 PGFGPGVVGVPAGVPGVPGAGIPVVPAGAGIPGAAPVGVSPAAAAAATAAKAAYGAAAGLVPGG 179
 QY 361 PGVVGSGIPTGYGAGSGFPGFVGVGIPGVAGVPSVGGVPGVGGVPGVGSISPEAQAAAA 420
 DB 180 PGVVGSGIPTGYGAGSGFPGFVGVGIPGVAGVPSVGGVPGVGGVPGVGSISPEAQAAAA 239
 QY 421 AKAAYKVGVTAAAAAATAAKAAYGAAAGLVPGVPGVAPGVGVPAGVGLAGVGVAPG 480
 DB 240 AKAAYK-----GLVPGVPGVAPGVGVPAGVGLAGVGVAPG 280
 QY 481 VGVAPGVGVPAGVPGVPGVAAAAAATAAKAAYGAAAGLVAGIPGILGVGGVPGVGLGVGA 540
 DB 281 VGVAPGVGVPAGVPGVPGVAAAAAATAAKAAYGAAAGLVAGIPGILGVGGVPGVGLGVGT 340
 QY 541 GVPGLGVGAGVPGFPGVPGVPGVAAAAAATAAKAAYGAAAGLVGGILGALGGVGI 588
 DB 341 GVPGLGVGAGVPGFPGVPGVPGVAAAAAATAAKAAYGAAAGLVGGILGALGGVGI 388

RESULT 26

AAR80253

ID AAR80253 standard; peptide; 988 AA.

XX AAR80253;

AC AAR80253;

XX 17-APR-1996 (first entry)

DT Polymer SCLP7.

DE Fibroin; elastin; repeat sequence; suture; thread; pin; gel; silk;

XX polymer; E.coli; EC3.

XX Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..76

FT /note= "polymer repeat block sequence"

XX W09524478-A1.

PN 14-SEP-1995.

PD 10-MAR-1995; 95WO-US002772.

PF 11-MAR-1994; 94US-00212237.

XX (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

XX Cappello J;

XX WPI; 1995-328270/42.

XX

Matches	338;	Conservative	49;	Mismatches	248;	Indels	178;	Gaps	46;
---------	------	--------------	-----	------------	------	--------	------	------	-----

QY		320	VPGAGIPVPGGAGIPGAHVPGVSPPEAAAKAAKAAKYGARPPGVGGIPIYGVGAGFP	379
			: :	
D _b		336	VPVG---VPGVGPVGPVGPVGGAGAGSGA--GAGSGAGAGS-----GAGAGSVP	386
			: :	
QY		380	GFGVGVGGIPGVAGVPSVGGVPGV-----GYPGVGISPEAQAAAAAKAYKYGVTTPAAAA	435
			: :	
D _b		387	GVGPVGPVGPV-GVPGV-GVPGVGPVGPVGPVGPV-PGVGGAGAGSGA--GAGSGAGAG	441
			: :	
QY		436	AKAATAQAQGLVPFPGVAPCGVAPAGVAPGVCLAPGVAPGVGPVAPGVGPVAPGIGP	495
			: : : : :	
D _b		442	SGAGA-----GSVPFPGV-PGVGV-PGVGV-PGVGV-PGVGV-PGVGV-PGVGG	489
			: : : :	
QY		496	GGVAATAAKAAKAAQLRAAAGLGCAGIPGLGV-GVGPVGLGV-GAGVPLGLV-GAGVP	552
			: : : : :	
D _b		490	AGAGSGAGAGSGAGAGSGAGSVPGVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPV	549
			: : : :	
QY		553	GFGAV-----PCALAAAANKY-----GAAPVGV-LGGLGALG----G	585
			: : : :	
D _b		550	GVGGAGAGSGAGAGSGAGAGSGAGAGSVPGVGPVGPVGPVGPVGPVGPVGPVGPVGP	609
			: : : :	
QY		586	VGIFG-GVVGAPAAAAAAXAAKAQFGLVGAAGLGLGVGGLGVPGV-----GL	637
			: : : :	
D _b		610	VGVPVGGAGAGSGAGAGSGAGAGSGAGAGSVPGVGPVGPVGPVGPVGPVGPVGPVGPV	669
			: : : :	
QY		638	G-----GIPTAAAAKAYCAGLAGLVLG---CAGQFLICGVAAKPCFGLSPI-FPG	685
			: : : :	
D _b		670	GVPGVGPVGGAGAGSGAGAGSGAGAGSGAGAGSVPGVGV---PGVPGVGPVGP	722
			: : : :	

RESULT 29	
ABP53473	
ID	ABP53473 standard; protein; 832 AA.
XX	
AC	ABP53473;
XX	
DT	20-NOV-2002 (first entry)
XX	
DE	Protein polymer SEUP8 polymer block amino acid sequence.
XX	
KW	protein crystallisation; elastin; collagen; keratin; controlled release;
KW	physical dimension

RESULT 30
AAR80251
ID ID AAR80251 standard; peptide; 936 AA.
XX
AC AAR80251;

XX	17-APR-1996	(first entry)	
XX	Polymer Selp0.		
XX	Fibroin; elastin; repeat sequence; suture; thread; pin; gel; silk;		
KW	polymer; E.coli; EC3.		
XX	Synthetic.		
OS			
XX	Key	Location/Qualifiers	
FT	Peptide	1..52	
FT		/note= "polymer repeat block sequence"	
XX	WO9524478-A1.		
XX	14-SEP-1995.		
XX	10-MAR-1995;	95WO-US002772.	
XX	11-MAR-1994;	94US-00212237.	
XX	(PROT-) PROTEIN POLYMER TECHNOLOGIES INC.		
FA			
XX	Cappello J;		
PI			
XX	WPI; 1995-328270/42.		
DR			
XX	Protein polymer comprising alternating blocks of fibroin and elastin		
PT	units - used to form a device e.g. a suture to keep separated viable		
PT	tissue together.		
XX			
XX	Example 1; Page 22-24; 46pp; English.		
FS			
XX	The sequences represented by AAR80251-R80257 are polymers constructed of		
CC	repeating blocks of fibroin-like (see AAR80249) and elastin-like (see		
CC	AAR80250) units. This sequence contains 18 repeats of a block consisting		
CC	of 8 elastin-like repeats followed by 2 fibroin-like repeats. The DNA		
CC	sequences encoding these polymers were inserted into plasmids which were		
CC	used to transform E.coli strain EC3. The polymers could then be isolated		
CC	from the fermented strains by standard centrifugation techniques. The		
CC	polymers are used to form a device (such as a suture, pin, thread, gel or		
CC	film) to keep separated viable tissue together. By varying the lengths of		
CC	each of the two repetitive units, and by altering the lengths of the blocks		
CC	moderately. By reducing the number of repeating units of this sequence, or		
CC	by increasing the number of units of the elastin like repeat, a faster		
CC	rate of resorption can be achieved. Of the polymers, this sequence had		
CC	the fastest resorption rate. The Selp4 (see AAR80255) and Selp5		
CC	(seeR80256) polymers showed no resorption after seven weeks. The other		
CC	three polymers showed intermediate resorption. No data was given for		
CC	Selp6 (see AAR80257)		
XX			
XX	Sequence 936 AA;		
XX			
XX	Query Match	31.5%; Score 1139.5; DB 2; Length 936;	
XX	Best Local Similarity	41.7%; Pred. No. 3.1e-58;	
XX	Matches 350; Conservative	44; Mismatches 228; Indels 217; Gaps 55;	
XX			
QY	2	GVPG-ATPG-GVPG- ---GVFPYFAGLALGGGALGPQ-----	33
DB	114	GVPGVGVPVGVPVGVPVGVPVGVPVGVPVGVPVGVPVGVPVGVPVGVPVGVPVGVP 173	
QY	34	-----GKPLKPVPG-VLGAAGLGLAGLCAFAVTPFGALVPGGVADAAAYKAA 80	
DB	174	GVGVPGVGVPVGVPVGVPVGVPVGVPVGVPVGVPVGVPVGVPVGVPVGVPVGVP 233	
QY	81	KAGAGLG- -GVPGVGGLVGSAGAVVPQFGAGVKFG- KVPGVGLPGV- YPGGVLPGARFPG 136	
DB	234	VPGVGVPGVGVPVGVPVGAGAGSGA- ---GAGSVPGVGVPVGVPVGVPVGVPVGVP 288	
QY	137	VGVLPGVPTGAGVKPKAPGVGGAPAG- -----IPGVPGPGPGPGVPL- GYPIKAPKLP 188	

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OM protein - protein search, using sw model

Run on: November 19, 2004, 15:19:20 ; Search time 10.014 Seconds
(without alignments)
1755.321 Million cell updates/sec

Title: US-09-743-818A-72

Perfect score: 253

Sequence: 1 AAGLAGIGELGVGVGVPG.....LGVGAGVPGFAGAGDEGVRR 49

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A_Geneseq_23Sep04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	ID	Description
1	253	100.0	216	2	AAW01310	Human tro
2	253	100.0	730	2	AAW46315	Human ela
3	253	100.0	731	3	AAW69068	Amino aci
4	253	100.0	731	4	AAW66657	Human ela
5	253	100.0	731	6	ABU08725	Human ela
6	253	100.0	731	7	ADL96420	Human ela
7	253	100.0	733	2	AAW56653	Synthetic
8	253	100.0	733	2	AAW01301	Amino aci
9	253	100.0	757	7	ABG75223	Human tro
10	253	100.0	757	7	ADP65160	Human tro
11	212	83.8	183	3	AAW01311	Human ela
12	212	83.8	183	3	AAW69138	Human tro
13	212	83.8	617	7	ADB64761	Amino aci
14	212	83.8	660	2	AAW01303	Human tro
15	212	83.8	663	7	ADM03792	Human tro
16	212	83.8	692	7	AAW40134	Human tro
17	212	83.8	698	2	AAW01302	Human tro
18	212	83.8	698	3	AAW69069	Human tro
19	212	83.8	711	7	AAW40132	Amino aci
20	212	83.8	712	3	AAW08630	Human tro
21	212	83.8	730	3	AAW08631	Fusion pr
22	212	83.8	730	5	AAW017360	Human ela
23	212	83.8	730	8	ADQ19747	Human sof
24	212	83.8	870	7	ADQ08527	Novel pro
25	208	82.2	472	4	AAW88422	Human mem

26	189	74.7	571	3	AAW69071	Amino aci
27	181	71.5	864	7	ADE56670	Rat Prote
28	159	62.8	34	1	AAW71455	Sequence
29	149	58.9	60	5	ABP53469	SELP8K DN
30	149	58.9	64	2	AAW80339	PPAS SELP
31	149	58.9	64	2	AAW80338	Protein p
32	149	58.9	64	2	AAW80340	PPAS SELP
33	149	58.9	64	2	AAW09211	SELP8 mon
34	149	58.9	64	2	AAW09212	SELP8 mon
35	149	58.9	64	2	AAW53538	Amino aci
36	149	58.9	64	2	AAW49726	SELP8K mo
37	149	58.9	64	2	AAW49725	SELP8 mon
38	149	58.9	64	2	AAW49727	SELP8E mo
39	149	58.9	64	3	AAW51881	Plasmid p
40	149	58.9	64	5	ABG31411	SELP8K mo
41	149	58.9	64	5	ABP53464	SELP8K mo
42	149	58.9	64	7	ABW01626	SELP8K mo
43	149	58.9	64	7	ABW01627	SELP8K mo
44	149	58.9	217	2	AAW80347	Protein p
45	149	58.9	223	2	AAW80348	Protein p
46	149	58.9	281	2	AAW49736	Protein p
47	149	58.9	287	2	AAW49737	Protein p
48	149	58.9	312	5	ABP53480	Protein p
49	149	58.9	378	2	AAW09219	SELP8K po
50	149	58.9	378	2	AAW53545	Amino aci
51	149	58.9	378	3	AAW51889	Plasmid p
52	149	58.9	378	5	ABG31419	SELP8K pr
53	149	58.9	378	7	ABW01635	Plasmid p
54	149	58.9	696	5	ABP53470	SELP8K re
55	149	58.9	696	5	ABP53482	Protein p
56	149	58.9	696	8	ADK51955	Repeat pr
57	149	58.9	768	5	ABP53481	Protein p
58	149	58.9	768	5	ABP53466	SELP8 rel
59	149	58.9	877	2	AAW80335	Protein p
60	149	58.9	877	2	AAW49724	Protein p
61	149	58.9	884	2	AAW80341	Protein p
62	149	58.9	884	2	AAW09213	SELP8K po
63	149	58.9	884	2	AAW53541	Expected
64	149	58.9	884	2	AAW49728	SELP8K po
65	149	58.9	884	3	AAW51882	Plasmid p
66	149	58.9	884	5	ABG31412	SELP8K po
67	149	58.9	884	7	ABW01628	Plasmid p
68	149	58.9	968	5	AAW18320	Silk elas
69	149	58.9	1002	2	AAW09218	SELP8K po
70	149	58.9	1002	2	AAW53544	Amino aci
71	149	58.9	1002	2	AAW51888	Plasmid p
72	149	58.9	1002	5	ABG31418	SELP8K pr
73	149	58.9	1011	3	ABW01634	Plasmid p
74	149	58.9	1011	3	AAW78287	SELP8K pr
75	149	58.9	1011	5	ABG69277	SELP8K pr
76	149	58.9	1011	7	ABG69277	Silk/Elas
77	149	58.9	1170	2	AAW26351	Recombina
78	149	58.9	1170	2	AAW26351	SELP8K syn
79	149	58.9	1412	2	AAW53527	Amino aci
80	149	58.9	1413	1	AAW82957	Amino aci
81	149	58.9	1413	2	AAW41008	ESBI prot
82	149	58.9	1413	2	AAW26343	ESBI mult
83	149	58.9	1464	3	AAW78278	ESBI synt
84	149	58.9	1465	5	ABG69268	ESBI prot
85	149	58.9	1465	7	AAW49727	Recombina
86	149	58.9	2055	1	AAW82960	SELP2 pro
87	149	58.9	2055	2	AAW41011	SELP2 mul
88	149	58.9	2055	2	AAW26346	SELP2 syn
89	149	58.9	2055	2	AAW53522	Amino aci
90	149	58.9	2055	3	AAW78281	SELP2 ami
91	149	58.9	2055	5	ABG69271	Silk/Elas
92	149	58.9	2055	7	AAW49726	Recombina
93	149	58.9	2257	1	AAW82961	SELP3 pro
94	149	58.9	2257	2	AAW41012	SELP3 mul
95	149	58.9	2257	2	AAW26347	SELP3 syn
96	149	58.9	2257	2	AAW53523	Amino aci
97	149	58.9	2257	3	AAW78282	SELP3 ami
98	149	58.9	2257	5	ABG69272	Silk/Elas

99 149 58.9 2257 7 ADE44977 Ade44977 Recombina
100 148.5 58.7 65 3 AAY51880 Aay51880 Crosslink

ALIGNMENTS

RESULT 1
AAY01310 ID AAY01310 standard; protein; 216 AA.
XX AC AAY01310;
XX DT 07-JUN-1999 (first entry)
XX DE Human tropoelastin derivative SHEL26-36.
XX KW Tropoelastin; hRE; elastin; glycosaminoglycan; GAG-binding; medical;
XX KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
XX KW hand lotion; surgical implant; industrial product; human; SHEL; variant.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO9903886-A1.
XX PD 28-JAN-1999.
XX PF 17-JUL-1998; 98WO-AU000564.
XX PR 18-JUL-1997; 97AU-00008117.
XX PA (UNSY) UNIV SYDNEY.
XX PI Weiss AS;
XX DR WPI; 1999-132162/11.
XX PT New derivatives of human tropoelastin - with elastin-like or
XX PT macromolecular binding properties, useful e.g. as surgical implants.
XX PS Claim 35; Page 11; 82pp; English.
XX This invention relates to a derivative or variant of human tropoelastin
XX (hRE) having elastin-like and/or macromolecule (specifically
XX glycosaminoglycan (GAG))-binding properties. Cells containing vectors
XX comprising the nucleic acids encoding the variants or derivatives are
XX used to produce the proteins recombinantly. The tropoelastin derivatives
XX or hybrid proteins containing the derivatives are useful in medical,
XX pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
XX wrinkle or hand lotions, also as surgical implants, foods and industrial
XX products. The hybrid protein have controllable GAG-binding properties,
XX depending on presence or absence of a specific fragment, designated
XX peptide 26A, from hRE. The present sequence represents a human
XX tropoelastin derivative SHEL26-36
XX Sequence 216 AA;

Query Match 100.0%; Score 253; DB 2; Length 216;
Best Local Similarity 100.0%; Pred. No. 2.1e-17;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGVLGVGAGVPGFGAGADEGVR 49
Db 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGVLGVGAGVPGFGAGADEGVR 49

RESULT 2
AAW46315 ID AAW46315 standard; protein; 730 AA.
XX AC AAW46315;
XX

23-JUL-1998 (first entry)
Human elastin containing non-natural polypeptide MFU-1 sequence.
MFU-1; minimal functional unit; elastin; human; fibrous protein;
beta-sheet; coating; wound dressing.
Homo sapiens.
Key Location/Qualifiers
Protein 374..499
/note= "MFU-1 polypeptide"
WO9805685-A2.
12-FEB-1998.
07-AUG-1997; 97WO-CA000560.
07-AUG-1996; 96US-0023552P.
07-AUG-1997; 97US-00911364.
(PROT-) PROTEIN SPECIALTIES LTD.
(HOSP-) HOSPITAL FOR SICK CHILDREN.
Rothstein A, Keeley FW, Rothstein SJ;
WPI; 1998-145551/13.
New non-natural polypeptide with multiple beta-sheet, beta-turn
structures - particularly based on human elastin, useful for coating
prostheses, as wound dressings, etc., allows ingrowth of cells.
Claim 5; Fig 1B; 39pp; English.
This represents the human elastin sequence containing the minimal
functional unit (MFU)-1 polypeptide of the invention. This MFU-1 is a
polypeptide that has at least 3 beta-sheet/ beta-turn structures, but is
not a naturally occurring fibrous protein. Each beta-sheet structure has
3-7 (preferably 5-7) amino acids and the MFU polypeptide may include at
least 1 amino acid that can take part in crosslinking. The polypeptide
can also be derived from the sequences of animal elastin, lamprin and
spider silk protein. The MFU polypeptides are self-aligning peptides
having the same primary structure as part of a natural fibrous protein.
They are used to coat prostheses made of animal or synthetic material or
metal, particularly for use as blood vessel or heart valve replacements,
wound or burn dressings, or stents. They can be used in cosmetic, elastic
or high-tensile strength materials, e.g. ropes or parachute cord.
Prostheses based on the MFU allow penetration of endothelial cells, so
become permanent, living, tissue replacements. The MFU polypeptides have
better biocompatibility than known elastin-based materials. They are well
defined, homogeneous material and are easier to manipulate and produce
than full-length elastins. They are non-thrombogenic and non-immunogenic.
Materials can be made from 2 or more different MFU polypeptides to allow
properties to be tailored for particular applications, e.g. combining the
high extensibility of elastin and the high tensile strength of spider
silk protein

Sequence 730 AA;
Query Match 100.0%; Score 253; DB 2; Length 730;
Best Local Similarity 100.0%; Pred. No. 6.4e-17;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGVLGVGAGVPGFGAGADEGVR 49
Db 516 AAAGLGAGIPGLGVGVGVPGLGVGAGVPGVLGVGAGVPGFGAGADEGVR 564

RESULT 3
AAY69068 ID AAY69068 standard; protein; 731 AA.
XX

AA69068;
 30-MAY-2000 (first entry)
 Amino acid sequence of a human tropoelastin splice form.
 Tropoelastin; derivative; proteolysis; protease; antiwrinkle;
 hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;
 peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.
 Homo sapiens.
 Key Location/Qualifiers
 Cleavage-site 441..442
 Cleavage-site 503..504
 Cleavage-site 515..516
 Cleavage-site 564..565
 WO200004043-A1.
 27-JAN-2000.
 19-JUL-1999; 99WO-AU000580.
 17-JUL-1998; 98AU-00004723.
 (UNSY) UNIV SYDNEY.
 Weiss AS;
 WPI; 2000-182399/16.
 N-PSDB; AAZ61146.
 New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and cell growth.
 Disclosure; Page 107-109; 136pp; English.
 The present sequence represents a human tropoelastin splice form. The specification describes tropoelastin derivatives, in which a subsequence has been mutated so that susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is increased. The derivatives have with reduced susceptibility, and can be used where the wild-type protein would be degraded too easily, e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivatives, and other polypeptides containing tropoelastin derivative-derived protease-susceptibility sites, are useful in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents and for inducing chemotaxis. They are also useful for proliferation or growth inhibition, particularly of smooth muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets. Peptidomimetics that mimic the protease cleavage site in tropoelastin derivatives are competitive inhibitors of the protease, and are used for protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit protease activity that causes blood clotting
 Sequence 731 AA;
 Query Match 100.0%; Score 253; DB 3; Length 731;
 Best Local Similarity 100.0%; Pred. No. 6.4e-17;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAAGLGAGIPGLGVGVPGLVGAGVPGLVGAGVPGFAGADEGVRR 49
 Db 516 AAAGLGAGIPGLGVGVPGLVGAGVPGLVGAGVPGFAGADEGVRR 564
 RESULT 4
 AAB66657
 ID AAB66657 standard; protein; 731 AA.
 XX

AAB66657;
 05-APR-2001 (first entry)
 Human elastin protein without signal peptide.
 Minimal function unit; MFU; human; elastin prosthetic.
 Homo sapiens.
 WO2001006666-A2.
 04-JAN-2001.
 29-JUN-2000; 2000WO-US017829.
 29-JUN-1999; 99US-00340736.
 (PROT-) PROTEIN SPECIALTIES LTD.
 (HSCR-) HSC RES & DEV LP.
 Rothstein A, Keeley F, Rothstein S, Stahl R;
 WPI; 2001-102886/11.
 Novel polypeptides that comprise three beta-sheet/beta-turn structures and are not naturally occurring fibrous protein, used to produce prosthesis suitable for implantation into humans, and cosmetic materials.
 Claim 1; Fig 1; 39pp; English.
 The present invention relates to a minimal functional unit (MFU) of human elastin polypeptide. This protein is useful in a cosmetic material or a prosthetic material such as prosthesis for blood vessel replacements, for heart valve replacement, tissue replacement, for covering burns, for covering wounds and stents
 Sequence 731 AA;
 Query Match 100.0%; Score 253; DB 4; Length 731;
 Best Local Similarity 100.0%; Pred. No. 6.4e-17;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAAGLGAGIPGLGVGVPGLVGAGVPGLVGAGVPGFAGADEGVRR 49
 Db 516 AAAGLGAGIPGLGVGVPGLVGAGVPGLVGAGVPGFAGADEGVRR 564
 RESULT 5
 ABO08725
 ID ABO08725 standard; protein; 731 AA.
 AC ABO08725;
 XX 25-JUN-2003 (first entry)
 DE Human elastin mature protein.
 XX Human; elastin; minimal functioning unit; MFU;
 KW beta-sheet/beta-turn structure; fibrous protein; prosthesis;
 KW blood vessel replacement; heart replacement valve; burn; wound; lamprin;
 KW spider silk; cord; rope; parachute; cosmetic; platelet binding inhibitor;
 KW platelet activation inhibitor; non-thrombogenic; cell infiltration;
 KW non-immunogenic; biocompatible; high tensile strength; elasticity;
 plasticity.
 XX Homo sapiens.
 OS US6489446-B1.
 XX 03-DEC-2002.
 PD 29-JUN-1999; 99US-00340736.
 XX


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RESULT 7
AAR56653
ID AAR56653 standard; protein; 733 AA.
XX AC AAR56653;
XX DT 25-MAR-2003 (revised)
XX DT 22-MAR-1995 (first entry)
XX DE Synthetic human tropoelastin (SHEL).
XX KW Tropoelastin; pharmaceutical; surgical dressing.
XX OS Synthetic.
XX PN WO9414958-A1.
XX PD 07-JUL-1994.
XX PF 16-DEC-1993; 93WO-AU000655.
XX PR 22-DEC-1992; 92AU-00006520.
XX PR 28-JUN-1993; 93AU-00009661.
XX PA (UNSY ) UNIV SYDNEY.
XX PI Weiss AS; Martin SL;
XX WPI; 1994-263633/32.
XX DR N-PSDB; AAQ70941.
XX SQ Synthetic polynucleotide(s) - encode recombinant tropoelastins and
PT variants.
XX PS Disclosure; Page 30; 77pp; English.
XX CC Human synthetic tropoelastin is susceptible to hydrolytic breakdown of
CC the crosslinks. Such material may be useful in e.g. surgical
CC applications, where the gradual loss of material over time is intended.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 733 AA;

Query Match 100.0%; Score 253; DB 2; Length 733;
Best Local Similarity 100.0%; Pred. No. 6.5e-17;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFAGAGDEGVRR 49
Db 518 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFAGAGDEGVRR 566

RESULT 8
AAY01301
ID AAY01301 standard; protein; 733 AA.
XX AC AAY01301;
XX DT 07-JUN-1999 (first entry)
XX DE Amino acid sequence of synthetic human tropoelastin SHEL.
XX KW Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;
XX pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
XX hand lotion; surgical implant; industrial product; human; SHEL.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO9903886-A1.
XX PD 28-JAN-1999.

Query Match 100.0%; Score 253; DB 2; Length 733;
Best Local Similarity 100.0%; Pred. No. 6.5e-17;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFAGAGDEGVRR 49
Db 518 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFAGAGDEGVRR 566

RESULT 9
ABG75223
ID ABG75223 standard; protein; 757 AA.
XX AC ABG75223;
XX DT 12-FEB-2004 (first entry)
XX DE Human tropoelastin protein.
XX KW Human; tropoelastin; elastin; body vessel occlusion; stenosis;
XX KW vascular smooth muscle cell; elastin signaling; vasotrophic.
XX OS Homo sapiens.
XX PN WO2003082203-A2.
XX PD 09-OCT-2003.
XX PF 27-MAR-2003; 2003WO-US009391.
XX PR 27-MAR-2002; 2002US-0368084P.
XX PA (UTAH ) UNIV UTAH RES FOUND.
XX PI Li DY, Karnik S;
XX WPI; 2003-833516/77.

Use of an agent that promotes elastin signaling in smooth muscle cells
for e.g. decreasing or preventing occlusion of a body vessel by smooth
muscle cells, treating or preventing obstructive vascular disease, or

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XX PF 17-JUL-1998; 98WO-AU000564.
XX PR 18-JUL-1997; 97AU-00008117.
XX PA (UNSY ) UNIV SYDNEY.
XX PI Weiss AS;
XX WPI; 1999-132162/11.
XX DR N-PSDB; AAX27704.
XX PT New derivatives of human tropoelastin - with elastin-like or
XX macromolecular binding properties, useful e.g. as surgical implants.
XX PS Disclosure; Fig 1; 82pp; English.
XX CC The invention relates to a derivative or variant of human tropoelastin
XX (hTE) having elastin-like and/or macromolecule (specifically
XX glycosaminoglycan (GAG))-binding properties. Cells containing vectors
XX comprising the nucleic acids encoding the variants or derivatives are
XX used to produce the proteins recombinantly. The tropoelastin derivatives
XX or hybrid proteins containing the derivatives are useful in medical,
XX pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
XX wrinkle or hand lotions, also as surgical implants, foods and industrial
XX products. The hybrid protein have controllable GAG-binding properties,
XX depending on presence or absence of a specific fragment, designated
XX peptide 26A, from hTE. The present sequence represents the amino acid
XX sequence of the synthetic human tropoelastin SHEL
XX SQ Sequence 733 AA;

Query Match 100.0%; Score 253; DB 2; Length 733;
Best Local Similarity 100.0%; Pred. No. 6.5e-17;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFAGAGDEGVRR 49
Db 518 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFAGAGDEGVRR 566

RESULT 9
ABG75223
ID ABG75223 standard; protein; 757 AA.
XX AC ABG75223;
XX DT 12-FEB-2004 (first entry)
XX DE Human tropoelastin protein.
XX KW Human; tropoelastin; elastin; body vessel occlusion; stenosis;
XX KW vascular smooth muscle cell; elastin signaling; vasotrophic.
XX OS Homo sapiens.
XX PN WO2003082203-A2.
XX PD 09-OCT-2003.
XX PF 27-MAR-2003; 2003WO-US009391.
XX PR 27-MAR-2002; 2002US-0368084P.
XX PA (UTAH ) UNIV UTAH RES FOUND.
XX PI Li DY, Karnik S;
XX WPI; 2003-833516/77.

Use of an agent that promotes elastin signaling in smooth muscle cells
for e.g. decreasing or preventing occlusion of a body vessel by smooth
muscle cells, treating or preventing obstructive vascular disease, or

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CC The invention relates to a novel method for diagnosing and analysing
CC autoimmune disease or arthritides. The method comprises obtaining a
CC patient sample containing mRNA, analysing gene expression using the mRNA
CC that results in a gene expression signature of the mRNA, and using that
CC gene expression signature to diagnose or analyse the autoimmune disease
CC or arthritides in the patient, where gene expression of at least 60% of
CC the genes correlates with that of the gene signature. The invention
CC further comprises: a treatment of rheumatoid arthritis; identification of
CC genes for targeting in the treatment of rheumatoid arthritis in a mammal
CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
CC analyses of autoimmune disease or rheumatoid arthritis; screening the
CC efficacy of a candidate drug in vitro for the treatment of collagen-
CC induced arthritis; and reducing the symptoms associated with the following
CC induced arthritis. The compositions of the invention have the following
CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
CC antigout, antiinflammatory, dermatological, and immunomodulatory. The
CC methods and compositions of the present invention are useful for
CC diagnosing and treating autoimmune disease or arthritides, such as
CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
CC immune disease caused by an infectious agent. This sequence represents a
CC protein sequence relating to the genes used in the analysis and treatment
CC of autoimmune diseases or arthritides. Note: This sequence is not shown
CC in the specification. It has been supplied in an electronic format from
CC WIPO.

XX Sequence 757 AA;
SQ Query Match 100.0%; Score 253; DB 7; Length 757;
Best Local Similarity 100.0%; Pred. No. 6.7e-17; Mismatches 0; Indels 0; Gaps 0;
Matches 49; Conservative 0;

QY 1 AAAGLGAGIGPLGVGVGPGLVGAGVPGLVGAGVPGFAGAGADEGVRR 49
|||||
DB 542 AAAGLGAGIGPLGVGVGPGLVGAGVPGLVGAGVPGFAGAGADEGVRR 590
|||||

RESULT 11
AAV01311
ID AAY01311 standard; protein; 183 AA.
XX AC AAY01311;
XX DT 07-JUN-1999 (first entry)
XX DE Human tropoelastin derivative SHEL26-36 (excluding exon 26A product).
XX KW Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;
KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
KW hand lotion; surgical implant; industrial product; human; SHEL; variant.
XX OS Homo sapiens.
OS Synthetic.
XX PN WO9903886-A1.
XX PD 28-JAN-1999.
XX PF 17-JUL-1998; 98WO-AU000564.
XX PR 18-JUL-1997; 97AU-00008117.
XX PA (UNSY) UNIV SYDNEY.
XX PI Weiss AS;
XX DR WPI; 1999-132162/11.
XX PT New derivatives of human tropoelastin - with elastin-like or
PT macromolecular binding properties, useful e.g. as surgical implants.
XX PS Claim 39; Page 11; 82pp; English.

PT preventing stenosis.
XX Claim 24; Page 138-141; Opp; English.
XX The present invention relates to the use of an agent that promotes
CC elastin signaling in smooth muscle cells for decreasing or preventing
CC occlusion of a body vessel by smooth muscle cells, decreasing vascular
CC obstruction, promoting actin stress fiber formation or actin
CC polymerisation, increasing F:G actin ratio in a smooth muscle cell,
CC treating or preventing obstructive vascular disease (e.g. restenosis), or
CC preventing stenosis. The agent that promotes elastin signaling in smooth
CC muscle cells is useful for decreasing or preventing occlusion of a body
CC vessel by smooth muscle cells, decreasing vascular obstruction, promoting
CC actin stress fiber formation or actin polymerization, increasing F:G
CC actin ratio in a smooth muscle cell, treating or preventing obstructive
CC vascular disease (e.g. restenosis following angioplasty), or preventing
CC stenosis. It is also useful in manufacturing a medicament for the
CC treatment or prevention of occlusion of a vessel. The present sequence is
CC the human tropoelastin protein as shown in the exemplification of the
CC invention

XX Sequence 757 AA;
SQ Query Match 100.0%; Score 253; DB 7; Length 757;
Best Local Similarity 100.0%; Pred. No. 6.7e-17; Mismatches 0; Indels 0; Gaps 0;
Matches 49; Conservative 0;

QY 1 AAAGLGAGIGPLGVGVGPGLVGAGVPGLVGAGVPGFAGAGADEGVRR 49
|||||
DB 542 AAAGLGAGIGPLGVGVGPGLVGAGVPGLVGAGVPGFAGAGADEGVRR 590
|||||

RESULT 10
ADP65160
ID ADP65160 standard; protein; 757 AA.
XX AC ADP65160;
XX DT 12-AUG-2004 (first entry)
XX DE Human elastin.
XX KW autoimmune disease; arthritis; gene expression analysis;
KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
KW antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;
KW immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;
KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
KW immune; human.
XX OS Homo sapiens.
XX PN WO2003072827-A1.
XX PD 04-SEP-2003.
XX PF 31-OCT-2002; 2002WO-US035433.
XX PR 31-OCT-2001; 2001US-0336220P.
XX PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
XX PI Hirsch R, Thorton SL;
XX DR WPI; 2003-712740/67.
XX GENBANK; NP_000492.
XX Diagnosing and analyzing autoimmune disease using gene expression
PT profiles and microarray technology, useful for diagnosing and treating
PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
PT gout.
XX Disclosure; Page; 56pp; English.

XX The invention relates to a derivative or variant of human tropoelastin
 CC (hTE) having elastin-like and/or macromolecule (specifically
 CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors
 CC comprising the nucleic acids encoding the variants or derivatives are
 CC used to produce the proteins recombinantly. The tropoelastin derivatives
 CC or hybrid proteins containing the derivatives are useful in medical,
 CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
 CC wrinkle or hand lotions, also as surgical implants, foods and industrial
 CC products. The hybrid protein have controllable GAG-binding properties,
 CC depending on presence or absence of a specific fragment, designated
 CC peptide 26A, from hTE. The present sequence represents a human
 CC tropoelastin derivative SHEL26-36 excluding exon 26A product
 XX
 SQ Sequence 183 AA;

Query Match 83.8%; Score 212; DB 2; Length 183;
 Best Local Similarity 100.0%; Pred. No. 1.9e-13;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVGAGVPGFGA 41
 |||||
 Db 1 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVGAGVPGFGA 41

RESULT 12

AA69138
 ID AAY69138 standard; protein; 183 AA.

XX
 AC AAY69138;

XX
 DT 30-MAY-2000 (first entry)

XX Amino acid sequence of a human tropoelastin derivative.

XX Tropoelastin; derivative; proteolysis; protease; antiwrinkle;
 KW hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;
 KW peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.
 XX
 OS Homo sapiens.

XX WO200004043-A1.

XX 27-JAN-2000.

XX 19-JUL-1999; 99WO-AU000580.

XX 17-JUL-1998; 98AU-00004723.

XX (UNSY) UNIV SYDNEY.

XX Weiss AS;

XX WPI; 2000-182399/16.

XX New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and
 PT cell growth.

XX Disclosure; Page 134-135; 136pp; English.

XX The present sequence represents a human tropoelastin derivative, which is
 CC representative of tropoelastin derivatives of the invention. In the
 CC tropoelastin derivatives of the invention a subsequence has been mutated
 CC so that susceptibility to proteolysis is reduced or eliminated, or a
 CC subsequence has been inserted so that susceptibility to proteolysis is
 CC increased. The derivatives have with reduced susceptibility, and can be
 CC used where the wild-type protein would be degraded too easily, e.g. in
 CC contact with serum or wound exudate. The tropoelastin derivatives provide
 CC competitive inhibition of protease activity. The tropoelastin
 CC derivatives, and other polypeptides containing tropoelastin derivative-
 CC derived protease-susceptibility sites, are useful in human or veterinary
 CC medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents
 CC and for inducing chemotaxis. They are also useful for proliferation or

CC growth inhibition, particularly of smooth muscle cells, epithelial or
 CC endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets.
 CC Peptidomimetics that mimic the protease cleavage site in tropoelastin
 CC derivatives are competitive inhibitors of the protease, and are used for
 CC protecting against lung damage caused by elastin, for inhibiting or
 CC controlling localized growth of cancers or metastases, or to limit
 CC protease activity that causes blood clotting

XX Sequence 183 AA;

Query Match 83.8%; Score 212; DB 3; Length 183;
 Best Local Similarity 100.0%; Pred. No. 1.9e-13;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVGAGVPGFGA 41
 |||||
 Db 1 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVGAGVPGFGA 41

RESULT 13

ADB64761
 ID ADB64761 standard; protein; 617 AA.

XX
 AC ADB64761;

XX
 DT 04-DEC-2003 (first entry)

XX Human protein encoded by clone NT2RP70003110.

XX Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;
 KW cell regeneration; membrane protein; signal transduction-related protein;
 KW transcription-related protein; osteoporosis; neurological disease;
 KW cancer; tumour.

XX Homo sapiens.

XX EP1308459-A2.

XX 07-MAY-2003.

XX 28-MAR-2002; 2002EP-00007401.

XX 05-NOV-2001; 2001JP-00379298.

XX 25-JAN-2002; 2002US-00350978.

XX (HELI-) HELIX RES INST.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 PI Seki N, Yoshikawa T, Otsuka M, Nagahara K, Masuho Y;

XX WPI; 2003-450961/43.
 DR N-PSDB; ADB62791.

XX New polynucleotides and polypeptides, useful for developing a diagnostic
 PT marker or medicines for regulation of their expression and activity, or
 PT as targets of gene therapy.

XX Claim 1; Page; 222pp; English.

XX The invention discloses a polynucleotide comprising a sequence selected
 CC from 1970 fully defined nucleotide sequences which encode novel
 CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
 CC or its partial peptide, an antibody binding to the polypeptide or peptide
 CC of the polynucleotide, immunologically assaying the polypeptide or
 CC peptide of the polynucleotide by contacting the polypeptide or peptide
 CC with the antibody of the encoded protein, and observing the binding
 CC between the two, a transformant carrying the polynucleotide in an
 CC expressible manner and an antisense polynucleotide. The oligonucleotide
 CC is useful as a primer for synthesising the polynucleotide, or as a probe
 CC for detecting the polynucleotide. The polynucleotides and encoded
 CC proteins are useful as pharmaceutical agents and many disease-related

CC genes may be included in them, for developing a diagnostic marker or
 CC medicines for regulation of their expression and activity, or as targets
 CC of gene therapy. The genes are involved in tissue and/or cell
 CC regeneration. Membrane proteins, signal transduction-related proteins,
 CC transcription-related proteins, disease-related proteins and genes
 CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
 CC neurological diseases, cancer, tumors). The cDNA may be used to regulate
 CC the activity or expression of the encoded protein to treat diseases. The
 CC sequence presented is a protein of the invention. Note: Some of the
 CC sequence data for this patent is not represented in the printed
 CC specification, but is based on sequence information supplied by the
 CC European Patent Office.

XX SQ Sequence 617 AA;
 Query Match 83.8%; Score 212; DB 7; Length 617;
 Best Local Similarity 100.0%; Pred. No. 5.9e-13;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGLGGAGIPGLGVGVGVPGLGVGAGVPGVGAGVPGFGA 41
 Db 453 AAAGLGGAGIPGLGVGVGVPGLGVGAGVPGVGAGVPGFGA 493

RESULT 14
 AAY01303
 ID AAY01303 standard; protein; 660 AA.

XX AC AAY01303;
 XX 07-JUN-1999 (first entry)
 XX Human tropoelastin derivative SHEldeltamodified.
 XX Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;
 KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
 KW hand lotion; surgical implant; industrial product; human; SHEL.

XX Homo sapiens.
 OS Synthetic.
 XX WO9903886-A1.
 XX 28-JAN-1999.
 XX 17-JUL-1998; 98WO-AU000564.
 XX 18-JUL-1997; 97AU-00008117.
 XX (UNSY) UNIV SYDNEY.
 XX Weiss AS;
 XX WPI; 1999-132162/11.
 DR N-PSDB; AAX27705.
 XX New derivatives of human tropoelastin - with elastin-like or
 PT macromolecular binding properties, useful e.g. as surgical implants.
 XX Claim 7; Fig 3; 82pp; English.

XX The invention relates to a derivative or variant of human tropoelastin
 CC (hTE) having elastin-like and/or macromolecule (specifically
 CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors
 CC comprising the nucleic acids encoding the variants or derivatives are
 CC used to produce the proteins recombinantly. The tropoelastin derivatives
 CC or hybrid proteins containing the derivatives are useful in medical,
 CC pharmaceutical, veterinary and cosmetic applications. e.g. as anti-
 CC wrinkle or hand lotions, also as surgical implants, foods and industrial
 CC products. The hybrid protein have controllable GAG-binding properties,
 CC depending on presence or absence of a specific fragment, designated
 CC peptide 26A, from hTE. The present sequence represents a human
 CC tropoelastin derivative SHEldeltamodified

XX SQ Sequence 660 AA;
 Query Match 83.8%; Score 212; DB 2; Length 660;
 Best Local Similarity 100.0%; Pred. No. 6.3e-13;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGLGGAGIPGLGVGVGVPGLGVGAGVPGVGAGVPGFGA 41
 Db 479 AAAGLGGAGIPGLGVGVGVPGLGVGAGVPGVGAGVPGFGA 519

RESULT 15
 ADM03792
 ID ADM03792 standard; protein; 663 AA.

XX AC ADM03792;
 XX 20-MAY-2004 (first entry)
 XX Human protein of the invention SEQ ID NO:2477.
 XX human; gene therapy; diagnostic marker; pharmaceutical.
 KW Homo sapiens.
 OS EPI347046-A1.
 XX 24-SEP-2003.
 XX 12-APR-2002; 2002EP-00008400.
 XX 22-MAR-2002; 2002JP-00137785.
 XX (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Iehli S;
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
 XX WPI; 2003-723558/69.
 DR N-PSDB; ADM01349.

XX New polynucleotides and polypeptides are useful in gene therapy, for
 PT developing a diagnostic marker or medicines for regulating their
 PT expression and activity, or as a target of gene therapy.

XX Claim 1; SEQ ID NO 2477; 305pp; English.

XX The invention relates to a novel human polynucleotide and the encoded
 CC polypeptide. A polynucleotide of the invention may have a use in gene
 CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
 CC as a primer for synthesizing the polynucleotide or as a probe for
 CC detecting the polynucleotide. The polynucleotides ADM03758 are
 CC useful in gene therapy, for developing a diagnostic marker or medicines
 CC for regulating their expression and activity, or as a target of gene
 CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
 CC are useful as pharmaceutical agents. The present sequence represents a
 CC protein sequence of the invention.

XX SQ Sequence 663 AA;

Query Match 83.8%; Score 212; DB 7; Length 663;
 Best Local Similarity 100.0%; Pred. No. 6.3e-13;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGLGGAGIPGLGVGVGVPGLGVGAGVPGVGAGVPGFGA 41
 Db 481 AAAGLGGAGIPGLGVGVGVPGLGVGAGVPGVGAGVPGFGA 521

RESULT 16
 ADE40134

CC	cytostatic, anorectic, antidiabetic, immunosuppressive, anti-HIV,
CC	neuroprotective, nootropic, antiparkinsonian, antiasthmatic and
CC	gynaecological activities and may be useful in diagnosing, treating or
CC	preventing NOVX-associated disorders including cardiomyopathy,
CC	atherosclerosis, hypertension, cancer, obesity, diabetes, AIDS, multiple
CC	sclerosis, graft-versus-host disease, Alzheimer's disease, Parkinson's
CC	disease, asthma or fertility disorders. Furthermore, the polypeptides may
CC	be utilised as vaccines whilst the nucleic acids may be used as
CC	hybridisation probes, in gene therapy, chromosome mapping, tissue typing,
CC	preventive medicine and pharmacogenomics. The current sequence is that of
CC	the human NOV protein of the invention.
XX	
XX	
SQ	Sequence 692 AA;
Query Match	83.8%; Score 212; DB 7; Length 692;
Best Local Similarity	100.0%; Pred. No. 6.5e-13;
Matches 41;	Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 AAAGLGAGTGLGVGVGVPGLGVGAGVPLGVGAGVPGFGA 41
Db	510 AAAGLGAGTGLGVGVGVPGLGVGAGVPLGVGAGVPGFGA 550
RESULT 17	
AAAY01302	
ID	AAAY01302 standard; protein; 698 AA.
XX	
AC	AAAY01302;
XX	
DT	07-JUN-1999 (first entry)
XX	
DE	Human tropoelastin variant SHELDelta26A.
XX	
KW	Tropoelastin; hHE; elastin; glycosaminoglycan; GAG-binding; medical;
KW	pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
KW	hand lotion; surgical implant; industrial product; human; SHEL; variant.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	W03903886-A1.
XX	
PD	28-JAN-1999.
XX	
PF	17-JUL-1998; 98WO-AU0000564.
XX	
PR	18-JUL-1997; 97AU-00008117.
XX	
FA	(UNSY) UNIV SYDNEY.
XX	
PT	Weiss AS;
XX	
XX	WPI; 1999-132162/11.
DR	
XX	
PT	New derivatives of human tropoelastin - with elastin-like or
XX	macromolecular binding properties, useful e.g. as surgical implants.
XX	
PS	Claim 13; Fig 2; 82pp; English.
XX	
CC	The invention relates to a derivative or variant of human tropoelastin
CC	(hTE) having elastin-like and/or macromolecule (specifically
CC	glycosaminoglycan (GAG))-binding properties. Cells containing vectors
CC	comprising the nucleic acids encoding the variants or derivatives are
CC	used to produce the proteins recombinantly. The tropoelastin derivatives
CC	or hybrid proteins containing the derivatives are useful in medical,
CC	pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
CC	wrinkle or hand lotions, also as surgical implants, foods and industrial
CC	products. The hybrid protein have controllable GAG-binding properties,
CC	depending on presence or absence of a specific fragment, designated
CC	peptide 26A, from hTE. The present sequence represents the synthetic
CC	human tropoelastin variant SHELDelta26A
XX	
SQ	Sequence 698 AA;

Mon Nov 22 12:42:43 2004

us-09-743-818a-72.rag

Query Match 83.8%; Score 212; DB 2; Length 698;
 Best Local Similarity 100.0%; Pred. No. 6.6e-13;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAAGLGGAGIPGLGVGVGPGGLGVGAGVPGGLGVGAGVPGFGA 41
 DB 516 AAAGLGGAGIPGLGVGVGPGGLGVGAGVPGGLGVGAGVPGFGA 556

RESULT 18
 AAY69069
 ID AAY69069 standard; protein; 698 AA.

XX AC AAY69069;
 XX DT 30-MAY-2000 (first entry)
 XX XX Amino acid sequence of a human reduced tropoelastin derivative.
 DE Tropoelastin; derivative; SHEL-delta-26a; SHEL; proteolysis; protease;
 KW antiwrinkle; hand lotion; bulking agent; chemotaxis; proliferation;
 KW growth inhibition; peptidomimetic; lung damage; elastin; cancer;
 KW metastasis; blood clotting.

XX OS Synthetic.
 OS Homo sapiens.
 XX WO200004043-A1.

XX PD 27-JAN-2000.
 XX PF 19-JUL-1999; 99WO-AU000580.
 XX PR 17-JUL-1998; 98AU-00004723.
 XX PA (UNSY) UNIV SYDNEY.

XX PI Weiss AS;
 XX DR WPI; 2000-182399/16.
 XX DR N-PSDB; AAZ61144.

XX PT New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and cell growth.
 XX PS Disclosure; Page 110-112; 136pp; English.

XX CC The present sequence represents a human reduced tropoelastin derivative, designated SHEL-delta-26a. The sequence is produced by removing exon 26a of SHEL (SHEL not defined). The protein is representative of tropoelastin derivatives of the invention, in which a subsequence has been mutated so that susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is increased. The derivatives have with reduced susceptibility, and can be used where the wild-type protein would be degraded too easily, e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivative-derived protease-susceptibility sites, are useful in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents and for inducing chemotaxis. They are also useful for proliferation or growth inhibition, particularly of smooth muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets. Peptidomimetics that mimic the protease cleavage site in tropoelastin derivatives are competitive inhibitors of the protease, and are used for protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit protease activity that causes blood clotting

XX SQ Sequence 698 AA;

Query Match 83.8%; Score 212; DB 3; Length 698;

Best Local Similarity 100.0%; Pred. No. 6.6e-13;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAAGLGGAGIPGLGVGVGPGGLGVGAGVPGGLGVGAGVPGFGA 41
 DB 516 AAAGLGGAGIPGLGVGVGPGGLGVGAGVPGGLGVGAGVPGFGA 556

RESULT 19
 ADE40132
 ID ADE40132 standard; protein; 711 AA.

XX AC ADE40132;
 XX DT 29-JAN-2004 (first entry)
 XX XX Human NOV16a protein - SEQ ID 38.

XX KW NOVX; cardiac; antiarteriosclerotic; hypotensive; cytostatic; anorectic;
 KW antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic;
 KW antiparkinsonian; antiasthmatic; gynaecological; cardiomyopathy;
 KW atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;
 KW multiple sclerosis; graft-versus-host disease; Alzheimer's; Parkinson's;
 KW asthma; fertility disorder; vaccine; gene therapy; chromosome mapping;
 KW tissue typing; human; NOV.

XX OS Homo sapiens.

XX FN WO2003064589-A2.

XX PD 07-AUG-2003.

XX PF 02-AUG-2002; 2002WO-US024483.

XX PR 02-AUG-2001; 2001US-0309501P.
 PR 03-AUG-2001; 2001US-0310291P.
 PR 07-AUG-2001; 2001US-0310544P.
 PR 08-AUG-2001; 2001US-0310951P.
 PR 09-AUG-2001; 2001US-0311292P.
 PR 13-AUG-2001; 2001US-0311979P.
 PR 16-AUG-2001; 2001US-0312892P.
 PR 17-AUG-2001; 2001US-0313201P.
 PR 17-AUG-2001; 2001US-0313415P.
 PR 20-AUG-2001; 2001US-0313643P.
 PR 20-AUG-2001; 2001US-0313702P.
 PR 21-AUG-2001; 2001US-0314031P.
 PR 23-AUG-2001; 2001US-0314466P.
 PR 28-AUG-2001; 2001US-0315403P.
 PR 29-AUG-2001; 2001US-0315853P.
 PR 17-SEP-2001; 2001US-0322716P.
 PR 21-SEP-2001; 2001US-0323994P.
 PR 14-DEC-2001; 2001US-0340233P.
 PR 05-FEB-2002; 2002US-0354591P.
 PR 19-MAR-2002; 2002US-0365478P.
 PR 19-APR-2002; 2002US-0373814P.
 PR 19-APR-2002; 2002US-0373825P.
 PR 19-APR-2002; 2002US-0373989P.
 PR 23-APR-2002; 2002US-0374632P.
 PR 07-JUN-2002; 2002US-0386971P.
 PR 01-AUG-2002; 2002US-00210172.

(CURA-) CURAGEN CORP.

XX PA (CURA-) CURAGEN CORP.
 XX PI Kekuda R, Miller CE, Patturajan M, Pena CEA, Rieger DK;
 PI Shimkets RA, Zerhusen BD, Li L, Ji W, Padigaru M, Casman SJ;
 PI Voss EZ, Boldog FL, Gorman L, Leite MW, Vernet CAM, Anderson DW;
 PI Guo X, Zhong M, Gerlach VL, Hjalt T, Rastelli L, Spytek KA;
 PI Edinger SR, Ellerman K, Malyankar UM, Macdougall JR, Stone DJ;
 PI Alsobrook JP, Lepley DM, Burgess CE, Majumder K, Wolenc AR;
 PI Smithson G;
 XX WPI; 2003-663472/62.
 DR N-PSDB; ADE40131.

XX New NOVX polypeptides and nucleic acids, useful for preventing or
 PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
 PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.
 XX
 PS Claim 1; SEQ ID NO 38; 560pp; English.
 XX
 CC The invention relates to a novel NOVX polypeptide. The polypeptide of the
 CC invention demonstrates cardiant, antiarteriosclerotic, hypertensive,
 CC cytotatic, anorectic, antidiabetic, immunosuppressive, anti-HIV,
 CC neuroprotective, nootropic, antiparkinsonian, antiasthmatic and
 CC gynaecological activities and may be useful in diagnosing, treating or
 CC preventing NOVX-associated disorders including cardiomyopathy,
 CC atherosclerosis, hypertension, cancer, obesity, diabetes, AIDS, multiple
 CC sclerosis, graft-versus-host disease, Alzheimer's disease, Parkinson's
 CC disease, asthma or fertility disorders. Furthermore, the polypeptides may
 CC be utilised as vaccines whilst the nucleic acids may be used as
 CC hybridisation probes, in gene therapy, chromosome mapping, tissue typing,
 CC preventive medicine and pharmacogenomics. The current sequence is that of
 CC the human NOV protein of the invention.
 XX
 SQ Sequence 711 AA;

Query Match 83.8%; Score 212; DB 7; Length 711;
 Best Local Similarity 100.0%; Pred. No. 6.7e-13;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAAGLGAGTGLGVGVGPGTGLGVGAGVPGTGLGVGAGVPGTGA 41
 DB 547 AAAGLGAGTGLGVGVGPGTGLGVGAGVPGTGLGVGAGVPGTGA 587

RESULT 20
 AAB08630
 ID AAB08630 standard; peptide; 712 AA.
 AC AAB08630;
 XX
 XX Amino acid sequence of a human elastin polypeptide.
 DE
 XX
 XX Tropoelastin; elastin; elastic fibre; smooth muscle cell proliferation;
 KW smooth muscle cell differentiation; smooth muscle cell migration;
 KW smooth muscle cell function; atherosclerosis; restenosis; aneurysm;
 KW vascular bypass graft stenosis; transplant arteriopathy; dissection;
 KW SVAS; hypertension; transplant arteriopathy.
 XX
 OS Homo sapiens.
 XX
 XX WO200050068-A2.
 XX
 XX 31-AUG-2000.
 XX
 XX 28-FEB-2000; 2000WO-US002526.
 XX
 XX 26-FEB-1999; 99US-00258217.
 XX
 XX (UTAH) UNIV UTAH RES FOUND.
 XX
 XX Keating MT, Li DY;
 XX
 XX WPI; 2000-533134/48.
 XX
 XX Elastin based compositions useful for treating atherosclerosis,
 PT restenosis, vascular bypass graft stenosis, transplant arteriopathy,
 PT aneurysm, dissection SVAS and/or hypertension.
 XX
 XX Example 3; Page 46; 79pp; English.
 PS
 XX
 XX The present sequence represents a human elastin. Peptides derived from
 CC elastin are used in compositions of the invention. The specification

CC describes elastin based compositions that are potent regulators of smooth
 CC muscle cell proliferation, differentiation and migration in vivo. The
 CC elastin-based compositions comprise at least one elastic fibre, elastins,
 CC tropoelastins (or fragments of them) which have biological activities
 CC comprising: inhibiting the proliferation of smooth muscle cells in vivo;
 CC stimulating the differentiation of smooth muscle cells in vivo; and
 CC regulating the migration of smooth muscle cells in vivo. The compositions
 CC may be used for the prophylaxis or treatment of a disorder characterized
 CC by diminished capacity to regulate smooth muscle cell function such as
 CC atherosclerosis, restenosis, vascular bypass graft stenosis, transplant
 CC arteriopathy, aneurysm and/or dissection. Disorders which may be treated
 CC also include SVAS (undefined), hypertension, and transplant arteriopathy
 XX

SQ Sequence 712 AA;

Query Match 83.8%; Score 212; DB 3; Length 712;
 Best Local Similarity 100.0%; Pred. No. 6.7e-13;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAAGLGAGTGLGVGVGPGTGLGVGAGVPGTGLGVGAGVPGTGA 41
 DB 548 AAAGLGAGTGLGVGVGPGTGLGVGAGVPGTGLGVGAGVPGTGA 588

RESULT 21
 AAB08631
 ID AAB08631 standard; peptide; 730 AA.
 AC AAB08631;
 XX
 XX 20-DEC-2000 (first entry)
 XX
 XX Fusion protein comprising human elastin and c-myc.
 DE
 XX
 XX Tropoelastin; elastin; elastic fibre; smooth muscle cell proliferation;
 KW smooth muscle cell differentiation; smooth muscle cell migration;
 KW smooth muscle cell function; atherosclerosis; restenosis; aneurysm;
 KW vascular bypass graft stenosis; transplant arteriopathy; dissection;
 KW SVAS; hypertension; transplant arteriopathy.
 XX
 OS Synthetic.
 OS Homo sapiens.
 OS Unidentified.
 XX
 XX WO200050068-A2.
 XX
 XX 31-AUG-2000.
 XX
 XX 28-FEB-2000; 2000WO-US002526.
 XX
 XX 26-FEB-1999; 99US-00258217.
 XX
 XX (UTAH) UNIV UTAH RES FOUND.
 XX
 XX Keating MT, Li DY;
 XX
 XX WPI; 2000-533134/48.
 XX
 XX Elastin based compositions useful for treating atherosclerosis,
 PT restenosis, vascular bypass graft stenosis, transplant arteriopathy,
 PT aneurysm, dissection SVAS and/or hypertension.
 XX
 XX Example 3; Page 48; 79pp; English.
 PS
 XX
 XX The present sequence represents a fusion protein, comprising human
 CC elastin and c-myc, preceded by a His tag. The protein is used in
 CC compositions of the invention. The specification describes elastin based
 CC compositions that are potent regulators of smooth muscle cell
 CC proliferation, differentiation and migration in vivo. The elastin-based
 CC compositions comprise at least one elastic fibre, elastins, tropoelastins
 CC (or fragments of them) which have biological activities comprising:
 CC inhibiting the proliferation of smooth muscle cells in vivo; stimulating
 CC the differentiation of smooth muscle cell in vivo; and regulating the

CC migration of smooth muscle cells in vivo. The compositions may be used
CC for the prophylaxis or treatment of a disorder characterized by
CC diminished capacity to regulate smooth muscle cell function such as
CC atherosclerosis, restenosis, vascular bypass graft stenosis, transplant
CC arteriopathy, aneurysm and/or dissection. Disorders which may be treated
CC also include SVAS (undefined), hypertension, and transplant arteriopathy
XX
SQ Sequence 730 AA;

Query Match 83.8%; Score 212; DB 3; Length 730;
Best Local Similarity 100.0%; Pred. No. 6.9e-13;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFGA 41
DB 557 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFGA 597

RESULT 22
AAO17360
ID AAO17360 standard; protein; 730 AA.

XX AAO17360;
DT 19-JUL-2002 (first entry)
DE Human elastin.

XX Human; endometriosis; DNA chip; fibronectin; p27; reticulocalbin;
KW aldehyde dehydrogenase 6; gravin; phospholipase C epsilon; elastin;
KW insulin-like growth factor binding protein-2; alpha-2 type IV collagen;
KW transmembrane receptor PTK7; collagen type XVIII alpha 1;
KW platelet derived growth factor receptor alpha; laminin M chain;
KW subtilisin like protein PACE4; nidogen.

XX Homo sapiens.

OS

XX EPI191107-A2.

XX 27-MAR-2002.

XX 21-AUG-2001; 2001EP-00250300.

XX 25-SEP-2000; 2000DE-01048633.

XX (SCHD) SCHERING AG.

XX Hess-Stump H, Haendler B, Kraetzschmar J, Kreft B, Winterhager E;
PI Regidor P, Scotti S;
XX WPI; 2002-317413/36.

XX In vitro diagnosis and monitoring of endometriosis, comprises detecting
PT reduced expression of specific gene products, e.g. from the fibronectin
PT gene.

XX Claim 1; Page 15-16; 21pp; German.

XX The present invention relates to a method for the in vitro diagnosis of
CC endometriosis by determining the amount of gene product from at least one
CC specific gene in a patient sample and comparing this with the amount of
CC gene product in a control sample. A reduced level is indicative of
CC endometriosis. The gene products may be fibronectin, p27, reticulocalbin,
CC aldehyde dehydrogenase 6, gravin, phospholipase C epsilon, elastin,
CC insulin-like growth factor binding protein-2, alpha-2 type IV collagen,
CC transmembrane receptor PTK7, collagen type XVIII alpha 1, platelet
CC derived growth factor receptor alpha, laminin M chain, subtilisin like
CC protein PACE4 or nidogen. The method is useful for initial diagnosis of
CC endometriosis, and also for monitoring progress and treatment of the
CC disease. The present sequence is human elastin

XX Sequence 730 AA;

Query Match 83.8%; Score 212; DB 5; Length 730;
Best Local Similarity 100.0%; Pred. No. 6.9e-13;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFGA 41
DB 548 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFGA 588

RESULT 23
ADQ19747
ID ADQ19747 standard; protein; 730 AA.

XX ADQ19747;
DT 26-AUG-2004 (first entry)

XX Human soft tissue sarcoma-upregulated protein - SEQ ID 2566.

XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.

XX Homo sapiens.

XX WO2004048938-A2.

XX 10-JUN-2004.

XX 26-NOV-2003; 2003WO-US038193.

XX 26-NOV-2002; 2002US-0429739P.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Aziz N, Ginsburg WM, Zlotnik A;

XX WPI; 2004-441208/41.

XX Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.

XX Example 2; SEQ ID NO 2566; 210pp; English.

XX The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC protein of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.

XX Sequence 730 AA;

Query Match 83.8%; Score 212; DB 8; Length 730;
Best Local Similarity 100.0%; Pred. No. 6.9e-13;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFGA 41
DB 548 AAAGLGAGIPGLGVGVPGVLGVGAGVPGVLGVGAGVPGFGA 588

RESULT 24
ADE08527
ID ADE08527 standard; protein; 870 AA.

XX

AC ADE08527;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Novel protein (useful for identifying genetic disorders) #682.
 XX
 KW novel gene; novel protein; tissue marker; molecular weight marker;
 KW chromosome marker; genetic disorder.
 XX
 OS Unidentified.
 XX
 XX WO2003054152-A2.
 PN
 XX
 PD 03-JUL-2003.
 PD
 XX
 PF 10-DEC-2002; 2002WO-US039555.
 PF
 XX
 PR 10-DEC-2001; 2001US-0339739P.
 PR
 PR 11-DEC-2001; 2001US-0339453P.
 PR
 PR 14-MAR-2002; 2002US-0365091P.
 PR
 PR 14-MAR-2002; 2002US-0365384P.
 PR
 PR 12-APR-2002; 2002US-0372381P.
 PR
 PR 12-APR-2002; 2002US-0372615P.
 PR
 PR 22-APR-2002; 2002US-00128558.
 PR
 PR 24-APR-2002; 2002US-0376045P.
 PR
 XX
 PA (HYSE-) HYSEQ INC.
 PA
 PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
 PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;
 PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
 XX
 DR WPI; 2003-569235/53.
 DR N-PSDB; ADE07616.
 DR
 XX
 PT New polynucleotides, useful for expressing recombinant proteins for
 PT analysis, characterization or therapeutic use, or as markers for tissues
 PT in which the corresponding protein is preferentially expressed.
 XX
 PS Claim 20; SEQ ID NO 1593; 1177pp; English.
 PS
 CC The invention comprises the amino acid and coding sequences of novel
 CC proteins. The DNA and protein sequences of the invention are useful as:
 CC markers for tissues in which the corresponding protein is preferentially
 CC expressed; as molecular weight markers on gels; as chromosome markers or
 CC tags; to identify chromosomes or to map related gene positions; and to
 CC compare with endogenous DNA sequences in patients to identify potential
 CC genetic disorders. The present amino acid sequence represents a protein
 CC of the invention.
 XX
 SQ Sequence 870 AA;
 SQ
 Query Match 83.8%; Score 212; DB 7; Length 870;
 Best Local Similarity 100.0%; Pred. No. 8.1e-13;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPLGLGVGAGVPGFGA 41
 DB 613 AAAGLGAGIPGLGVGVGVPGLGVGAGVPLGLGVGAGVPGFGA 653
 RESULT 25
 AAB88422
 ID AAB88422 standard; protein; 472 AA.
 XX
 AC AAB88422;
 XX
 DT 23-MAY-2001 (first entry)
 DT
 DE Human membrane or secretory protein clone PSEC0191.
 XX
 KW Human; secretory protein; membrane protein; vaccine; gene therapy;
 KW rheumatoid arthritis; diabetes.

XX Homo sapiens.
 OS
 XX EPI067182-A2.
 PN
 XX 10-JAN-2001.
 PD
 XX
 PF 07-JUL-2000; 2000EP-00114090.
 PF
 XX
 PR 08-JUL-1999; 99JP-00194179.
 PR
 PR 11-JAN-2000; 2000JP-00118775.
 PR
 PR 02-MAY-2000; 2000JP-00183766.
 PR
 XX (HELI-) HELIX RES INST.
 PA
 XX
 PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
 PI WPI; 2001-093989/11.
 DR N-PSDB; AAF93849.
 DR
 XX
 PT Nucleic acids encoding secretory proteins/membrane proteins, useful in
 PT gene therapy or as candidate target molecules in drug development.
 XX
 PS Claim 1; SEQ ID NO 212; 609pp + Sequence Listing; English.
 PS
 CC This invention relates to nucleic acid sequences AAF93744 - AAF93916
 CC which encode human secretory or membrane proteins represented by AAB88317
 CC - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and
 CC AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the
 CC invention. The invention also includes methods for the production of
 CC antibodies directed against the proteins, and cDNA sequences, which can
 CC be used in vaccines. The polynucleotide sequences can be used in gene
 CC therapy. The polynucleotide sequences and the proteins they encode may be
 CC used in the prevention, treatment and diagnosis of diseases associated
 CC with inappropriate secretory protein/membrane protein expression. The
 CC nucleic acids and complementary sequences may also be used as DNA probes
 CC in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect
 CC and quantitate the presence of similar nucleic acid sequences in samples.
 CC They may also be used to study the expression and function of secretory
 CC proteins/membrane polypeptides and their role in metabolism. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC against them and in assays to identify modulators (agonists and
 CC antagonists) of expression and activity. The antibodies and antagonists
 CC may also be used as therapeutic agents to down regulate expression and
 CC activity. The antibodies may also be used as diagnostic agents for
 CC detecting the presence of the polypeptides in samples (e.g. by enzyme
 CC linked immunosorbant assay (ELISA)). Examples of diseases which may be
 CC treated include rheumatoid arthritis and diabetes
 XX
 SQ Sequence 472 AA;
 SQ
 Query Match 82.2%; Score 208; DB 4; Length 472;
 Best Local Similarity 97.6%; Pred. No. 1.1e-12;
 Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AAAGLGAGIPGLGVGVGVPGLGVGAGVPLGLGVGAGVPGFGA 41
 DB 316 AAAGLGAGIPGLGVGVGVPGLGVGAGVPLGLGVGAGVPGFGA 356
 RESULT 26
 AAY69071
 ID AAY69071 standard; protein; 571 AA.
 XX
 AC AAY69071;
 XX
 DT 30-MAY-2000 (first entry)
 DT
 DE Amino acid sequence of a human tropoelastin derivative.
 XX
 KW Tropoelastin; derivative; proteolysis; protease; antiwrinkle;
 KW hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;
 KW peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.

XX	OS	Homo sapiens.	14-AUG-2002; 2002WO-US025765.	PF
XX	PN	WO200004043-A1.	14-AUG-2001; 2001US-0312147P.	PR
XX	PD	27-JAN-2000.	01-NOV-2001; 2001US-0346382P.	PR
XX	PF	19-JUL-1999; 99WO-AU0000580.	26-NOV-2001; 2001US-0333347P.	PR
XX	PR	17-JUL-1998; 98AU-00004723.	(GEHO) GEN HOSPITAL CORP.	XX
XX	PA	(UNSY) UNIV SYDNEY.	(FARB) BAYER AG.	XX
XX	PI	Weiss AS;	Woolf C, D'urso D, Befort K, Costigan M;	XX
XX	DR	WPI; 2000-182399/16.	WPI; 2003-268312/26.	XX
XX	PT	New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and cell growth.	GENBANK; Q99372.	DR
XX	PS	Disclosure; Page 115-117; 136pp; English.	Claim 1; Page; 1017pp; English.	XX
XX	CC	The present sequence represents a human tropoelastin derivative, which is representative of tropoelastin derivatives of the invention. In the tropoelastin derivatives of the invention a subsequence has been mutated so that susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is increased. The derivatives have with reduced susceptibility, and can be used where the wild-type protein would be degraded too easily, e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivatives, and other polypeptides containing tropoelastin derivative-derived protease-susceptibility sites, are useful in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents and for inducing chemotaxis. They are also useful for proliferation or growth inhibition, particularly of smooth muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets. Peptidomimetics that mimic the protease cleavage site in tropoelastin derivatives are competitive inhibitors of the protease, and are used for protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit protease activity that causes blood clotting.	The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene injury (CCI) and spared nerve injury (SNI)) in a rat protein (shown in table 2 of therapy). The sequence presented is a rat protein (shown in table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.	XX
XX	SQ	Sequence 571 AA;	Sequence 864 AA;	SQ
XX	QY	Query Match 74.7%; Score 189; DB 3; Length 571; Best Local Similarity 94.9%; Pred. No. 1e-10; Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	Query Match 71.5%; Score 181; DB 7; Length 864; Best Local Similarity 78.3%; Pred. No. 9e-10; Matches 36; Conservative 1; Mismatches 7; Indels 2; Gaps 1	QY
XX	DB	1 AAAGLGAGIPGLGVGVGPGVLGVGAGVPGVLGVGAGVPGF 39 516 AAAGLGAGIPGLGVGVGPGVLGVGAGVPGVLGVGAGVPGF 554	1 AAAGLGAGIPGLGVGVGPGVLGVGAGVPGVLGVGAGVPGF 46 622 AAAGLGAGVPGVLGVGAGVPGFAGAG--GFGAGAGVPGFAGAGVPG 665	DB
XX	RESULT 27	AD56670	RESULT 28	XX
XX	ID	AD56670 standard; protein; 864 AA.	AAP71455	XX
XX	AC	AD56670;	ID AAP71455 standard; peptide; 34 AA.	XX
XX	DT	29-JAN-2004 (first entry)	AC AAP71455;	XX
XX	DE	Rat Protein Q99372, SEQ ID NO 2524.	XX	XX
XX	XX	Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;	DT 25-MAR-2003 (revised)	DT
XX	KW	chronic constriction injury; CCI; spared nerve injury; SNI; Chung.	DT 09-JAN-2003 (revised)	DT
XX	OS	Rattus norvegicus.	DT 13-JUN-1991 (first entry)	XX
XX	XX	WO2003016475-A2.	DE Sequence of chemotactic peptides which is incorporated into the surface of a prosthetic device.	DE
XX	PD	27-FEB-2003.	XX Fibroblast; elastic fibres; tissue regeneration; skin tissue;	XX
XX	XX		KW Blood vessel walls.	KW

XX	OS	Homo sapiens.	14-AUG-2002; 2002WO-US025765.	PF
XX	PN	WO200004043-A1.	14-AUG-2001; 2001US-0312147P.	PR
XX	PD	27-JAN-2000.	01-NOV-2001; 2001US-0346382P.	PR
XX	PF	19-JUL-1999; 99WO-AU0000580.	26-NOV-2001; 2001US-0333347P.	PR
XX	PR	17-JUL-1998; 98AU-00004723.	(GEHO) GEN HOSPITAL CORP.	XX
XX	PA	(UNSY) UNIV SYDNEY.	(FARB) BAYER AG.	XX
XX	PI	Weiss AS;	Woolf C, D'urso D, Befort K, Costigan M;	XX
XX	DR	WPI; 2000-182399/16.	WPI; 2003-268312/26.	XX
XX	PT	New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and cell growth.	GENBANK; Q99372.	DR
XX	PS	Disclosure; Page 115-117; 136pp; English.	Claim 1; Page; 1017pp; English.	XX
XX	CC	The present sequence represents a human tropoelastin derivative, which is representative of tropoelastin derivatives of the invention. In the tropoelastin derivatives of the invention a subsequence has been mutated so that susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is increased. The derivatives have with reduced susceptibility, and can be used where the wild-type protein would be degraded too easily, e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivatives, and other polypeptides containing tropoelastin derivative-derived protease-susceptibility sites, are useful in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents and for inducing chemotaxis. They are also useful for proliferation or growth inhibition, particularly of smooth muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets. Peptidomimetics that mimic the protease cleavage site in tropoelastin derivatives are competitive inhibitors of the protease, and are used for protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit protease activity that causes blood clotting.	The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene injury (CCI) and spared nerve injury (SNI)) in a rat protein (shown in table 2 of therapy). The sequence presented is a rat protein (shown in table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.	XX
XX	SQ	Sequence 571 AA;	Sequence 864 AA;	SQ
XX	QY	Query Match 74.7%; Score 189; DB 3; Length 571; Best Local Similarity 94.9%; Pred. No. 1e-10; Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	Query Match 71.5%; Score 181; DB 7; Length 864; Best Local Similarity 78.3%; Pred. No. 9e-10; Matches 36; Conservative 1; Mismatches 7; Indels 2; Gaps 1	QY
XX	DB	1 AAAGLGAGIPGLGVGVGPGVLGVGAGVPGVLGVGAGVPGF 39 516 AAAGLGAGIPGLGVGVGPGVLGVGAGVPGVLGVGAGVPGF 554	1 AAAGLGAGIPGLGVGVGPGVLGVGAGVPGVLGVGAGVPGF 46 622 AAAGLGAGVPGVLGVGAGVPGFAGAG--GFGAGAGVPGFAGAGVPG 665	DB
XX	DE	RESULT 27 ADE56670 ID ADE56670 standard; protein; 864 AA.	RESULT 28 AAP71455 ID AAP71455 standard; peptide; 34 AA.	DE
XX	AC	ADE56670;	AC AAP71455;	AC
XX	DT	29-JAN-2004 (first entry)	25-MAR-2003 (revised)	DT
XX	DE	Rat Protein Q99372, SEQ ID NO 2524.	09-JAN-2003 (revised)	DE
XX	XX	Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;	13-JUN-1991 (first entry)	XX
XX	KW	chronic constriction injury; CCI; spared nerve injury; SNI; Chung.	Sequence of chemotactic peptides which is incorporated into the surface of a prosthetic device.	KW
XX	OS	Rattus norvegicus.	Fibroblast; elastic fibres; tissue regeneration; skin tissue;	OS
XX	XX	WO2003016475-A2.	Blood vessel walls.	XX
XX	PN	27-FEB-2003.		PN
XX	PD			PD
XX	XX			XX

Mon Nov 22 12:42:43 2004

```
XX
PI Cappelletto J;
XX
DR WPI; 1995-320413/41.
DR N-PSDB; AAQ98722.
XX
PT Protein polymers comprising repeating units and sequences - capable of
PT enzyme-catalysed covalent bond formation useful as a biocompatible
PT material for wound closure and tissue repair.
XX
XX Example 7; Page 63; 138pp; English.
PS
XX The sequence of the protein polymer adhesion substrate (PPAS) SELP8K
CC monomer sequence. The gene sequence is altered from the native SELP8
CC sequence (AAQ98718) by the introduction of a polymorphism at pos. 90 of
CC the SELP8 sequence. The sequence was used to produce the PPAS SELP8K
CC (AAR80341). The protein can be used as a polymer substrate in a
CC isopeptide cross-linking reaction catalysed by a transglutaminase
CC enzymatic activity, e.g. Factor VIII or XIII. The polymers can be used in
CC biological systems where in situ formation of a biocompatible material
CC with structural integrity is required e.g. as medical adhesives and
CC sealants or for wound closure or tissue repair
XX
SQ Sequence 64 AA;
Query Match 58.9%; Score 149; DB 2; Length 64;
Best Local Similarity 61.1%; Pred. No. 1.1e-07;
Matches 33; Conservative 5; Mismatches 8; Indels 8; Gaps 3;
QY 1 AAAGLGAGIGPLGV-GVGVPLGV-----GAGVPLGV-GAGVPGFGAGADEG 46
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 6 AGAGSGVGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 59
Search completed: November 19, 2004, 16:28:42
Job time : 10.014 secs
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OM protein - protein search, using sw model

Run on: November 19, 2004, 15:19:20 ; Search time 105.249 Seconds
(without alignments)
1755.321 Million cell updates/sec

Title: US-09-743-818a-71

Perfect score: 2680

Sequence: 1 GGVPDCAIPGGVPGGVFPVGA.....GGVAAAKSAKVAAKQLR 515

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: A_genseq_23Sep04.*

2: Genseqpl1980s.*

3: Genseqpl1990s.*

4: Genseqpl2000s.*

5: Genseqpl2001s.*

6: Genseqpl2002s.*

7: Genseqpl2003as.*

8: Genseqpl2003bs.*

9: Genseqpl2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	2680	100.0	515	3	AAY69135 Amino aci
2	2680	100.0	571	3	AAY69071 Amino aci
3	2680	100.0	698	2	AAY01302 Human tro
4	2680	100.0	698	3	AAY69069 Amino aci
5	2680	100.0	730	2	AAW46315 Human ela
6	2680	100.0	731	4	AAY69068 Human ela
7	2680	100.0	731	4	AAY69068 Human ela
8	2680	100.0	733	2	AAB66657 Human ela
9	2680	100.0	733	2	AAB66657 Human ela
10	2680	100.0	733	2	AAY01301 Amino aci
11	2680	100.0	757	7	ABG75223 Human tro
12	2672	99.7	731	7	ADP65160 Human ela
13	2670	99.6	731	6	ADP65160 Human ela
14	2667.5	99.5	711	7	ABU08725 Human ela
15	2667	99.5	730	5	AAO17360 Human ela
16	2667	99.5	730	8	AAO17360 Human ela
17	2663	99.4	712	3	AAO17360 Human ela
18	2663	99.4	730	3	AAO17360 Human ela
19	2431	90.7	692	7	ADP65160 Human ela
20	2353	87.8	870	7	ADP65160 Human ela
21	2328	86.9	660	2	ADP65160 Human ela
22	2306.5	86.1	663	2	ADP65160 Human ela
23	2129.5	79.5	617	7	ADP65160 Human ela
24	1675.5	62.5	864	7	ADP65160 Human ela
25	1314	49.0	472	4	AAO17360 Human ela

26	911.5	34.0	745	2	AAY31682	Aay31682 Alanine-c
27	890	33.2	988	2	AAR80253	Aar80253 Polymer s
28	890	33.2	988	5	ABP53474	Abp53474 Protein p
29	872	32.5	832	2	AAR80252	Aar80252 Polymer s
30	872	32.5	832	5	ABP53473	Abp53473 Protein p
31	870	32.5	936	2	AAR80251	Aar80251 Polymer s
32	870	32.5	936	5	ABP53472	Abp53472 Protein p
33	864	32.2	1056	2	AAR80254	Aar80254 Polymer s
34	864	32.2	1056	5	ABP53475	Abp53475 Protein p
35	850	31.7	972	2	AAR80255	Aar80255 Polymer s
36	850	31.7	972	5	ABP53476	Abp53476 Protein p
37	849.5	31.7	1412	2	AAW53519	Aaw53519 Amino aci
38	849.5	31.7	1413	1	AAW53519	Aaw53519 Amino aci
39	849.5	31.7	1413	1	AAW53519	Aaw53519 Amino aci
40	849.5	31.7	1413	2	AAW53519	Aaw53519 Amino aci
41	849.5	31.7	1464	3	AAW53519	Aaw53519 Amino aci
42	849.5	31.7	1465	5	ABG69268	Abg69268 Elastin-l
43	849.5	31.7	1465	5	ABG69268	Abg69268 Elastin-l
44	848.5	31.7	1002	2	AAW03218	Aaw03218 SELP0K po
45	848.5	31.7	1002	2	AAW03218	Aaw03218 SELP0K po
46	848.5	31.7	1002	3	AAW53544	Aaw53544 Amino aci
47	848.5	31.7	1002	5	ABG31418	Abg31418 SELP0K pr
48	848.5	31.7	1002	7	ABW01634	Abw01634 Plasmid p
49	847	31.6	1040	5	ABP53478	Abp53478 Protein p
50	846.5	31.6	696	8	ADK51953	Adk51953 Repeat pr
51	844.5	31.5	968	5	AAE18320	Aae18320 Silk elas
52	844.5	31.5	2257	1	AAW02961	Aaw02961 SELP3 pro
53	844.5	31.5	2257	2	AAW02961	Aaw02961 SELP3 pro
54	844.5	31.5	2257	2	AAW02961	Aaw02961 SELP3 mul
55	844.5	31.5	2257	2	AAW02961	Aaw02961 SELP3 mul
56	844.5	31.5	2257	3	AAW02961	Aaw02961 SELP3 mul
57	844.5	31.5	2257	3	AAW02961	Aaw02961 SELP3 mul
58	844.5	31.5	2257	3	AAW02961	Aaw02961 SELP3 mul
59	843.5	31.5	696	8	ADK51955	Adk51955 Repeat pr
60	842.5	31.4	696	5	ABP53470	Abp53470 SELP9K re
61	842.5	31.4	696	5	ABP53470	Abp53470 SELP9K re
62	842.5	31.4	768	5	ABP53466	Abp53466 SELP8 rel
63	842.5	31.4	768	5	ABP53466	Abp53466 SELP8 rel
64	842.5	31.4	877	2	AAW03335	Aaw03335 Protein p
65	841.5	31.4	877	2	AAW03335	Aaw03335 Protein p
66	841.5	31.4	936	2	AAW03335	Aaw03335 Protein p
67	841.5	31.4	936	3	AAW03335	Aaw03335 Protein p
68	841.5	31.4	936	3	AAW03335	Aaw03335 Protein p
69	841.5	31.4	936	3	AAW03335	Aaw03335 Protein p
70	837	31.2	768	5	ABP53481	Abp53481 Protein p
71	837	31.2	768	5	ABP53481	Abp53481 Protein p
72	837	31.2	884	2	AAW09213	Aaw09213 SELP8K po
73	837	31.2	884	2	AAW09213	Aaw09213 SELP8K po
74	837	31.2	884	2	AAW09213	Aaw09213 SELP8K po
75	837	31.2	884	2	AAW09213	Aaw09213 SELP8K po
76	837	31.2	884	3	AAW09213	Aaw09213 SELP8K po
77	837	31.2	884	3	AAW09213	Aaw09213 SELP8K po
78	834.5	31.1	1024	5	ABW01628	Abw01628 Plasmid p
79	834.5	31.1	1024	5	ABW01628	Abw01628 Plasmid p
80	829	30.9	768	5	ABP53477	Abp53477 Protein p
81	822.5	30.7	2055	1	AAW02960	Aaw02960 SELP2 pro
82	822.5	30.7	2055	2	AAW02960	Aaw02960 SELP2 pro
83	822.5	30.7	2055	2	AAW02960	Aaw02960 SELP2 mul
84	822.5	30.7	2055	2	AAW02960	Aaw02960 SELP2 mul
85	822.5	30.7	2055	3	AAW02960	Aaw02960 SELP2 syn
86	822.5	30.7	2055	3	AAW02960	Aaw02960 SELP2 syn
87	822.5	30.7	2055	5	ABG69271	Abg69271 Silk/Elas
88	804.5	30.0	780	8	ADK51951	Adk51951 Repeat pr
89	793	29.6	966	3	AAW51893	Aaw51893 SELP0K-CS
90	793	29.6	966	3	AAW51893	Aaw51893 SELP0K-CS
91	793	29.6	966	3	AAW51893	Aaw51893 SELP0K-CS
92	793	29.6	966	7	ABW01639	Abw01639 Plasmid p
93	784.5	29.3	450	5	AAU77399	Aau77399 Elastin-l
94	778.5	29.0	1085	2	AAU77399	Aau77399 Elastin-l
95	777.5	29.0	773	5	AAW50045	Aaw50045 N. clavip
96	777.5	29.0	773	5	AAW50045	Aaw50045 N. clavip
97	774.5	28.9	975	5	ABW05207	Abw05207 Elastin m
98	774	28.9	782	2	AAU77399	Aau77399 Elastin m

Qy 1 GGVPGAI PGGVPGGVFFYPNGNLGALGGGALGPGGKPLKPPVGGGLACAGLGLGAGFAFPV 60

CC increased. The derivatives have with reduced susceptibility, and can be
 CC used where the wild-type protein would be degraded too easily, e.g. in
 CC contact with serum or wound exudate. The tropoelastin derivatives provide
 CC competitive inhibition of protease activity. The tropoelastin
 CC derivatives, and other polypeptides containing tropoelastin derivative-
 CC derived protease-susceptibility sites, are useful in human or veterinary
 CC medicine, cosmetics (e.g. anti-wrinkle or hand lotions), as bulking agents
 CC and for inducing chemotaxis. They are also useful for proliferation or
 CC growth inhibition, particularly of smooth muscle cells, epithelial or
 CC endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets.
 CC Peptidomimetics that mimic the protease cleavage site in tropoelastin
 CC derivatives are competitive inhibitors of the protease, and are used for
 CC protecting against lung damage caused by elastin, for inhibiting or
 CC controlling localized growth of cancers or metastases, or to limit
 CC protease activity that causes blood clotting

XX Sequence 571 AA;

Query Match 100.0%; Score 2680; DB 3; Length 571;
 Best Local Similarity 100.0%; Pred. No. 6e-153;
 Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGVPAIPGGVPGGVFYPGAGLGGGALGPGKPLKPVPGGLAGAGLGAFFAVT 60
 DB |||||
 QY 1 GGVPAIPGGVPGGVFYPGAGLGGGALGPGKPLKPVPGGLAGAGLGAFFAVT 60
 DB |||||
 QY 61 FPGALVPGGVADAAAYKAAKAGAGLGGVPGVGGVGSAGAVVPPGAGVPGKVPVGL 120
 DB |||||
 QY 61 FPGALVPGGVADAAAYKAAKAGAGLGGVPGVGGVGSAGAVVPPGAGVPGKVPVGL 120
 DB |||||
 QY 121 PGVPGGVLPGARPPGVPGVPGAGVPGKPKAPGVGGAFAGIPGVGPPGPPGVLGY 180
 DB |||||
 QY 121 PGVPGGVLPGARPPGVPGVPGAGVPGKPKAPGVGGAFAGIPGVGPPGPPGVLGY 180
 DB |||||
 QY 181 PIKAPKLPGGYGLPYTTGKLPYGVGPGVAGAGKAGVPTGTGVPQAAAAKAAKAF 240
 DB |||||
 QY 181 PIKAPKLPGGYGLPYTTGKLPYGVGPGVAGAGKAGVPTGTGVPQAAAAKAAKAF 240
 DB |||||
 QY 241 GAGAAGVLPFGARPPGVPGVPGVPGKPKAPGVGGAFAGIPGVGPPGPPGVLGY 300
 DB |||||
 QY 241 GAGAAGVLPFGARPPGVPGVPGAGLGGALGPGKPLKPVPGGLAGAGLGAFFAVT 300
 DB |||||
 QY 301 PGFGPGVVGVPAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPG 360
 DB |||||
 QY 301 PGFGPGVVGVPAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPG 360
 DB |||||
 QY 361 PGVPGGVIPYGVGAGGPPGFGVGGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 420
 DB |||||
 QY 361 PGVPGGVIPYGVGAGGPPGFGVGGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 420
 DB |||||
 QY 421 AKAAKYGVGTTPAAAAKAAKAAQFGLVPGVAPGVGVPAGVPGVAPGVGVPAG 480
 DB |||||
 QY 421 AKAAKYGVGTTPAAAAKAAKAAQFGLVPGVAPGVGVPAGVPGVAPGVGVPAG 480
 DB |||||
 QY 481 VGVAPGVGVPAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPG 515
 DB |||||
 QY 481 VGVAPGVGVPAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPG 515
 DB |||||

RESULT 3

AAAY01302

ID AAAY01302 standard; protein; 698 AA.

XX AC

XX AAAY01302;

XX DT

XX 07-JUN-1999 (first entry)

XX DE

XX Human tropoelastin variant SHELDelta26A.

XX KW

XX Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;

XX KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;

XX KW hand lotion; surgical implant; industrial product; human; SHEL; variant.

XX XX

OS Homo sapiens.
 OS Synthetic.
 XX WO9903886-A1.
 XX 28-JAN-1999.
 XX 17-JUL-1998; 98WO-AU000564.
 XX 18-JUL-1997; 97AU-00008117.
 XX (UNSY) UNIV SYDNEY.
 XX Weiss AS;
 XX WPI; 1999-132162/11.
 XX New derivatives of human tropoelastin - with elastin-like or
 XX macromolecular binding properties, useful e.g. as surgical implants.
 XX Claim 13; Fig 2; 82pp; English.
 XX The invention relates to a derivative or variant of human tropoelastin
 XX (hTE) having elastin-like and/or macromolecule (specifically
 XX glycosaminoglycan (GAG))-binding properties. Cells containing vectors
 XX comprising the nucleic acids encoding the variants or derivatives are
 XX used to produce the proteins recombinantly. The tropoelastin derivatives
 XX or hybrid proteins containing the derivatives are useful in medical,
 XX pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
 XX wrinkle or hand lotions, also as surgical implants, foods and industrial
 XX products. The hybrid protein have controllable GAG-binding properties,
 XX depending on presence or absence of a specific fragment, designated
 XX peptide 26A, from hTE. The present sequence represents the synthetic
 XX human tropoelastin variant SHELDelta26A
 XX Sequence 698 AA;

Query Match 100.0%; Score 2680; DB 2; Length 698;
 Best Local Similarity 100.0%; Pred. No. 7.1e-153;
 Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGVPAIPGGVPGGVFYPGAGLGGGALGPGKPLKPVPGGLAGAGLGAFFAVT 60
 DB |||||
 QY 1 GGVPAIPGGVPGGVFYPGAGLGGGALGPGKPLKPVPGGLAGAGLGAFFAVT 60
 DB |||||
 QY 61 FPGALVPGGVADAAAYKAAKAGAGLGGVPGVGGVGSAGAVVPPGAGVPGKVPVGL 120
 DB |||||
 QY 61 FPGALVPGGVADAAAYKAAKAGAGLGGVPGVGGVGSAGAVVPPGAGVPGKVPVGL 120
 DB |||||
 QY 121 PGVPGGVLPGARPPGVPGVPGVPGKPKAPGVGGAFAGIPGVGPPGPPGVLGY 180
 DB |||||
 QY 121 PGVPGGVLPGARPPGVPGVPGAGLGGALGPGKPLKPVPGGLAGAGLGAFFAVT 180
 DB |||||
 QY 181 PIKAPKLPGGYGLPYTTGKLPYGVGPGVAGAGKAGVPTGTGVPQAAAAKAAKAF 240
 DB |||||
 QY 181 PIKAPKLPGGYGLPYTTGKLPYGVGPGVAGAGKAGVPTGTGVPQAAAAKAAKAF 240
 DB |||||
 QY 241 GAGAAGVLPFGARPPGVPGVPGVPGKPKAPGVGGAFAGIPGVGPPGPPGVLGY 300
 DB |||||
 QY 241 GAGAAGVLPFGARPPGVPGVPGAGLGGALGPGKPLKPVPGGLAGAGLGAFFAVT 300
 DB |||||
 QY 301 PGFGPGVVGVPAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPG 360
 DB |||||
 QY 301 PGFGPGVVGVPAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPG 360
 DB |||||
 QY 361 PGVPGGVIPYGVGAGGPPGFGVGGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 420
 DB |||||
 QY 361 PGVPGGVIPYGVGAGGPPGFGVGGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 420
 DB |||||
 QY 421 AKAAKYGVGTTPAAAAKAAKAAQFGLVPGVAPGVGVPAGVPGVAPGVGVPAG 480
 DB |||||
 QY 421 AKAAKYGVGTTPAAAAKAAKAAQFGLVPGVAPGVGVPAGVPGVAPGVGVPAG 480
 DB |||||

XX Claim 5; Fig 1B; 39pp; English.

XX This represents the human elastin sequence containing the minimal functional unit (MFU)-1 polypeptide of the invention. This MFU-1 is a polypeptide that has at least 3 beta-sheet/ beta-turn structures, but is not a naturally occurring fibrous protein. Each beta-sheet structure has 3-7 (preferably 5-7) amino acids and the MFU polypeptide may include at least 1 amino acid that can take part in crosslinking. The polypeptide can also be derived from the sequences of animal elastin, lamprin and spider silk protein. The MFU polypeptides are self-aligning peptides having the same primary structure as part of a natural fibrous protein. They are used to coat prostheses made of animal or synthetic material or metal, particularly for use as blood vessel or heart valve replacements, wound or burn dressings, or stents. They can be used in cosmetic, elastic or high-tensile strength materials, e.g. ropes or parachute cord. Prostheses based on the MFU allow penetration of endothelial cells, so become permanent, living, tissue replacements. The MFU polypeptides have better biocompatibility than known elastin-based materials. They are well defined, homogeneous material and are easier to manipulate and produce than full-length elastins. They are non-thrombogenic and non-immunogenic. Materials can be made from 2 or more different MFU polypeptides to allow properties to be tailored for particular applications, e.g. combining the high extensibility of elastin and the high tensile strength of spider silk protein

XX SQ Sequence 730 AA;

Query Match 100.0%; Score 2680; DB 2; Length 730;
 Best Local Similarity 100.0%; Pred. No. 7.4e-153;
 Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGVPGAIPGGVPGGVPGYFPGAGLGGALGGGKPLKPVPGGLAGAGLGAGGAPPAVT 60
 DB 1 GGVPGAIPGGVPGGVPGYFPGAGLGGALGGGKPLKPVPGGLAGAGLGAGGAPPAVT 60

QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVSAGAVVPPQAGVKPGVGL 120
 DB 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVSAGAVVPPQAGVKPGVGL 120

QY 121 PGVYPGVLPGARFPGVGLPGVPTGAGVKPKAGVGGAFAGTGTGVPQAAAAAAXKAF 180
 DB 121 PGVYPGVLPGARFPGVGLPGVPTGAGVKPKAGVGGAFAGTGTGVPQAAAAAAXKAF 180

QY 181 PIKAPKLPGGYGLPYTTGKLPYGYGPGGAGAGKAGYPTGTGVPQAAAAAAXKAF 240
 DB 181 PIKAPKLPGGYGLPYTTGKLPYGYGPGGAGAGKAGYPTGTGVPQAAAAAAXKAF 240

QY 241 GAGAGVLPGVGAGVPGVPGAIPIGIGTAGVGTAAAAAAXKAGYGAAGLVPGG 300
 DB 241 GAGAGVLPGVGAGVPGVPGAIPIGIGTAGVGTAAAAAAXKAGYGAAGLVPGG 300

QY 301 PGFGVGVPGVPGAGVPGVPGAGIPVVPAGIPGAAPGVVSPAAAAAAXKAGYGAR 360
 DB 301 PGFGVGVPGVPGAGVPGVPGAGIPVVPAGIPGAAPGVVSPAAAAAAXKAGYGAR 360

QY 361 PGVGVGGIPTTYGVGAGGFPFGVGVGGIPGVAGVPSVGVPGVGVGVPISPEAQAAA 420
 DB 361 PGVGVGGIPTTYGVGAGGFPFGVGVGGIPGVAGVPSVGVPGVGVGVPISPEAQAAA 420

QY 421 AKAAKYGTGTAAAAAAXKAAQAGLVPGVGAPGVGAPGVGAPGVGAPG 480
 DB 421 AKAAKYGTGTAAAAAAXKAAQAGLVPGVGAPGVGAPGVGAPGVGAPG 480

QY 481 VGVAPGVGAPGIGPGGVAAXKAAKAAQRL 515
 DB 481 VGVAPGVGAPGIGPGGVAAXKAAKAAQRL 515

RESULT 6
 AAY69068
 ID AAY69068 standard; protein; 731 AA.
 XX

AC AAY69068;
 XX
 DT 30-MAY-2000 (first entry)
 XX
 DE Amino acid sequence of a human tropoelastin splice form.
 XX
 KW Tropoelastin, derivative; proteolysis; protease; antiwrinkle;
 KW hand lotion; bulking agent; chemotaxis; proliferation; growth inhibition;
 KW peptidomimetic; lung damage; elastin; cancer; metastasis; blood clotting.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Cleavage-site 441..442
 FT Cleavage-site 503..504
 FT Cleavage-site 515..516
 FT Cleavage-site 564..565
 XX
 PN WO200004043-A1.
 XX
 PD 27-JAN-2000.
 XX
 PF 13-JUL-1999; 99WO-AU000580.
 XX
 PR 17-JUL-1998; 98AU-00004723.
 XX
 PA (UNSY) UNIV SYDNEY.
 XX
 PI Weiss AS;
 XX
 DR WPI: 2000-182399/16.
 XX
 DR N-PSDB; AAZ61146.
 XX
 PT New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and cell growth.
 XX
 PS Disclosure; Page 107-109; 136pp; English.
 XX
 CC The present sequence represents a human tropoelastin splice form. The specification describes tropoelastin derivatives, in which a subsequence has been mutated so that susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is increased. The derivatives have with reduced susceptibility, and can be used where the wild-type protein would be degraded too easily, e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivatives, and other polypeptides containing tropoelastin derivative-derived protease-susceptibility sites, are useful in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents and for inducing chemotaxis. They are also useful for proliferation or growth inhibition, particularly of smooth muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets. Peptidomimetics that mimic the protease cleavage site in tropoelastin derivatives are competitive inhibitors of the protease, and are used for protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit protease activity that causes blood clotting

Query Match 100.0%; Score 2680; DB 3; Length 731;
 Best Local Similarity 100.0%; Pred. No. 7.4e-153;
 Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGVPGAIPGGVPGGVPGYFPGAGLGGALGGGKPLKPVPGGLAGAGLGAGGAPPAVT 60
 DB 1 GGVPGAIPGGVPGGVPGYFPGAGLGGALGGGKPLKPVPGGLAGAGLGAGGAPPAVT 60

QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVSAGAVVPPQAGVKPGVGL 120
 DB 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGLGVSAGAVVPPQAGVKPGVGL 120

QY 121 PGVYPGVLPGARFPGVGLPGVPTGAGVKPKAGVGGAFAGTGTGVPQAAAAAAXKAF 180
 DB 121 PGVYPGVLPGARFPGVGLPGVPTGAGVKPKAGVGGAFAGTGTGVPQAAAAAAXKAF 180

QY 181 PIKAPKLPGGYGLPYTTGKLPYGYGPGGAGAGKAGYPTGTGVPQAAAAAAXKAF 240
 DB 181 PIKAPKLPGGYGLPYTTGKLPYGYGPGGAGAGKAGYPTGTGVPQAAAAAAXKAF 240

QY 241 GAGAGVLPGVGAGVPGVPGAIPIGIGTAGVGTAAAAAAXKAGYGAAGLVPGG 300
 DB 241 GAGAGVLPGVGAGVPGVPGAIPIGIGTAGVGTAAAAAAXKAGYGAAGLVPGG 300

QY 301 PGFGVGVPGVPGAGVPGVPGAGIPVVPAGIPGAAPGVVSPAAAAAAXKAGYGAR 360
 DB 301 PGFGVGVPGVPGAGVPGVPGAGIPVVPAGIPGAAPGVVSPAAAAAAXKAGYGAR 360

QY 361 PGVGVGGIPTTYGVGAGGFPFGVGVGGIPGVAGVPSVGVPGVGVGVPISPEAQAAA 420
 DB 361 PGVGVGGIPTTYGVGAGGFPFGVGVGGIPGVAGVPSVGVPGVGVGVPISPEAQAAA 420

QY 421 AKAAKYGTGTAAAAAAXKAAQAGLVPGVGAPGVGAPGVGAPGVGAPG 480
 DB 421 AKAAKYGTGTAAAAAAXKAAQAGLVPGVGAPGVGAPGVGAPGVGAPG 480

QY 481 VGVAPGVGAPGIGPGGVAAXKAAKAAQRL 515
 DB 481 VGVAPGVGAPGIGPGGVAAXKAAKAAQRL 515

RESULT 6
 AAY69068
 ID AAY69068 standard; protein; 731 AA.
 XX

Db	121	PGVYPGVLPFGARPGVGVLPGVPTGAGVKPAPGVGGAFAGIPGVGPGPQGVPLGY	180
Qy	181	PIKAPKLPGGYGLPYTTGKLPYGYGGVAGAGKAGYPTGTGVPQAAAAAKAAKF	240
Db	181	PIKAPKLPGGYGLPYTTGKLPYGYGGVAGAGKAGYPTGTGVPQAAAAAKAAKF	240
Qy	241	GAGNAGVLPVGGGAGVPGVPGAIPGIGGIAGVGTAAAAAATAAAYGAAAGLVPGG	300
Db	241	GAGAAGVLPVGGGAGVPGVPGAIPGIGGIAGVGTAAAAAATAAAYGAAAGLVPGG	300
Qy	301	PGFGPVVGVFAGVPGVPGGAGIPVWPGAGIPGAAPGVSPPEAAAKAAAKAYGAR	360
Db	301	PGFGPVVGVFAGVPGVPGGAGIPVWPGAGIPGAAPGVSPPEAAAKAAAKAYGAR	360
Qy	361	PGVGVGGIPTVYGVGAGGFGGFGVGGIPGVAGVPSVGGVPGVGGISPEAQAAAA	420
Db	361	PGVGVGGIPTVYGVGAGGFGGFGVGGIPGVAGVPSVGGVPGVGGISPEAQAAAA	420
Qy	421	AKAAKYGVGTTPAAAAAATAAATAAQAQGLVPGVGVAPGVGVAPGVGLAPGVGVAPG	480
Db	421	AKAAKYGVGTTPAAAAAATAAATAAQAQGLVPGVGVAPGVGVAPGVGLAPGVGVAPG	480
Qy	481	GVGAPGVGVAPGIPGGGVAAAAAKAAKAAQAQLR	515
Db	481	GVGAPGVGVAPGIPGGGVAAAAAKAAKAAQAQLR	515
RESULT 7			
AA066657			
ID	AA066657	standard; protein; 731 AA.	
XX	AA066657;		
AC	AA066657;		
XX	05-APR-2001 (first entry)		
XX	Human elastin protein without signal peptide.		
DE	Minimal function unit; MFU; human; elastin prosthetic.		
XX	Homo sapiens.		
OS	WO2001006666-A2.		
XX	04-JAN-2001.		
XX	29-JUN-2000; 2000WO-US017829.		
XX	29-JUN-1999; 99US-00340736.		
XX	(PROT-) PROTEIN SPECIALTIES LTD.		
PA	(HSCR-) HSC RES & DEV LP.		
XX	Rothstein A, Keeley F, Rothstein S, Stahl R;		
PI	WPI; 2001-102886/11.		
DR	Novel polypeptides that comprise three beta-sheet/beta-turn structures		
XX	and are not naturally occurring fibrous protein, used to produce		
PT	prosthesis suitable for implantation into humans, and cosmetic materials		
PT	Claim 1; Fig 1; 39pp; English.		
XX	The present invention relates to a minimal functional unit (MFU) of human		
XX	elastin polypeptide. This protein is useful in a cosmetic material or a		
CC	prosthetic material such as prosthesis for blood vessel replacements, for		
CC	heart valve replacement, tissue replacement, for covering burns, for		
CC	covering wounds and stents		
XX	Sequence 731 AA;		
SQ	Query Match	100.0%; Score 2680; DB 4; Length 731;	

PS Disclosure; Page 30; 77pp; English.
 XX Human synthetic tropoelastin is susceptible to hydrolytic breakdown of
 CC the crosslinks. Such material may be useful in e.g. surgical
 CC applications, where the gradual loss of material over time is intended.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 733 AA;
 Query Match
 Best Local Similarity 100.0%; Score 2680; DB 2; Length 733;
 Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGVPGAIPGVGGVPGAGLGGALPGGKPLKVPVPGGLAGAGLGAFFAVT 60
 Db |||||
 QY 3 GGVPGAIPGVGGVPGAGLGGALPGGKPLKVPVPGGLAGAGLGAFFAVT 62
 Db |||||
 QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVSGAGVVPQAGVKPGVGVGL 120
 Db |||||
 QY 63 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVSGAGVVPQAGVKPGVGVGL 122
 Db |||||
 QY 121 PGVYPGVLPGARFPVGGVLPVPTGAGVKPAGVGGAFAGIPGVPGPGPQPGVPLGY 180
 Db |||||
 QY 123 PGVYPGVLPGARFPVGGVLPVPTGAGVKPAGVGGAFAGIPGVPGPGPQPGVPLGY 182
 Db |||||
 QY 181 PIKAPKLPGGYGLPYTTGKLPYGYGPGVAGAGKAGYPTGTGVPQAAAAAATAAKAF 240
 Db |||||
 QY 183 PIKAPKLPGGYGLPYTTGKLPYGYGPGVAGAGKAGYPTGTGVPQAAAAAATAAKAF 242
 Db |||||
 QY 241 GAGAAGVLPVGGAGVPGVPGAIPGIGGIAGVGTTPAAAAAATAAKAAYGAAAGLVPGG 300
 Db |||||
 QY 243 GAGAAGVLPVGGAGVPGVPGAIPGIGGIAGVGTTPAAAAAATAAKAAYGAAAGLVPGG 302
 Db |||||
 QY 301 PGFPGVGVPGAGVPGVPGAGIPVVPAGIPGAAVPGVSPAAAAAATAAKAAYGAR 360
 Db |||||
 QY 303 PGFPGVGVPGAGVPGVPGAGIPVVPAGIPGAAVPGVSPAAAAAATAAKAAYGAR 362
 Db |||||
 QY 361 PGVGGVGIPTVYGVGAGFPFGVGVGIPGVAGVPSVGGVPGVGVGISPAAAAA 420
 Db |||||
 QY 363 PGVGGVGIPTVYGVGAGFPFGVGVGIPGVAGVPSVGGVPGVGVGISPAAAAA 422
 Db |||||
 QY 421 AKAAYGVGTTPAAAAAATAAKAAYQFGLVPGVAGVPGVAGVPGVGLAPGVGVAPG 480
 Db |||||
 QY 481 VGVAPGVGVAPGIPGPGVAAAAAATAAKAAYQAQLR 515
 Db |||||
 QY 483 VGVAPGVGVAPGIPGPGVAAAAAATAAKAAYQAQLR 517
 Db |||||
 RESULT 9
 ID AAY01301
 AC AAY01301;
 DT 07-JUN-1999 (first entry)
 XX
 DE Amino acid sequence of synthetic human tropoelastin SHEL.
 XX
 KW Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;
 KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
 KW hand lotion; surgical implant; industrial product; human; SHEL.
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9903886-A1.
 XX
 PD 28-JAN-1999.
 XX
 EF 17-JUL-1998; 98WO-AU000564.
 XX

PR 18-JUL-1997; 97AU-00008117.
 XX (UNSY) UNIV SYDNEY.
 PA Weiss AS;
 PI
 XX WPI; 1999-132162/11.
 DR N-PSDB; AAX27704.
 XX
 PT New derivatives of human tropoelastin - with elastin-like or
 XX macromolecular binding properties, useful e.g. as surgical implants.
 PS Disclosure; Fig 1; 82pp; English.
 XX
 CC The invention relates to a derivative or variant of human tropoelastin
 CC (hTE) having elastin-like and/or macromolecule (specifically
 CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors
 CC comprising the nucleic acids encoding the variants or derivatives are
 CC used to produce the proteins recombinantly. The tropoelastin derivatives
 CC or hybrid proteins containing the derivatives are useful in medical,
 CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
 CC wrinkle or hand lotions, also as surgical implants, foods and industrial
 CC products. The hybrid protein have controllable GAG-binding properties,
 CC depending on presence or absence of a specific fragment, designated
 CC peptide 28A, from hTE. The present sequence represents the amino acid
 CC sequence of the synthetic human tropoelastin SHEL.
 SQ Sequence 733 AA;
 Query Match
 Best Local Similarity 100.0%; Score 2680; DB 2; Length 733;
 Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGVPGAIPGVGGVPGAGLGGALPGGKPLKVPVPGGLAGAGLGAFFAVT 60
 Db |||||
 QY 3 GGVPGAIPGVGGVPGAGLGGALPGGKPLKVPVPGGLAGAGLGAFFAVT 62
 Db |||||
 QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVSGAGVVPQAGVKPGVGVGL 120
 Db |||||
 QY 63 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVSGAGVVPQAGVKPGVGVGL 122
 Db |||||
 QY 121 PGVYPGVLPGARFPVGGVLPVPTGAGVKPAGVGGAFAGIPGVPGPGPQPGVPLGY 180
 Db |||||
 QY 123 PGVYPGVLPGARFPVGGVLPVPTGAGVKPAGVGGAFAGIPGVPGPGPQPGVPLGY 182
 Db |||||
 QY 181 PIKAPKLPGGYGLPYTTGKLPYGYGPGVAGAGKAGYPTGTGVPQAAAAAATAAKAF 240
 Db |||||
 QY 183 PIKAPKLPGGYGLPYTTGKLPYGYGPGVAGAGKAGYPTGTGVPQAAAAAATAAKAF 242
 Db |||||
 QY 241 GAGAAGVLPVGGAGVPGVPGAIPGIGGIAGVGTTPAAAAAATAAKAAYGAAAGLVPGG 300
 Db |||||
 QY 243 GAGAAGVLPVGGAGVPGVPGAIPGIGGIAGVGTTPAAAAAATAAKAAYGAAAGLVPGG 302
 Db |||||
 QY 301 PGFPGVGVPGAGVPGVPGAGIPVVPAGIPGAAVPGVSPAAAAAATAAKAAYGAR 360
 Db |||||
 QY 303 PGFPGVGVPGAGVPGVPGAGIPVVPAGIPGAAVPGVSPAAAAAATAAKAAYGAR 362
 Db |||||
 QY 361 PGVGGVGIPTVYGVGAGFPFGVGVGIPGVAGVPSVGGVPGVGVGISPAAAAA 420
 Db |||||
 QY 363 PGVGGVGIPTVYGVGAGFPFGVGVGIPGVAGVPSVGGVPGVGVGISPAAAAA 422
 Db |||||
 QY 421 AKAAYGVGTTPAAAAAATAAKAAYQFGLVPGVAGVPGVAGVPGVGLAPGVGVAPG 480
 Db |||||
 QY 481 VGVAPGVGVAPGIPGPGVAAAAAATAAKAAYQAQLR 515
 Db |||||
 QY 483 VGVAPGVGVAPGIPGPGVAAAAAATAAKAAYQAQLR 517
 Db |||||
 RESULT 10
 ID ABG75223
 ID ABG75223 standard; protein; 757 AA.

[illegible]

Dd	267	GAGAAGVLPVGAGVPVPGAIPGIGGIAGVGTPTAAAAAAXAAKATGAAGLVPGG	326
Qy	301	PGFGPGVVGVPGAGVPGVGPVPGAGIPVPPGAGIPGAAPGVWSPPEAAAKAAKAAYGAR	360
Dd	327	PGFGPGVVGVPGAGVPGVGPVPGAGIPVPPGAGIPGAAPGVWSPPEAAAKAAKAAYGAR	386
Qy	361	PGVGVGGIPTYGCAGGPPGFGVGVGGIPGVAGVPSVGGVPGVGVPGVGSPEAQAAA	420
Dd	387	PGVGVGGIPTYGVGAGGPPGFGVGVGGIPGVAGVPSVGGVPGVGVPGVGSPEAQAAA	446
Qy	421	AKAARYGVGTPTAAAAAAXAAKAAQAQFGLVPGVGVPAFCVAVACGVAGPVGVLAPGVGVAPG	480
Dd	447	AKAARYGVGTPTAAAAAAXAAKAAQAQFGLVPGVGVPAFCVAVACGVAGPVGVLAPGVGVAPG	506
Qy	481	VGVAPGVGVPAFCVAVACGVAGPVGVLAPGVGVPAFCVAVACGVAGPVGVLAPGVGVAPG	515
Dd	507	VGVAPGVGVPAFCVAVACGVAGPVGVLAPGVGVPAFCVAVACGVAGPVGVLAPGVGVAPG	541
RESULT 11			
ADP65160			
ID	ADP65160 standard; protein; 757 AA.		
XX	AC ADP65160;		
XX	12-AUG-2004 (first entry)		
DT	Human elastin.		
DE			
XX	autoimmune disease; arthritis; gene expression analysis;		
KW	rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;		
KW	antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;		
KW	immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;		
KW	fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;		
KW	immune; human.		
XX			
OS	Homo sapiens.		
XX			
FN	WO2003072827-Al.		
XX			
PD	04-SEP-2003.		
XX			
PF	31-OCT-2002; 2002WO-US035433.		
XX			
PR	31-OCT-2001; 2001US-0336220P.		
XX	(CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.		
XX			
PI	Hirsch R, Thorton SL;		
XX			
DR	WPI; 2003-712740/67.		
XX	GENBANK; NP_000492.		
DR			
PT	Diagnosing and analyzing autoimmune disease using gene expression		
PT	profiles and microarray technology, useful for diagnosing and treating		
PT	rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and		
PT	gout.		
XX			
PS	Disclosure; Page; 56pp; English.		
XX			
CC	The invention relates to a novel method for diagnosing and analysing a		
CC	autoimmune disease or arthritides. The method comprises obtaining a		
CC	patient sample containing mRNA, analysing gene expression using the mRNA		
CC	that results in a gene expression signature of the mRNA, and using that		
CC	gene expression signature to diagnose or analyse the autoimmune disease		
CC	or arthritides in the patient, where gene expression of at least 60% of		
CC	the genes correlates with that of the gene signature. The invention		
CC	further comprises: a treatment of rheumatoid arthritis; identification		
CC	genes for targeting in the treatment of rheumatoid arthritis in a mamma		
CC	other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an		
CC	array or gene chip, specific for rheumatoid arthritis; diagnosis or		
CC	analyses of autoimmune disease or rheumatoid arthritis; screening the		

CC efficacy of a candidate drug in vitro for the treatment of collagen-
CC induced arthritis; and reducing the symptoms associated with collagen-
CC induced arthritis. The compositions of the invention have the following
CC activities: immunosuppressive, antiinflammatory, antirheumatic, antiarthritic, osteopathic,
CC antigout, antiinflammatory, dermatological, and immunomodulatory. The
CC methods and compositions of the present invention are useful for
CC diagnosing and treating autoimmune disease or arthritis, such as
CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
CC immune disease caused by an infectious agent. This sequence represents a
CC protein sequence relating to the genes used in the analysis and treatment
CC of autoimmune diseases or arthritis. Note: This sequence is not shown
CC in the specification. It has been supplied in an electronic format from
CC WIPO.

XX Sequence 757 AA;

Query Match 100.0%; Score 2680; DB 7; Length 757;
Best Local Similarity 100.0%; Pred. No. 7.6e-153;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGVPGAIPGGVPGGVYFPGAGLGGGALGGGKPLKPVPGGLAGAGLGAFFAVT 60
Db 27 GGVPGAIPGGVPGGVYFPGAGLGGGALGGGKPLKPVPGGLAGAGLGAFFAVT 86
QY 61 FPGALVPGGVADAAAYKAAKAGAGLGGVPGVGGGLGVSGAGAVVPGAGVPGKVPVGL 120
Db 87 FPGALVPGGVADAAAYKAAKAGAGLGGVPGVGGGLGVSGAGAVVPGAGVPGKVPVGL 146
QY 121 PGVYPGVLPGARFPFGVLPVGTAGVKPKAGVGGAGAGIPGVPGVPGVPGVGL 180
Db 147 PGVYPGVLPGARFPFGVLPVGTAGVKPKAGVGGAGAGIPGVPGVPGVPGVGL 206
QY 181 PIKAPKLPGGGLPYTTGKLPYGVPGGVGAAGKAGYPTGTGVPQAAAAAKAAKF 240
Db 207 PIKAPKLPGGGLPYTTGKLPYGVPGGVGAAGKAGYPTGTGVPQAAAAAKAAKF 266
QY 241 GAGAAGVLPGGVAGVPGVPGAGIPVPGAGIPGAAPGVPGVSPAAAAAKAAKAAKF 300
Db 267 GAGAAGVLPGGVAGVPGVPGAGIPVPGAGIPGAAPGVPGVSPAAAAAKAAKAAKF 326
QY 301 PGFGPGVWVPGVAGVPGVPGAGIPVPGAGIPGAAPGVPGVSPAAAAAKAAKAAKF 360
Db 327 PGFGPGVWVPGVAGVPGVPGAGIPVPGAGIPGAAPGVPGVSPAAAAAKAAKAAKF 386
QY 361 PGVYVGGIPTYGVAGGFFGFGVGGIPGVAGVSPVSGVPGVGGVPGVSPAAAA 420
Db 387 PGVYVGGIPTYGVAGGFFGFGVGGIPGVAGVSPVSGVPGVGGVPGVSPAAAA 446
QY 421 AKAAKYGVTTPAAAAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 480
Db 447 AKAAKYGVTTPAAAAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 506
QY 481 VGVAPGVGVPAGIPGGVAAAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 515
Db 507 VGVAPGVGVPAGIPGGVAAAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 541

RESULT 12

ADL96420
ID ADL96420 standard; protein; 731 AA.

XX AC ADL96420;

XX DT 20-MAY-2004 (first entry)

XX DE Human elastin protein fragment.

XX KW fibrous protein; prosthesis; elastin; lamprin; spider silk protein;
XX KW blood vessel; wound; burn healing; collagen.

XX OS Homo sapiens.

XX

FH Key Location/Qualifiers
FT Region 19..160
FT Region /note="region specifically claimed in claim 6"
FT Region 188..367
FT Region /note="region specifically claimed in claim 6"
FT Region 374..499
FT Region /note="region specifically claimed in claim 6"
FT Region 607..717
FT Region /note="region specifically claimed in claim 6"
PN US2003166846-A1.
XX 04-SEP-2003.
XX 28-SEP-2001; 2001US-00964662.
PR 07-AUG-1996; 96US-0023522P.
PR 07-AUG-1997; 97US-00911364.
PR 29-JUN-1999; 99US-00340736.
XX (ROTH/) ROTHSTEIN A.
PA (KEEL/) KEELEY F.
PA (ROTH/) ROTHSTEIN S.
Rothstein A, Keeley F, Rothstein S;
WPI; 2003-898105/82.

Polypeptide for constructing human elastin-like prostheses such as tubes
for blood vessel replacement and sheets for other uses such as wound or
burn healing, comprises three beta sheets and three beta turns.

Claim 5; Fig 1B; 17pp; English.

This invention describes a polypeptide that comprises three beta
sheet/beta turn structures and that is not a naturally occurring fibrous
protein. The invention also describes a prosthesis comprising an animal,
metal or synthetic material, where the surface is coated with the
polypeptide, a cosmetic material comprising the polypeptide, an elastic
material comprising the polypeptide, a high tensile strength material
comprising the polypeptide, a material comprising two or more
polypeptides selected from (a) a polypeptide consisting essentially of a
portion of the polypeptide comprising at least three beta sheet/beta turn
structures, (b) a polypeptide consisting essentially of a portion of the
amino acid sequence of an animal elastin comprising at least three beta
sheets/beta turns, (c) a polypeptide consisting essentially of a portion
of lamprin comprising at least three beta sheets/beta turns, and (d) a
polypeptide consisting essentially of a spider silk protein comprising at
least three beta sheets/beta turns, a polypeptide having the primary
structure of a portion of a naturally occurring fibrous protein and a
secondary structure comprising at least three beta sheets/beta turns,
where each of the beta sheet/beta turn structures comprises from 3 to
about 7 amino acids and the polypeptide is not a naturally occurring
fibrous protein. The minimal functional unit (MFU) of the invention is
useful to construct human elastin-like prostheses such as tubes for blood
vessel replacement and sheets for other uses such as wound or burn
healing. Alternatively the MFU can be co-aggregated with other proteins,
for example collagen, to provide prosthesis material that resembles the
natural structural materials of the body. The MFU based material is
subject to infiltration of cells growing in the patient, including
endothelial cells, and the prosthesis can become a permanent living
tissue replacement. The material is more biocompatible than other elastin
-containing materials proposed for prostheses.

Sequence 731 AA;

Query Match

Best Local Similarity 99.7%; Score 2672; DB 7; Length 731;

Matches 514; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGVPGAIPGGVPGGVYFPGAGLGGGALGGGKPLKPVPGGLAGAGLGAFFAVT 60
Db 1 GGVPGAIPGGVPGGVYFPGAGLGGGALGGGKPLKPVPGGLAGAGLGAFFAVT 60

QY	61	FPGALVPGGVADAAAAAAYKAAKAGAGLGGVPGVGGGLGVSAGAVVPPQAGVKKPKVPGVGL	120
Db	61	FPGALVPGGVADAAAAAAYKAAKAGAGLGGVPGVGGGLGVSAGAVVPPQAGVKKPKVPGVGL	120
QY	121	PGVYPGGVLPGARFPGGVGLPGVPTGAGVKKPKAPGVGGAFAGIPGVGPGPGPGVPLGY	180
Db	121	PGVYPGGVLPGARFPGGVGLPGVPTGAGVKKPKAPGVGGAFAGIPGVGPGPGPGVPLGY	180
QY	181	PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAGKAGYPTGTGVPQAAAAAAYKAAAKF	240
Db	181	PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAGKAGYPTGTGVPQAAAAAAYKAAAKF	240
QY	241	GAGAAGVLPVGGGAGVPGVPGAIPIGIGIAGVGTTPAAAAAAYKAAKAAKAAAGLVPGG	300
Db	241	GAGAAGVLPVGGGAGVPGVPGAIPIGIGIAGVGTTPAAAAAAYKAAKAAKAAAGLVPGG	300
QY	301	PGFGVGVVPGAGVPGVPGAGIPVVPAGITPGAAVPGVVSPEAAKAAKAAKYGAR	360
Db	301	PGFGVGVVPGAGVPGVPGAGIPVVPAGITPGAAVPGVVSPEAAKAAKAAKYGAR	360
QY	361	PGVGVGGIPTTYGVGAGGPGFGVGGIPGVAGVPSVGGVPGVGGVPGVGISSPEAQAAAA	420
Db	361	PGVGVGGIPTTYGVGAGGPGFGVGGIPGVAGVPSVGGVPGVGGVPGVGISSPEAQAAAA	420
QY	421	AKAAKYGVGTTPAAAAAAYKAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGVAPG	480
Db	421	AKAAKYGVGTTPAAAAAAYKAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGVAPG	480
QY	481	VGVAFGVGVAPGIGPGGVAAAAAAYKAAKAAKAAQLR	515
Db	481	VGVAFGVGVAPGIGPGGVAAAAAAYKAAKAAKAAQLR	515
RESULT 13			
ABU08725			
ID	ABU08725	standard; protein; 731 AA.	
XX	AC	ABU08725;	
XX	DT	25-JUN-2003 (first entry)	
DE	DE	Human elastin mature protein.	
XX	KW	Human; elastin; minimal functioning unit; MFU;	
KW	KW	beta-sheet/beta-turn structure; fibrous protein; prosthesis;	
KW	KW	blood vessel replacement; heart replacement valve; burn; wound; lamprin;	
KW	KW	spider silk; cord; rope; parachute; cosmetic; platelet binding inhibitor;	
KW	KW	platelet activation inhibitor; non-thrombogenic; cell infiltration;	
KW	KW	non-immunogenic; biocompatible; high tensile strength; elasticity.	
OS	OS	Homo sapiens.	
XX	XX	US6489446-B1.	
XX	XX	03-DEC-2002.	
XX	XX	29-JUN-1999; 99US-00340736.	
XX	XX	07-AUG-1996; 96US-0023522P.	
PR	PR	07-AUG-1997; 97US-00911364.	
XX	XX	(HSCR-) HSC RES & DEV LP.	
PA	PA	(PROT-) PROTEIN SPECIALTIES LTD.	
XX	XX	Rothstein A, Keeley F, Rothstein S;	
XX	XX	WPI; 2003-391056/37.	
XX	XX	Novel polypeptide useful in prosthesis, has a secondary structure	
PT	PT	characterized by three beta-sheet/beta-turn structures, and is not a	
PT	PT	naturally occurring fibrous protein.	
Claim 1; Fig 1B; 21pp; English.			
The invention describes a polypeptide (1) comprising a minimal			
functioning unit (MFU) which is present in the sequence of human elastin			
and comprised of at least three beta-sheet/beta-turn structures, and at			
least one amino acid residue that participates in cross-linking, and not			
a naturally occurring fibrous protein. The MFU material can be used to			
construct human elastin-like prostheses such as tubes for blood vessel			
replacement, heart replacement valves and sheets for other uses such as			
burns or wounds to promote healing. MFUs can be co-aggregated with other			
proteins, for e.g. collagen, to provide prosthesis material that			
resembles the natural structural materials of the body. MFUs modeled on			
lamprin and other fibrous proteins e.g. spider silk, can be used to make			
in cords and ropes for use in parachutes and in cosmetics. Coating			
synthetic prosthesis with MFUs modeled on human elastin significantly			
inhibits platelet binding and activation. The human-like MFU material is			
more biocompatible than other elastin-containing materials. In contrast			
to solubilised fragments of elastin used before, an MFU is a single			
peptide of defined composition. The MFU is considerably smaller than the			
parent protein, simpler in structure, easier to produce or express in			
quantity, to handle in solution and to manipulate for experimental and			
practical purposes. Like other elastin preparations, the MFU is non-			
thrombogenic and provides a friendly environment for cell infiltration.			
Being composed entirely of a human elastin sequence, MFU is non-			
immunogenic, thus providing a truly biocompatible material. MFUs modeled			
on lamprin and other fibrous proteins can be used to make a variety of			
materials having high tensile strength, elasticity and plasticity of			
their parent proteins. This is the amino acid sequence of mature human			
elastin on which the MFU peptides of the invention are based			
Sequence 731 AA;			
Query Match 99.6%; Score 2670; DB 6; Length 731;			
Best Local Similarity 99.6%; Pred. No. 2.9e-152;			
Matches 513; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
QY	1	GGVPGAIPGGVPGGVFPYAGIAGLGGALGPGGKPLKVPVGLGAGLGAAGLGAAPAVT	60
Db	1	GGVPGAIPGGVPGGVFPYAGIAGLGGALGPGGKPLKVPVGLGAGLGAAGLGAAPAVT	60
QY	61	FGALVPGGVADAAAAAYKAAKAGAGLGGVPGVGGGLGVSAGAVVPPQAGVKKPKVPGVGL	120
Db	61	FGALVPGGVADAAAAAYKAAKAGAGLGGVPGVGGGLGVSAGAVVPPQAGVKKPKVPGVGL	120
QY	121	PGVYPGGVLPGARFPGGVGLPGVPTGAGVKKPKAPGVGGAFAGIPGVGPGPGPGVPLGY	180
Db	121	PGVYPGGVLPGARFPGGVGLPGVPTGAGVKKPKAPGVGGAFAGIPGVGPGPGPGVPLGY	180
QY	181	PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAGKAGYPTGTGVPQAAAAAAYKAAAKF	240
Db	181	PIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAGKAGYPTGTGVPQAAAAAAYKAAAKF	240
QY	241	GAGAAGVLPVGGGAGVPGVPGAIPIGIGIAGVGTTPAAAAAAYKAAKAAKAAAGLVPGG	300
Db	241	GAGAAGVLPVGGGAGVPGVPGAIPIGIGIAGVGTTPAAAAAAYKAAKAAKAAAGLVPGG	300
QY	301	PGFGVGVVPGAGVPGVPGAGIPVVPAGITPGAAVPGVVSPEAAKAAKAAKYGAR	360
Db	301	PGFGVGVVPGAGVPGVPGAGIPVVPAGITPGAAVPGVVSPEAAKAAKAAKYGAR	360
QY	361	PGVGVGGIPTTYGVGAGGPGFGVGGIPGVAGVPSVGGVPGVGGVPGVGISSPEAQAAAA	420
Db	361	PGVGVGGIPTTYGVGAGGPGFGVGGIPGVAGVPSVGGVPGVGGVPGVGISSPEAQAAAA	420
QY	421	AKAAKYGVGTTPAAAAAAYKAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGVAPG	480
Db	421	AKAAKYGVGTTPAAAAAAYKAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGVAPG	480
QY	481	VGVAFGVGVAPGIGPGGVAAAAAAYKAAKAAKAAQLR	515
Db	481	VGVAFGVGVAPGIGPGGVAAAAAAYKAAKAAKAAQLR	515

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RESULT 14
ADE40132
ID ADE40132 standard; protein; 711 AA.
XX
AC ADE40132;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human NOV16a protein - SEQ ID 38.
XX
KW NOVX; cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic;
KW antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nontropic;
KW antiparkinsonian; antiasthmatic; gynaecological; cardiomyopathy;
KW atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;
KW multiple sclerosis; graft-versus-host disease; Alzheimer's; Parkinson's;
KW asthma; fertility disorder; vaccine; gene therapy; chromosome mapping;
KW tissue typing; human; NOV.
XX
OS Homo sapiens.
XX
PN WO2003064589-A2.
XX
PD 07-AUG-2003.
XX
PF 02-AUG-2002; 2002WO-US024483.
XX
PR 02-AUG-2001; 2001US-0309501P.
PR 03-AUG-2001; 2001US-0310291P.
PR 07-AUG-2001; 2001US-0310544P.
PR 08-AUG-2001; 2001US-0310951P.
PR 09-AUG-2001; 2001US-0311292P.
PR 13-AUG-2001; 2001US-0311799P.
PR 16-AUG-2001; 2001US-0312892P.
PR 17-AUG-2001; 2001US-0313201P.
PR 17-AUG-2001; 2001US-0313415P.
PR 20-AUG-2001; 2001US-0313643P.
PR 21-AUG-2001; 2001US-0313702P.
PR 23-AUG-2001; 2001US-0314031P.
PR 28-AUG-2001; 2001US-0314466P.
PR 29-AUG-2001; 2001US-0315403P.
PR 17-SEP-2001; 2001US-0322716P.
PR 21-SEP-2001; 2001US-0323994P.
PR 14-DEC-2001; 2001US-0340233P.
PR 05-FEB-2002; 2002US-0354591P.
PR 19-MAR-2002; 2002US-0365478P.
PR 19-APR-2002; 2002US-0373814P.
PR 19-APR-2002; 2002US-0373825P.
PR 23-APR-2002; 2002US-0373989P.
PR 07-JUN-2002; 2002US-0374632P.
PR 01-AUG-2002; 2002US-0386971P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Kekuda R, Miller CE, Patturajan M, Pena CEA, Rieger DK;
PI Shinkets RA, Zerhusen BD, Li L, Ji W, Padigaru M, Casman SJ;
PI Voss EZ, Boldog FL, Gorman L, Leite MW, Vernet CAM, Anderson DW;
PI Guo X, Zhong M, Gerlach VL, Hjal T, Rastelli L, Spytek KA;
PI Edinger SR, Ellerman K, Malyankar UM, Macdougall JR, Stone DJ;
PI Alsobrook JP, Lepley DM, Burgess CE, Majumder K, Wolenc AR;
PI Smithson G;
XX
WPI; 2003-663472/62.
DR N-PSDB; ADE40131.
XX
XX
New NOVX polypeptides and nucleic acids, useful for preventing or
treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX

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PS Claim 1; SEQ ID NO 38; 560pp; English.
XX
CC The invention relates to a novel NOVX polypeptide. The polypeptide of the
CC invention demonstrates cardiant, antiarteriosclerotic, hypotensive,
CC cytostatic, anorectic, antidiabetic, immunosuppressive, anti-HIV,
CC neuroprotective, nontropic, antiparkinsonian, antiasthmatic and
CC gynaecological activities and may be useful in diagnosing and
CC preventing NOVX-associated disorders including cardiomyopathy,
CC atherosclerosis, hypertension, cancer, obesity, diabetes, multiple
CC sclerosis, graft-versus-host disease, Alzheimer's disease, Parkinson's
CC disease, asthma or fertility disorders. Furthermore, the polypeptides may
CC be utilised as vaccines whilst the nucleic acids may be used as
CC hybridisation probes, in gene therapy, chromosome mapping, tissue typing,
CC preventive medicine and pharmacogenomics. The current sequence is that of
CC the human NOV protein of the invention.
XX
SQ Sequence 711 AA;
Query Match 99.5%; Score 2667.5; DB 7; Length 711;
Best Local Similarity 99.0%; Pred. No. 41e-152;
Matches 515; Conservative 0; Mismatches 0; Indels 5; Gaps 1;
QY 1 GGVPGAIPGGVPGGVYFGAGLGGALGGALGGKPLKEVPGGLAGAGLGAFFPVT 60
Db |||||
QY 27 GGVPGAIPGGVPGGVYFGAGLGGALGGALGGKPLKEVPGGLAGAGLGAFFPVT 86
Db |||||
QY 61 PFGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGGLGVA -----GAVVPQAGVKPGKV 115
Db |||||
QY 87 PFGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGGLGVAAPSVPGAVPQAGVKPGKV 146
Db |||||
QY 116 PGVGLPGVPGVLPGARFPGVPGVLPVPTGAGVKAPGVGGAGFAGIPGVPGGPGPG 175
Db |||||
QY 147 PGVGLPGVPGVLPGARFPGVPGVLPVPTGAGVKAPGVGGAGFAGIPGVPGGPGPG 206
Db |||||
QY 176 VPLGVPKAPKLPGGYGLPYTTGKLPYGYGGVAGAGKAGYPTGTGVPQAAAAAAK 235
Db |||||
QY 207 VPLGVPKAPKLPGGYGLPYTTGKLPYGYGGVAGAGKAGYPTGTGVPQAAAAAAK 266
Db |||||
QY 236 AAAFGAGAGVLPVGGAGVPGVPGAIPGTGGTAGVGTAAAAAATAKAAKYGAAAG 295
Db |||||
QY 267 AAAFGAGAGVLPVGGAGVPGVPGAIPGTGGTAGVGTAAAAAATAKAAKYGAAAG 326
Db |||||
QY 296 LVFGGPGFGVGVPGAGVPGVPGAIPVVPAGIPVVPAGIPVVPAGIPVVPAGIPV 355
Db |||||
QY 327 LVFGGPGFGVGVPGAGVPGVPGAIPVVPAGIPVVPAGIPVVPAGIPVVPAGIPV 386
Db |||||
QY 356 KYGAREPGVGGIPTTYGVGAGGPGPGVGGIPVVPAGIPVVPAGIPVVPAGIPV 415
Db |||||
QY 387 KYGAREPGVGGIPTTYGVGAGGPGPGVGGIPVVPAGIPVVPAGIPVVPAGIPV 446
Db |||||
QY 416 QAAAAAATAKYGVTAAAAAATAKAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGV 475
Db |||||
QY 447 QAAAAAATAKYGVTAAAAAATAKAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGV 506
Db |||||
QY 476 GVAPGVGVAPGVGVAPGVPGIPGGVAAAAAATAKAAKAAQOLR 515
Db |||||
QY 507 GVAPGVGVAPGVGVAPGVPGIPGGVAAAAAATAKAAKAAQOLR 546
Db |||||
RESULT 15
AAO17360
ID AAO17360 standard; protein; 730 AA.
XX
AC AAO17360;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human elastin.
XX
KW Human; endometriosis; DNA chip; fibronectin; p27; reticulocalbin;
KW aldehyde dehydrogenase 6; gravin; phospholipase C epsilon; elastin;
KW insulin-like growth factor binding protein-2; alpha-2 type IV collagen;
KW transmembrane receptor PTK7; collagen type XVIII alpha 1;

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KW platelet derived growth factor receptor alpha; laminin M chain;
KW subtilisin like protein PACE4; nidogen.
OS Homo sapiens.
XX EP1191107-A2.
XX PD 27-MAR-2002.
XX PF 21-AUG-2001; 2001EP-00250300.
XX PR 25-SEP-2000; 2000DE-01048633.
XX PA (SCHD) SCHERING AG.
XX Hess-Stump H, Haendler B, Kraetzschmar J, Kreft B, Winterhager E;
PI Regidor P, Scotti S;
XX WPI; 2002-317413/36.
DR In vitro diagnosis and monitoring of endometriosis, comprises detecting
XX reduced expression of specific gene products, e.g. from the fibronectin
PT gene.
XX Claim 1; Page 15-16; 21pp; German.

XX The present invention relates to a method for the in vitro diagnosis of
XX endometriosis by determining the amount of gene product from at least one
XX specific gene in a patient sample and comparing this with the amount of
XX gene product in a control sample. A reduced level is indicative of
XX endometriosis. The gene products may be fibronectin, p27, reticulocalbin,
XX aldehyde dehydrogenase 6, gravin, phospholipase C epsilon, elastin,
XX insulin-like growth factor binding protein-2, alpha-2 type IV collagen,
XX transmembrane receptor PK7, collagen type XVIII alpha 1, platelet
XX derived growth factor receptor alpha, laminin M chain, subtilisin like
XX protein PACE4 or nidogen. The method is useful for initial diagnosis of
XX endometriosis, and also for monitoring progress and treatment of the
XX disease. The present sequence is human elastin
XX

XX Sequence 730 AA;
Query Match 99.5%; Score 2667; DB 5; Length 730;
Best Local Similarity 98.8%; Pred. No. 4.4e-152;
Matches 515; Conservative 0; Mismatches 0; Indels 6; Gaps 1;
QY 1 GGVPGAIPGGVPGGVFYPGAGLGGALGGALPGGKPLKPVPGGLAGAGLGAFAFPAVT 60
DB 27 GGVPGAIPGGVPGGVFYPGAGLGGALGGALPGGKPLKPVPGGLAGAGLGAFAFPAVT 86
QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVFGVGLGSAGAVVPPQAGVPGKVPVGL 120
DB 87 FPGALVPGGVADAAAAYKAAKAGAGLGGVFGVGLGSAGAVVPPQAGVPGKVPVGL 146
QY 121 PGVYPGVLPGARFPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 180
DB 147 PGVYPGVLPGARFPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 206
QY 181 PIKAPKLPGGVGLPYTTCKLPYGGVPGVAGAGKAGYPTGTGVPQAAAAAAYKAAKAF 240
DB 207 PIKAPKLPGGVGLPYTTCKLPYGGVPGVAGAGKAGYPTGTGVPQAAAAAAYKAAKAF 266
QY 241 GAGAGVLPVGGAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 300
DB 267 GAGAGVLPVGGAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 326
QY 301 PGFPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 360
DB 327 PGFPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 386
QY 361 PGVYPGVLPGARFPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 420
DB 387 PGVYPGVLPGARFPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 446

QY 421 AKAAKYGVTGTPAAAAAAYKAAKAGAGLGGVFGVGLGSAGAVVPPQAGVPGKVPVGL 474
DB 447 AKAAKYGVTGTPAAAAAAYKAAKAGAGLGGVFGVGLGSAGAVVPPQAGVPGKVPVGL 506
QY 475 VGVAPGVGVPAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 515
DB 507 VGVAPGVGVPAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 547

RESULT 16
ADQ19747 ADQ19747 standard; protein; 730 AA.
XX AC ADQ19747;
XX 26-AUG-2004 (first entry)
DT Human soft tissue sarcoma-upregulated protein - SEQ ID 2566.
XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
XX Homo sapiens.
OS WO2004048938-A2.
XX PN 10-JUN-2004.
XX PD 26-NOV-2003; 2003WO-US038193.
XX PF 26-NOV-2002; 2002US-0429739P.
XX PR (PROT-) PROTEIN DESIGN LABS INC.
XX PA Aziz N, Ginsburg WM, Zlotnik A;
PI WPI; 2004-441208/41.
DR Early detection of soft tissue sarcoma comprises determining expression
XX of a gene in a first soft tissue sample and a normal soft tissue sample
XX and comparing the gene expression, also useful in treating soft tissue
XX sarcoma.
XX Example 2; SEQ ID NO 2566; 210pp; English.

XX The invention relates to a novel method for detecting soft tissue sarcoma
XX which comprises obtaining a first soft tissue sample from an individual,
XX and a normal soft tissue sample from the same or different individual,
XX and determining the expression of a gene in both samples, where a higher level
XX expression of the gene in both soft tissue samples indicates the
XX presence of soft tissue sarcoma. The method of the invention has
XX presence of soft tissue sarcoma. The method of the invention has
XX cytotatic applications and may be useful for detecting soft tissue
XX sarcoma, possibly via gene therapy or vaccine production. The nucleic
XX acid sequences may be useful in diagnostic and screening applications.
XX The current sequence is that of a human soft tissue sarcoma-upregulated
XX protein of the invention. The current sequence is not shown within the
XX specification per se but was submitted in CD format by the inventor.

XX Sequence 730 AA;
Query Match 99.5%; Score 2667; DB 8; Length 730;
Best Local Similarity 98.8%; Pred. No. 4.4e-152;
Matches 515; Conservative 0; Mismatches 0; Indels 6; Gaps 1;
QY 1 GGVPGAIPGGVPGGVFYPGAGLGGALGGALPGGKPLKPVPGGLAGAGLGAFAFPAVT 60
DB 27 GGVPGAIPGGVPGGVFYPGAGLGGALGGALPGGKPLKPVPGGLAGAGLGAFAFPAVT 86
QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVFGVGLGSAGAVVPPQAGVPGKVPVGL 120
DB 87 FPGALVPGGVADAAAAYKAAKAGAGLGGVFGVGLGSAGAVVPPQAGVPGKVPVGL 146
QY 121 PGVYPGVLPGARFPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 180

Mon Nov 22 12:42:42 2004

31-AUG-2000.
28-FEB-2000; 2000WO-US002526.
26-FEB-1999; 99US-00258217.
(UTAH) UNIV UTAH RES FOUND.
Keating MT, Li DY;
WPI; 2000-533134/48.
Elastin based compositions useful for treating atherosclerosis,
restenosis, vascular bypass graft stenosis, transplant arteriopathy,
aneurysm, dissection SVAS and/or hypertension.
Example 3; Page 48; 79pp; English.
The present sequence represents a fusion protein, comprising human
elastin and c-myc, preceded by a His tag. The protein is used in
compositions of the invention. The specification describes elastin based
compositions that are potent regulators of smooth muscle cell
proliferation, differentiation and migration in vivo. The elastin-based
compositions comprise at least one elastic fibre, elastins, tropoelastins
(or fragments of them) which have biological activities comprising:
inhibiting the proliferation of smooth muscle cells in vivo; stimulating
the differentiation of smooth muscle cell in vivo; and regulating the
migration of smooth muscle cells in vivo. The compositions may be used
for the prophylaxis or treatment of a disorder characterized by
diminished capacity to regulate smooth muscle cell function such as
atherosclerosis, restenosis, vascular bypass graft stenosis, transplant
arteriopathy, aneurysm and/or dissection. Disorders which may be treated
also include SVAS (undefined), hypertension, and transplant arteriopathy
SQ Sequence 730 AA;
Query Match 99.4%; Score 2663; DB 3; Length 730;
Best Local Similarity 98.7%; Pred. No. 7.7e-152;
Matches 514; Conservative 0; Mismatches 1; Indels 6; Gaps 1;
1 GGVPGAIPGGVPGGVYFGAGLGGALGGALGGKPLKVPVGGLAGAGLGGAGLGAFFAVT 60
36 GGVPGAIPGGVPGGVYFGAGLGGALGGALGGKPLKVPVGGLAGAGLGGAGLGAFFAVT 95
61 FGALVPGGVADAAAAAAYAAKAGAGLGGVPGVGLGVSAGAVPQPGVPGVGL 120
96 FGALVPGGVADAAAAAAYAAKAGAGLGGVPGVGLGVSAGAVPQPGVPGVGL 155
121 PGVYPGGVLPGARPPGVGLPGVPTGAGVFKPAGVCGAFAGIPGVPGPGPQGVPLGY 180
156 PGVYPGGVLPGARPPGVGLPGVPTGAGVFKPAGVCGAFAGIPGVPGPGPQGVPLGY 215
181 PIKAPKLPGGGLPYTTTKLPGYGGVGAAGKAGYPTGTGVPQAAAAAATAAKAF 240
216 PIKAPKLPGGGLPYTTTKLPGYGGVGAAGKAGYPTGTGVPQAAAAAATAAKAF 275
241 GAGAAGVLPVGGAGVPGVPGAIPGIGGAGVGTTPAAAAAATAAKAYGAAGLVPGG 300
276 GAGAAGVLPVGGAGVPGVPGAIPGIGGAGVGTTPAAAAAATAAKAYGAAGLVPGG 335
301 PGFGGVVGVPGAGVPGVPGAGIPVVPAGIPGAAPVGVVSPAAAAAATAAKAYGAR 360
336 PGFGGVVGVPGAGVPGVPGAGIPVVPAGIPGAAPVGVVSPAAAAAATAAKAYGAR 395
361 PGVGGGIPTYGVGAGGFPFGVGGIPGVAGVPSVGGVPGVGGVPGVGISPEAAAAA 420
396 PGVGGGIPTYGVGAGGFPFGVGGIPGVAGVPSVGGVPGVGGVPGVGISPEAAAAA 455
421 AKAAYGVGTAAAAAATAAKAAQF-----GLVPGVGVAPGVGVAPGVGLAPG 474
456 AKAAYGVGTAAAAAATAAKAAQFALLNLGLVPGVGVAPGVGVAPGVGLAPG 515
475 VGVPAGVGVAPGVGVAPGIPGPGGVAAAKSAKVAQAQLR 515

516 VGVPAGVGVAPGVGVAPGIPGPGGVAAAKSAKVAQAQLR 556

|||||

Db

RESULT 19

ADE40134

ID ADE40134 standard; protein; 692 AA.

XX AC ADE40134;

XX AC ADE40134;

DT 29-JAN-2004 (first entry)

DE Human NOV16b protein - SEQ ID 40.

XX NOVX; cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic;
XX anti-diabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic;
XX antiparkinsonian; antiasthmatic; gynaecological; cardiomyopathy;
XX atherosclerosis; hypertension; cancer; diabetes; AIDS;
XX multiple sclerosis; graft-versus-host disease; Alzheimer's; Parkinson's;
XX asthma; fertility disorder; vaccine; gene therapy; chromosome mapping;
XX tissue typing; human; NOV.

XX Homo sapiens.

OS WO2003064589-A2.

XX 07-AUG-2003.

XX 02-AUG-2002; 2002WO-US024483.

XX 02-AUG-2001; 2001US-0309501P.

XX 03-AUG-2001; 2001US-0310291P.

XX 07-AUG-2001; 2001US-0310544P.

XX 08-AUG-2001; 2001US-0310951P.

XX 09-AUG-2001; 2001US-0311292P.

XX 13-AUG-2001; 2001US-0311979P.

XX 16-AUG-2001; 2001US-0312892P.

XX 17-AUG-2001; 2001US-0313201P.

XX 17-AUG-2001; 2001US-0313415P.

XX 20-AUG-2001; 2001US-0313643P.

XX 20-AUG-2001; 2001US-0313702P.

XX 21-AUG-2001; 2001US-0314031P.

XX 23-AUG-2001; 2001US-0314466P.

XX 28-AUG-2001; 2001US-0315403P.

XX 29-AUG-2001; 2001US-0315853P.

XX 17-SEP-2001; 2001US-0322716P.

XX 21-SEP-2001; 2001US-0323944P.

XX 05-FEB-2002; 2002US-0354591P.

XX 19-MAR-2002; 2002US-0365478P.

XX 19-APR-2002; 2002US-0373814P.

XX 19-APR-2002; 2002US-0373825P.

XX 19-APR-2002; 2002US-0373989P.

XX 23-APR-2002; 2002US-0374632P.

XX 07-JUN-2002; 2002US-0386971P.

XX 01-AUG-2002; 2002US-00210172.

XX (CURA-) CURAGEN CORP.

XX Kekuda R, Miller CE, Patturajan M, Pena CEA, Rieger DK;

XX Shinkets RA, Zerhusen BD, Li L, Ji W, Padigar M, Casman ST;

XX Voss EZ, Boldog FL, Gorman L, Leite MW, Vernet CAM, Anderson DW;

XX Guo X, Zhong M, Gerlach VL, Hjal T, Rastelli L, Spytek KA;

XX Edinger SR, Eilerman K, Malyankar UM, Macdougall JR, Stone DJ;

XX Alsbrook JP, Lepley DM, Burgess CE, Majumder K, Wolenc AR;

XX Smithson G;

XX WPI; 2003-663472/62.

XX N-PSDB; ADE40133.

XX New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
PT

PT	pharmacogenomics.	
XX	Claim 1; SEQ ID NO 40; 560pp; English.	
XX		
CC	The invention relates to a novel NOVX polypeptide. The polypeptide of the invention demonstrates cardiant, antiarteriosclerotic, hypotensive, cyostatic, anorectic, antidiabetic, immunosuppressive, anti-HIV, neuroprotective, nootropic, antiparkinsonian, antiasthmatic and gynaecological activities and may be useful in diagnosing, treating or preventing NOVX-associated disorders including cardiomyopathy, atherosclerosis, hypertension, cancer, obesity, diabetes, AIDS, multiple sclerosis, graft-versus-host disease, Alzheimer's disease, Parkinson's disease, asthma or fertility disorders. Furthermore, the polypeptides may be utilised as vaccines whilst the nucleic acids may be used as hybridisation probes, in gene therapy, chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The current sequence is that of the human NOV protein of the invention.	
XX		
SQ	Sequence 692 AA;	
	Query Match	90.7%; Score 2431; DB 7; Length 692;
	Best Local Similarity	91.6%; Pred. No. 5.9e-138;
	Matches 477; Conservative	0; Mismatches 0; Indels 44; Gaps 2;
QY	1	GGVPGAIPGGVPGGVFYPCAGLGGALGGALPGGKPLKPVPGGLAGAGLGAFAFPAVT 60
Db	27	GGVPGAIPGGVPGGVFYPCAGLGGALGGALPGGKPLKPVPGGLAGAGLGAFAFPAVT 86
QY	61	PPGALVPGGVADAAAYAAKAGAGLGGVPGVGGGLVGSAGAVVPPQAGVKPKVPGVGL 120
Db	87	PPGALVPGGVADAAAYAAKAGAGLGGVPGVGGGLVGSAGAVVPPQAGVKPKV 141
QY	121	PGVYPGVLPGARFPGVGVLPQVPTGAGVKPKAPGVGGAFAPIGVGPPGPGVPLGY 180
Db	142	-----PGVGGNFAPIGVGPPGPGVPLGY 168
QY	181	PIKAPKLPGGYGLPYTTGKLPYGYPGGVAGAAKAGYPTGTGVGPQAAAAAKAAKF 240
Db	169	PIKAPKLPGGYGLPYTTGKLPYGYPGGVAGAAKAGYPTGTGVGPQAAAAAKAAKF 228
QY	241	GAGAGVLPVGGGAGVPGVPGAIPGIGIAGVGTAAAAAATAAAGLVPGG 300
Db	229	GAGAGVLPVGGGAGVPGVPGAIPGIGIAGVGTAAAAAATAAAGLVPGG 288
QY	301	PGFGPGVVVPGAGVPGVPGAGIPVWPGAGIPGAAPGVTSPEAAKAAKAYGAR 360
Db	289	PGFGPGVVVPGAGVPGVPGAGIPVWPGAGIPGAAPGVTSPEAAKAAKAYGAR 348
QY	361	PGVGVGIPITYGVGAGGFPFGVGGVGIQGVAGVPSVGGVPGVGGVPGVIGSPEACAAA 420
Db	349	PGVGVGIPITYGVGAGGFPFGVGGVGIQGVAGVPSVGGVPGVGGVPGVIGSPEACAAA 408
QY	421	AKAAKVGCTPAAAAAKAAKAAQF-----GLVPGVGVAPGVGVAPGVGVGLAPG 474
Db	409	AKAAKVGCTPAAAAAKAAKAAQFALLNLGLVPGVGVAPGVGVAPGVGVGLAPG 468
QY	475	VGVAPGVGVAPGVGVAPGIPGGVAAAAAKSAKAAKAAQLR 515
Db	469	VGVAPGVGVAPGVGVAPGIPGGVAAAAAKSAKAAKAAQLR 509
RESULT 20		
AD08527		
ID	AD08527 standard; protein; 870 AA.	
XX		
AC	AD08527;	
XX		
DT	29-JAN-2004 (first entry)	
XX		
DE	Novel protein (useful for identifying genetic disorders) #682.	
XX		
KW	novel gene; novel protein; tissue marker; molecular weight marker;	
KW	chromosome marker; genetic disorder	

Db 26 -----VPGGVADAAAAYKAAKAGAGLGGVPGVGGVAGVVPQAGVKGKVPQVGL 80
QY 121 PGVYPG-GVLPGARFFGVGLPGVPTGAGVKAPKAPGVGGAFAGIPGVGGPQPGVPLG 179
Db 81 PGVYPGFAGVPGARFFGVGLPGVPTGAGVKAPKAPGVGGAFAGIPGVGGPQPGVPLG 140
QY 180 YPIKAPKLPGGYGLPYTTTGLPYGYPGGVAGAGKAGYPTGTGVPQAAAAAATAA 239
Db 141 YPIKAPKLPGGYGLPYTTTGLPYGYPGGVAGAGKAGYPTGTGVPQAAAAAATAA 199
QY 240 FGAGAA--GVLPVGGAGVPGVPCAIPIGIGIAGVGTPTAAAAAATAAATAAAGLV 297
Db 200 FGAGAGFAGVPGVGGAGVPGVPCAIPIGIGIAGVGTPTAAAAAATAAATAAAGLV 259
QY 298 PGGFPGFPGVGVVPGFAG-VPGVGVPGAGIPVVPAGIPGAAGFAGVSPVGGVGGV 356
Db 260 PGGFPGFPGVGVVPGFAG-VPGVGVPGAGIPVVPAGIPGAAGFAGVSPVGGVGGV 319
QY 357 YGARPVGVGGIPVYGVGAGGFRGFGVGGIPGVAGVPSVGGVPGVGGVGGVSPBAQ 416
Db 320 YGARPVGVGGIPVYGVGAGGFRGFGVGGIPGVAGVPSVGGVPGVGGVGGVSPBAQ 379
QY 417 AAAAAKAAKYGVTPTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 476
Db 380 AAAAAKAAKYGVTPTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 439
QY 477 VAPGVGVAPGVGVPAGIPGPGVAAAAKAAKAAKAAKAAKAAKAAKAAKAAKAAK 515
Db 440 VAPGVGVAPGVGVPAGIPGPGVAAAAKAAKAAKAAKAAKAAKAAKAAKAAKAAK 478

RESULT 22
ADM03792
ID ADM03792 standard; protein; 663 AA.
XX ADM03792;
XX
DT 20-MAY-2004 (first entry)
DE Human protein of the invention SEQ ID NO:2477.
XX human; gene therapy; diagnostic marker; pharmaceutical.
XX Homo sapiens.
XX EPI347046-A1.
XX
PD 24-SEP-2003.
XX
XX 12-APR-2002; 2002EP-00008400.
XX
XX 22-MAR-2002; 2002JP-00137785.
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX WPI; 2003-723558/69.
DR N-PSDB; ADM01349.
XX
XX New polynucleotides and polypeptides are useful in gene therapy, for
PT developing a diagnostic marker or medicines for regulating their
PT expression and activity, or as a target of gene therapy.
XX
PS Claim 1; SEQ ID NO 2477; 305pp; English.
XX
XX The invention relates to a novel human polynucleotide and the encoded
CC polypeptide. A polynucleotide of the invention may have a use in gene
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
CC as a primer for synthesizing the polynucleotide or as a probe for

Db 466 PTVGVGAGGPGFGRGVGGIPGVAGVPGVGGVPGVGGVPGVGGVPGVGGVPGVGGV 525
QY 429 GTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 488
Db 526 GTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 585
QY 489 VAPGIGPGVAAAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAK 515
Db 586 VAPGIGPGVAAAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAK 612

RESULT 21
RAY01303
ID RAY01303 standard; protein; 660 AA.
XX
AC RAY01303;
XX
DT 07-JUN-1999 (first entry)
DE Human tropoelastin derivative SHELDeltamodified.
XX
XX Tropoelastin; hTE; elastin; glycosaminoglycan; GAG-binding; medical;
KW pharmaceutical; veterinary; cosmetic application; anti-wrinkle; food;
KW hand lotion; surgical implant; industrial product; human; SHEL.
XX
XX Homo sapiens.
XX Synthetic.
XX WO9903886-A1.
XX
PD 28-JAN-1999.
XX
PF 17-JUL-1998; 98WO-AU000564.
XX
PR 18-JUL-1997; 97AU-00008117.
XX
XX (UNSY) UNIV SYDNEY.
XX
XX Weiss AS;
PI
XX WPI; 1999-132162/11.
DR N-PSDB; AAX27705.
XX
PT New derivatives of human tropoelastin - with elastin-like or
PT macromolecular binding properties, useful e.g. as surgical implants.
XX
XX Claim 7; Fig 3; 82pp; English.
XX
XX The invention relates to a derivative or variant of human tropoelastin
XX (hTE) having elastin-like and/or macromolecule (specifically
CC glycosaminoglycan (GAG))-binding properties. Cells containing vectors
CC comprising the nucleic acids encoding the variants or derivatives are
CC used to produce the proteins recombinantly. The tropoelastin derivatives
CC or hybrid proteins containing the derivatives are useful in medical,
CC pharmaceutical, veterinary and cosmetic applications, e.g. as anti-
CC wrinkle or hand lotions, also as surgical implants, foods and industrial
CC products. The hybrid protein have controllable GAG-binding properties,
CC depending on presence or absence of a specific fragment, designated
CC peptide 26A, from hTE. The present sequence represents a human
XX tropoelastin derivative SHELDeltamodified
XX
XX Sequence 660 AA;
XX
XX Query Match 86.9%; Score 2328; DB 2; Length 660;
XX Best Local Similarity 89.0%; Pred. No. 8.4e-132;
XX Matches 462; Conservative 3; Mismatches 8; Indels 46; Gaps 5;
XX

QY 1 GGVPGAIPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 60
Db 2 GGVPGAIPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 25
QY 61 FGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVAGVVPQAGVKGKVPQVGL 120

CC detecting the polynucleotide. The polynucleotides ADM03758 are
CC useful in gene therapy, for developing a diagnostic marker or medicines
CC for regulating their expression and activity, or as a target of gene
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC are useful as pharmaceutical agents. The present sequence represents a
CC protein sequence of the invention.
XX
SQ Sequence 663 AA;

Query Match 86.1%; Score 2306.5; DB 7; Length 663;
Best Local Similarity 87.8%; Pred. No. 1.6e-130;
Matches 452; Conservative 0; Mismatches 2; Indels 61; Gaps 2;

QY 1 GGVPGAIPGGVPGGVYFPGAGLGGALGGKPLKPVPGGLAGAGLGAFFAVT 60
Db |||||
QY 27 GGVPGAIPGGVPGGVYFPGAGLGGALGGKPLKPVPGGLAGAGL 76
Db |||||
QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVGSAGAVVPGAGVPGKVPVGL 120
Db |||||
QY 77 -----AGLGGVPGVGGVGSAGAVVPGAGVPGKVPVGL 115
Db |||||
QY 121 PGVTPGGVLPGARPPGVGLPGVPTGAGVKPKAPGVGGAFAGIPGVPGFPGPQVPLGY 180
Db |||||
QY 116 PGVTPGGVLPGARPPGVGLPGVPTGAGVKPKAPGVGGAFAGIPGVPGFPGPQVPLGY 175
Db |||||
QY 181 PIKAPKLPGGYGLPYTTGKLPYGYGPGVGAAGKAGYPTGTGVPQAAAAAATAAKAF 240
Db |||||
QY 176 PIKAPKLPGGYGLPYTTGKLPYGYGPGVGAAGKAGYPTGTGVPQAAAAAATAAKAF 235
Db |||||
QY 241 GAGAAGVLPVGGAGVPGVPGCAIPGIGIAGVGTTPAAAAAATAAKAGLVPGG 300
Db |||||
QY 236 GAGAAGVLPVGGAGVPGVPGCAIPGIGIAGVGTTPAAAAAATAAKAGLVPGG 295
Db |||||
QY 301 PGFPGVVGVPAGVPGVPGVPGAGIPVVPAGIPGAAPVGVSPVSPVSPVSPVSPVSPV 360
Db |||||
QY 296 PGFPGVVGVPAGVPGVPGVPGAGIPVVPAGIPGAAPVGVSPVSPVSPVSPVSPVSPV 355
Db |||||
QY 361 PGVGVGGIPYGVGAGGFPFGVGVGIPGVAGVSPVSPVSPVSPVSPVSPVSPVSPVSPV 420
Db |||||
QY 356 PGVGVGGIPYGVGAGGFPFGVGVGIPGVAGVSPVSPVSPVSPVSPVSPVSPVSPVSPV 415
Db |||||
QY 421 AKAAYGVGTTPAAAAAATAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGVAPGVGVAPG 480
Db |||||
QY 416 AKAAYGVGTTPAAAAAATAAKAAQFGLV-----PG 445
Db |||||
QY 481 VGVAPGVGVAPGVPGVAAAAAATAAKAAQALR 515
Db |||||
QY 446 VGVAPGVGVAPGVPGVAAAAAATAAKAAQALR 480
Db |||||

RESULT 23
ADB64761
ID ADB64761 standard; protein; 617 AA.
XX AC ADB64761;
XX DT 04-DEC-2003 (first entry)
XX DE Human protein encoded by clone NT2RP70003110.
XX KW Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;
XX KW cell regeneration; membrane protein; signal transduction-related protein;
XX KW transcription-related protein; osteoporosis; neurological disease;
XX KW cancer; tumour.
XX OS Homo sapiens.
XX PN EPI308459-A2.
XX PD 07-MAY-2003.
XX PF 28-MAR-2002; 2002EP-00007401.
XX

PR 05-NOV-2001; 2001JP-00379298.
PR 25-JAN-2002; 2002US-00350978.
XX (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
DR WPI; 2003-450961/43.
DR N-PSDB; ADB62791.
XX
XX New polynucleotides and polypeptides, useful for developing a diagnostic
PT marker or medicines for regulation of their expression and activity, or
PT as targets of gene therapy.
XX
XX Claim 1; Page; 222pp; English.
XX
CC The invention discloses a polynucleotide comprising a sequence selected
CC from 1970 fully defined nucleotide sequences which encode novel
CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
CC or its partial peptide, an antibody binding to the polypeptide or peptide
CC of the polynucleotide, immunologically assaying the polypeptide or
CC peptide of the polynucleotide by contacting the polypeptide or peptide
CC with the antibody of the encoded protein, and observing the binding
CC expressible manner and a transformant carrying the polynucleotide in an
CC is useful as a primer for synthesising the polynucleotide. The oligonucleotide
CC for detecting the polynucleotide. The polynucleotides and encoded
CC proteins are useful as pharmaceutical agents and many disease-related
CC genes may be included in them, for developing a diagnostic marker or
CC medicines for regulation of their expression and activity, or as targets
CC of gene therapy. The genes are involved in tissue and/or cell
CC regeneration. Membrane proteins, signal transduction-related proteins,
CC transcription-related proteins, disease-related proteins and genes
CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
CC neurological diseases, cancer, tumours). The cDNA may be used to regulate
CC the activity or expression of the encoded protein to treat diseases. The
CC sequence presented is a protein of the invention. Note: Some of the
CC sequence data for this patent is not represented in the printed
CC specification, but is based on sequence information supplied by the
CC European Patent Office.
XX
SQ Sequence 617 AA;

Query Match 79.5%; Score 2129.5; DB 7; Length 617;
Best Local Similarity 82.5%; Pred. No. 6.2e-120;
Matches 425; Conservative 0; Mismatches 1; Indels 89; Gaps 4;

QY 1 GGVPGAIPGGVPGGVYFPGAGLGGALGGKPLKPVPGGLAGAGLGAFFAVT 60
Db |||||
QY 27 GGVPGAIPGGVPGGVYFPGAGLGGALGGKPLKPVPGGLAGAGLGAFFAVT 76
Db |||||
QY 61 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVGSAGAVVPGAGVPGKVPVGL 120
Db |||||
QY 77 FPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGVGSAGAVVPGAGVPGKVPVGL 136
Db |||||
QY 121 PGVTPGGVLPGARPPGVGLPGVPTGAGVKPKAPGVGGAFAGIPGVPGFPGPQVPLGY 180
Db |||||
QY 137 PGVTPGGVLPGARPPGVGLPGVPTGAGVKPKAPGVGGAFAGIPGVPGFPGPQVPLGY 162
Db |||||
QY 181 PIKAPKLPGGYGLPYTTGKLPYGYGPGVGAAGKAGYPTGTGVPQAAAAAATAAKAF 240
Db |||||
QY 163 PIKAPKLPGGYGLPYTTGKLPYGYGPGVGAAGKAGYPTGTGVPQAAAAAATAAKAF 222
Db |||||
QY 241 GAGAAGVLPVGGAGVPGVPGCAIPGIGIAGVGTTPAAAAAATAAKAGLVPGG 300
Db |||||
QY 223 GAGAAGVLPVGGAGVPGVPGCAIPGIGIAGVGTTPAAAAAATAAKAGLVPGG 282
Db |||||
QY 301 PGFPGVVGVPAGVPGVPGVPGAGIPVVPAGIPGAAPVGVSPVSPVSPVSPVSPVSPV 360
Db |||||
QY 283 PGFPGVVGVPAGVPGVPGVPGAGIPVVPAGIPGAAPVGVSPVSPVSPVSPVSPVSPV 342
Db |||||

PN EP1067182-A2.
 XX 10-JAN-2001.
 XX
 PF 07-JUL-2000; 2000EP-00114090.
 XX
 PR 08-JUL-1999; 99JP-00194179.
 PR 11-JAN-2000; 2000JP-00118775.
 PR 02-MAY-2000; 2000UP-00183766.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
 XX WPI; 2001-093989/11.
 DR N-PSDB; AAF93849.
 DR
 XX
 PT Nucleic acids encoding secretory proteins/membrane proteins, useful in
 PT gene therapy or as candidate target molecules in drug development.
 XX
 PS Claim 1; SEQ ID NO 212; 609pp + Sequence Listing; English.
 XX
 CC This invention relates to nucleic acid sequences AAF93744 - AAF93916
 CC which encode human secretory or membrane proteins represented by AAB88317
 CC - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and
 CC AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the
 CC invention. The invention also includes methods for the production of
 CC antibodies directed against the proteins, and cDNA sequences, which can
 CC be used in vaccines. The polynucleotide sequences can be used in gene
 CC therapy. The polynucleotide sequences and the proteins they encode may be
 CC used in the prevention, treatment and diagnosis of diseases associated
 CC with inappropriate secretory protein/membrane protein expression. The
 CC nucleic acids and complementary sequences may also be used as DNA probes
 CC in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect
 CC and quantitate the presence of similar nucleic acid sequences in samples.
 CC They may also be used to study the expression and function of secretory
 CC proteins/membrane polypeptides and their role in metabolism. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC against them and in assays to identify modulators (agonists and
 CC antagonists) of expression and activity. The antibodies and antagonists
 CC may also be used as therapeutic agents to down regulate expression and
 CC activity. The antibodies may also be used as diagnostic agents for
 CC detecting the presence of the polypeptides in samples (e.g. by enzyme
 CC linked immunosorbent assay (ELISA). Examples of diseases which may be
 CC treated include rheumatoid arthritis and diabetes
 XX
 SQ Sequence 472 AA;
 Query Match 49.0%; Score 1314; DB 4; Length 472;
 Best Local Similarity 55.1%; Pred. No. 3.7e-71;
 Matches 284; Conservative 3; Mismatches 2; Indels 226; Gaps 5;
 QY 1 GGVPGAIPGGVPGGVFPYAGLGGALGGKELKVPVGGLAGAGLGGAPPAVT 60
 Db |||||
 27 GGVPGAIPGGVPGGVFPYAGLGGALGGKELKVPVGGLAGAGLGGAGLGA 81
 QY 61 FPGALVPGGVADAAAYKAACAGAGLGGVPGVGGVSGAVVPGVPGKVPVGL 120
 Db |||||
 82 -----LGGVGI----- 87
 QY 121 PGVPGVLPGARFPGVGVLPVPTGAGVKPKAPGVGGAFAGIPGVPGPGVPLGY 180
 Db ----- 87
 88 ----- 87
 QY 181 PIKAPLPGVGLPVTGKLPVGYGPGGVAGAGKAGYPTGTGVPQAAAAAATAAF 240
 Db |||||
 88 -----PGVVGA-----GP----- 96
 QY 241 GAGAGVLPVGGAGVPGVPGVPAIPGIGGIAGVGTAAAAAATAAAYKAAGLVP 300
 Db |||||
 97 -----AAAAAATAAAYKAAGLVP 119
 QY 301 PGFPGVGVPGAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 360

Db 120 PGFPGVGVPGAGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 179
 QY 361 PGVGVGGIPTYGVGAGGPGFPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 420
 Db 180 PGVGVGGIPTYGVGAGGPGFPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 239
 QY 421 AKAAKYGVGTAAAAAATAAQAQFGLVPGVPGVPGVPGVPGVPGVPGVPGV 480
 Db 240 AKAAKY-----GLVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 280
 QY 481 VGVAPGVGVARGIGPGGVAAATAAATAAATAAATAAATAAATAAATAA 515
 Db 281 VGVAPGVGVARGIGPGGVAAATAAATAAATAAATAAATAAATAAATAA 315
 RESULT 26
 AAY31682
 ID AAY31682 standard; protein; 745 AA.
 XX
 AC AAY31682;
 XX
 DT 22-NOV-1999 (first entry)
 XX
 DE Alanine-containing elastomer, polymer IV.
 XX
 KW Elastomer; bioelastomer; polymer IV; tissue augmentation;
 KW tissue restoration; tissue reconstruction; tissue repair; implant;
 KW fibronectin cell attachment site.
 OS Synthetic.
 XX
 PN W09943271-A1.
 XX
 PD 02-SEP-1999.
 PF 26-FEB-1999; 99WO-US004440.
 XX
 PR 27-FEB-1999; 98US-0076297P.
 PR 29-MAY-1999; 98US-0087155P.
 XX
 PA (BIOE-) BIOELASTICS RES LTD.
 XX
 PI Urry DW, Parker TM, Glazer PA;
 XX
 DR WPI; 1999-540487/45.
 XX
 PT Augmentation or restoration of mammalian tissue by injecting solution of
 PT peptide polymer, used for soft or hard tissue reconstruction, especially
 PT of intervertebral disks.
 XX
 PS Claim 73; Page 106-109; 133pp; English.
 XX
 CC The present sequence represents novel alanine-containing polymer IV that
 CC has bioelastic properties. The invention provides a method of tissue
 CC augmentation by injecting a polymer comprising repeating peptide
 CC monomeric units selected from nonapeptide, pentapeptide and tetrapeptide
 CC separated by dynamic bridging segments. The polymer has an inverse
 CC temperature transition value (Tt) that is less than the tissue
 CC temperature, and is injected in water solution at coacervate
 CC concentration. The polymer is injected at periurethral or subdermal sites
 CC (for treatment of urinary incontinence or for cosmetic purposes), or into
 CC hard or soft tissue, e.g. for repair of traumatic injury. A specific
 CC application is restoration of intervertebral discs. Polymer IV has a Tt
 CC value of 28 deg
 XX
 SQ Sequence 745 AA;
 Query Match 34.0%; Score 911.5; DB 2; Length 745;
 Best Local Similarity 44.8%; Pred. No. 7.2e-47;
 Matches 265; Conservative 30; Mismatches 182; Indels 115; Gaps 40;


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Db      580 AGAGSGAGA 588
RESULT 28
ABP53474
ID      ABP53474 standard; protein; 988 AA.
XX      AC
XX      ABP53474;
DT      20-NOV-2002 (first entry)
XX      DE
XX      Protein polymer SEUP7 polymer block amino acid sequence.
XX      Protein crystallisation; elastin; collagen; keratin; controlled release;
XX      physical dimension.
XX      OS
XX      Synthetic.
XX      PN      US2002045567-A1.
XX      PD      18-APR-2002.
XX      PF      24-FEB-1997; 97US-00806029.
XX      PR      24-FEB-1997; 97US-00806029.
XX      PA      (CAPP/) CAPPELLO J.
XX      PA      (STED/) STEDRONSKY E R.
XX      PI      Cappello J, Stedronsky ER;
XX      PI      WPI; 2002-681318/73.
XX      PT
XX      PT      New composition comprising a repetitive polymer containing alternating
XX      PT      blocks of sequences that promote protein crystallization and sequences
XX      PT      that are elastin, collagen or keratin-like elements, useful for in vivo
XX      PT      drug delivery.
XX      PS
XX      Claim 19; Page 22; 32pp; English.
XX      CC
XX      The present invention describes a composition (C1) comprising: (a) a
XX      CC      protein polymer of at least 15kDa which comprises alternating blocks of
XX      CC      at least 2 units each of a sequence of 3-30 amino acids which promotes
XX      CC      protein crystallisation, and an amino acid sequence which is an elastin-
XX      CC      like element, a collagen-like element or a keratin-like element; and (b)
XX      CC      a biologically active substance. The composition acquires a non-liquid
XX      CC      form under physiological conditions. Also described: (1) delivering a
XX      CC      biologically active substance to a localized site in vivo, comprising
XX      CC      administering C1, where the biologically active substance is delivered
XX      CC      from the non-liquid to the localized site; and (2) altering the physical
XX      CC      dimensions of a body tissue of a mammal, comprising administering a C1.
XX      CC      The composition is used for the controlled release of biologically active
XX      CC      compounds in vivo. It can also be used to alter the physical dimensions
XX      CC      of a body tissue. The present sequence represents a protein polymer block
XX      CC      amino acid sequence from the present invention
XX      SQ
XX      Sequence 988 AA;
Query Match
Best Local Similarity 33.2%; Score 890; DB 5; Length 988;
Matches 258; Conservative 34; Mismatches 187; Indels 130; Gaps 35;
QY      2 GVPG-AIPG-GVPG---GVFPGAGLGGALGPG-----GXPLKPVGGLAGAG 48
Db      10 GVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGVP 69
QY      49 LGAGLGAFFAVTFPGALVPGGVADAAAAKAAKAGAGLG--GVPGVGLGVSGAVWPQ- 105
Db      70 SGAGAGSVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 129
QY      106 -----PGAGVKPKVPGVGLPGV-YPGGVLPFGARFPGVGLPGVPT--GAGV 149

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Db      130 AGAGSGAGSGAGAGSGAGSGAGSVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 188
QY      150 KPAPGVGGAPAG-----IPGVGPFPGPQPGVPL 178
Db      189 ---PGVGGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSVPGVPGV---PGVGP- 240
QY      179 GYPIKAPKLPG---GYGLPYTTGKLPYGYPGVPGVAGAGKAGYPTGTGTGVPQAAAAA 234
Db      241 GVGVPGVGVPGVGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 292
QY      235 KAAAKFGAGAGVLPVG--GAGVP--GVPG-AIPGIG---GIAGVCTPAAAAA 285
Db      293 GAGAGSGAG--AGSVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 351
QY      286 KAAKYGAAAGLVPG-----GPGFPGVVGVPAGVPGVPGVPGVPGVPGVPGVPGVPGV 338
Db      352 AGAGSGAGAGSGAGAGSGAGAGSGAGAGSVPGVPGVPGVPGVPGVPGVPGVPGVPGV 411
QY      339 PGVVSPEAAAKAAKAAKYGARPGVGGIPTYGVGAGGPGFPGVPGVGGIIPGV---AGV 394
Db      412 PGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 467
QY      395 PSVG---GVPGVG---GVPGVGISPEAQAAAAKAAKAAKAAKAAKAAKAAKAAKAAK 441
Db      468 PGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 526
QY      442 AAQFGLVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 501
Db      527 GAGAGSVPGVPGV--PGVGV--PGVGV--PGVGV--PGVGV--PGVGV--PGVGV--PGV 579
QY      502 AKSAAKVA 510
Db      580 AGAGSGAGA 588
RESULT 29
AAR80252
ID      AAR80252 standard; peptide; 832 AA.
XX      AC      AAR80252;
XX      DT      17-APR-1996 (first entry)
XX      DE      Polymer SEUP8.
XX      KW      Fibroin; elastin; repeat sequence; suture; thread; pin; gel; silk;
XX      KW      polymer; E.coli; EC3.
XX      OS      Synthetic.
XX      FH      Key
XX      FT      Peptide
XX      FT      Location/Qualifiers
XX      FT      1.64
XX      FT      /note= "polymer repeat block sequence"
XX      PN      WO9524478-A1.
XX      PD      14-SEP-1995.
XX      PF      10-MAR-1995; 95WO-US002772.
XX      PR      11-MAR-1994; 94US-00212237.
XX      PA      (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
XX      PI      Cappello J;
XX      PI      WPI; 1995-328270/42.
XX      PT      Protein polymer comprising alternating blocks of fibroin and elastin
XX      PT      units - used to form a device e.g. a suture to keep separated viable
XX      PT      tissue together.
XX      PS      Example 1; Page 25-27; 46pp; English.

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XX The sequences represented by AAR80251-R80257 are polymers constructed of
CC repeating blocks of fibroin-like (see AAR80249) and elastin-like (see
CC AAR80250) units. This sequence contains 13 repeats of a block consisting
CC of 8 elastin-like repeats followed by 4 fibroin-like repeats. The DNA
CC sequences encoding these polymers were inserted into plasmids which were
CC used to transform E.coli strain EC3. The polymers could then be isolated
CC from the fermented strains by standard centrifugation techniques. The
CC polymers are used to form a device (such as a suture, pin, thread, gel or
CC film) to keep separated viable tissue together. By varying the the ratio
CC of the two repetitive units, and by altering the lengths of the blocks of
CC each of them, the tensile properties of the polymer can altered
CC moderately. By reducing the number of repeating units of this sequence, or
CC by increasing the number of units of the elastin like repeat, a faster
CC rate of resorption can be achieved. Of the polymers, SELP0 (see AAR80251)
CC had the fastest resorption rate. The SELP4 (see AAR80255) and SELP5 (see
CC AAR80256) polymers showed no resorption after seven weeks. The other
CC three polymers showed intermediate resorption. No data was given for
CC SELP6 (see AAR80257)
XX
XX Sequence 832 AA;

Query Match 32.5%; Score 872; DB 2; Length 832;
Best Local Similarity 46.5%; Pred. No. 1.8e-44;
Matches 258; Conservative 30; Mismatches 161; Indels 106; Gaps 41;
QY 2 GVPG-AIPG-GVPG-----GVFPYFAGLGGALGGGKPLKPVPGGLAGAGLGA 55
DB 10 GVPGVGVPVGV 64
QY 56 FPAVTFPGALVPGGVADAAAAYKAAKAGAGLG--GVPGVGLGVAGAVVPQ---PGAGV 110
DB 65 VPGV 124
QY 111 KPGKVPVGLPGV--VPGVGLPGARFPGVGLPGVPT--GAGVFKAPGVGGAFAG----- 162
DB 125 GAGSVPGV 179
QY 163 -----IPGVG--PPGGPQPGV--LGYPKAPKPLPGVGLPYTTGKLPYGVG- 205
DB 180 SGAGAGSGAGSVPGV 223
QY 206 PG--GVAGAAKAGYPTGTGTGVPQAAAAAAYKAAKAFGAGAGV-LPGVG--GAGVPGV 261
DB 224 PGVGVPGVGG--AGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAG 280
QY 262 AIPGIGGIAGVGTAAAAAAYKAAKAGAGLG--GVPGVGLGVAGAVVPQ---PGAGV 319
DB 281 GVPGV--GVPGV 335
QY 320 VFGAGIPVPGAGIPGAAVPGVVSPAAAAKAAKAGYPTGTGTGVPQAAAAAAYK 379
DB 336 VPGVG---VPGV 386
QY 380 GFGVGVGGIPGVAGVPSVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGV 435
DB 387 GVGVPVGVGVGV--GVPGV--GVPGVGVGVGVGVGVGVGVGVGVGVGVGVGV 441
QY 436 AKAAKAAAFGLVPGVGVAPGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGV 495
DB 442 SGAGA-----GSVPGVGV--PGVGV--PGVGV--PGVGV--PGVGV--PGV 489
QY 496 GGVAATAAKAAKAAVAA 510
DB 490 AGAGSGAGAGSGAGA 504

RESULT 30
ABP53473
ID ABP53473 standard; protein; 832 AA.
XX
AC ABP53473;
XX

DT 20-NOV-2002 (first entry)
XX Protein polymer SELP8 polymer block amino acid sequence.
DE
XX Protein crystallisation; elastin; collagen; keratin; controlled release;
KW physical dimension.
XX
OS Synthetic.
XX
XX US2002045567-A1.
XX
XX 18-APR-2002.
XX
XX 24-FEB-1997; 97US-00806029.
XX
XX 24-FEB-1997; 97US-00806029.
XX
XX (CAPP// CAPPELLO J.
XX (STED// STEDRONSKY E R.
XX
XX Cappello J, Stedronsky ER;
XX
XX WPI; 2002-681318/73.
XX
XX New composition comprising a repetitive polymer containing alternating
PT blocks of sequences that promote protein crystallization and sequences
PT that are elastin, collagen or keratin-like elements, useful for in vivo
PT drug delivery.
XX
XX Claim 19; Page 22; 32pp; English.
XX
XX The present invention describes a composition (C1) comprising: (a) a
CC protein polymer of at least 15kDa which comprises alternating blocks of
CC at least 2 units each of a sequence of 3-30 amino acids which promotes
CC protein crystallisation, and an amino acid sequence which is an elastin-
CC like element, a collagen-like element or a keratin-like element; and (b)
CC a biologically active substance. The composition acquires a non-liquid
CC form under physiological conditions. Also described: (1) delivering a
CC biologically active substance to a localized site in vivo, comprising
CC administering C1, where the biologically active substance is delivered
CC from the non-liquid to the localized site; and (2) altering the physical
CC dimensions of a body tissue of a mammal, comprising administering a C1.
CC The composition is used for the controlled release of biologically active
CC compounds in vivo. It can also be used to alter the physical dimensions
CC of a body tissue. The present sequence represents a protein polymer block
CC amino acid sequence from the present invention
XX
XX Sequence 832 AA;
SQ
Query Match 32.5%; Score 872; DB 5; Length 832;
Best Local Similarity 46.5%; Pred. No. 1.8e-44;
Matches 258; Conservative 30; Mismatches 161; Indels 106; Gaps 41;
QY 2 GVPG-AIPG-GVPG-----GVFPYFAGLGGALGGGKPLKPVPGGLAGAGLGA 55
DB 10 GVPGVGVPVGV 64
QY 56 FPAVTFPGALVPGGVADAAAAYKAAKAGAGLG--GVPGVGLGVAGAVVPQ---PGAGV 110
DB 65 VPGV 124
QY 111 KPGKVPVGLPGV--VPGVGLPGARFPGVGLPGVPT--GAGVFKAPGVGGAFAG----- 162
DB 125 GAGSVPGV 179
QY 163 -----IPGVG--PPGGPQPGV--LGYPKAPKPLPGVGLPYTTGKLPYGVG- 205
DB 180 SGAGAGSGAGSVPGV 223
QY 206 PG--GVAGAAKAGYPTGTGTGVPQAAAAAAYKAAKAFGAGAGV-LPGVG--GAGVPGV 261
DB 224 PGVGVPGVGG--AGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAGSGAG 280